



51 IMVVSGLYLW WAKQRGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF  
 101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK  
 151 EVPWILELMP MPVSGTTVGE NGINPTEPNN IGNRRPFRAF NRFRALSVE  
 201 FAQRRGRGMD FVAGFYEL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

m218.seq  
 1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCCGC  
 51 CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC  
 101 TCGGTGCGGC AGGCGATTAT CTTTGGGAAA CGGCAGCTTC ACTGACCATT  
 151 ATTATGGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGCAGCGCAT  
 201 CAAGGCGATG CTGCTGCCGT CAAAAGGCAT GGCAGCTTCT TGGTGGCGGA  
 251 ATCTGCACGG CACGTTTGGA ACTTGGGTGT CGTTGATTTT GCTGTGTTC  
 301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGCGGCA AGTTCGTACA  
 351 GGCTTGGAGT CAGTTCCCTG CCGGTAAATG GGTGTGCGAA CCGAACCCCG  
 401 TTTCAGTCGT GCCGACCCAC GGCAGGTAT TGAATGACGG CAAGGTTAAG  
 451 GAAGTGCCGT GGGTTTGGG GCTTACGCCT ATGCCTGTTT CAGGGACGac  
 501 yGtgGGCAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAAACCG  
 551 TCGACCGCTT TCGCGGnGA AATCGGTTTC AAAGGGCGTT ATCAGTTGAA  
 601 TTTGCCCCAA GCGAGGACG GCGTATGGAC TTTGTCGAG GATTCTATGA  
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep  
 1 MVAVDPYTAK VVSTMPRNQG WYVTMDEIHS DMMLGAAGDY LLETAASLTI  
 51 IMVVSGLYLW WVKRRGIKAM LLPSKGXARS WWRNLHGTFG TWVSLILLLF  
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK  
 151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFRALSVE  
 201 FAQRRGRMD FVAGFYEL

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/g218

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYVTMDEIHS DMMLGAAGDY LLETAASLTI IMVVSGLYLW					
g218	MVAVDPYTAKVVNTMPRNQGWYHTMDEIHGDMMLGAAGDY LLETAASLTI IMVVSGLYLW					
	10	20	30	40	50	60
70	80	90	100	110	120	
m218.pep	WVKRRGIKAMLLPSKGXARS WWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
g218	WAKQRGIKAMLLPPKSRARS WWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKVKEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
g218	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKVKEVPWILELMPMPVSGTTVGENINPTEPNN					
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRFRALSVEFAQRRGRMD FVAGFYEL					
g218	IGNRRPFRAFNRFRALSVEFAQRRGRMD FVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

## a218.seq

```

1   ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51  CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTCGAC AGGTGATTAT CTTTGGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GCGCGGCGAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GCGCGCTTCT TGGTGGCGGA
251 ATCTGCACGG CGCGTTTGA ACTTGGGTGT CGTTGATTTT ACTGTGTTC
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCCGG CAGGCAAATG GGGTGTGCAA CCGAACCTTG
401 TTTCACTCGT GCCGACCCAC GCGCAGGTAT TGAATGACGG CAAGGTAAAG
451 GAAGTGCCGT GGGTTTGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAAACCG
551 TCGACCGTTT TCGCGG.GA AATCGGTTTC AAAGGCGTT ATCAGCTGAA
601 TTTCCCCAAA GCGCAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA
201 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

## a218.pep

```

1   MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51  IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRALSAE
201 FAQRRGRMD FVAGFYEL

```

## m218/a218 95.9% identity in 218 aa overlap

m218.pep	10	20	30	40	50	60
	MVAVDPYTAKVVSTMPRNQGWYYTMDEIHS DMMLGAAGDY LLETAASLTIIMVVSGLYLW					
a218	:     :     :     :					
	10	20	30	40	50	60
	MVAVDPYTAKVVSTMPRNQGWYYAMDEIHS DMMLGSTGDY LLETAASLTIIMIISGLYLW					
m218.pep	70	80	90	100	110	120
	WVKRRGIKAMLLPSKGXARSWWRNLHGTFGTWVSLILLFLCLSGIAWAGIWGGKFVQAWS					
a218	:     :     :     :					
	70	80	90	100	110	120
	WVKRRGIKAMLLPPKGRARSWWRNLHGAFGTWVSLILLFLCLSGIAWAGIWGGKFVQAWS					
m218.pep	130	140	150	160	170	180
	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKVPEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
a218	:     :     :     :					
	130	140	150	160	170	180
	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKVPEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
m218.pep	190	200	210			
	LETVDRFARXNRFQRALSVEFAQRRGRMD FVAGFYEL					
a218	:     :					
	LETVDRFARXNRFQRALSVEFAQRRGRMD FVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 775>:

```
g219.seq
1   atgacggcaa ggtaaggaa gtgccgtgga ttttggagct tatgcctatg
51  cctgtctcag ggacgactgt gggtgaaaac ggcattaacc ccaccgagcc
101 caataacatt ggaaaccgtc gaccgtttcg cgcgggaaat cggtttcaaa
151 gggcgttatc agttgaattt gcccaaaggc gaggacgggg tatggacttt
201 gtgcgaggat tctatgagtt atgacatgat cagcccgttt gccgaccgca
251 cggtagatat cgaccagtac agcggcgaga ttcttgccga catccgtttt
301 gacgattaca acccgttcgg caaatattat gcggcaagca ttgcgctgca
351 tatggggact ttgggctggg ggagcgtgtt ggccaacgtc gtgttctgcc
401 ttgccgtgat tttatcggc atcagcggct gcgtgatgtg gtggaacgc
451 cgtccgtccg gcgtggcggg cattgttcct ccggcgcaaa aaatcaaact
501 gcccgctctg tgggcgatgg cattgccgct gctgttgatt gcactgcttt
551 tcccgaccgc gctgcttgcc attgccgtga tttggctgtt ggataccttg
601 ctgctgtcgc ggattcctgt gttgaggaaa tggtttaaat ga
```

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

```
g219.pep
1   MTARLRKCRG FWSLCLCLSQ GRLWVKALT PPSPITLETV DRFAREIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGEILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLNV VFCLAVIFIG ISGCVMWKR
151 RPSGVAGIVP PAQIKLPVW WAMALPLLLI ALLEPTALLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

```
m219.seq
1   ATGACGGCAA GGTTAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGaCyGt gGGCAAAGAC GGCATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGCTTTGC GCGGnGAAAT CCGTTTCAAA
151 GGGCGTTATC AGTTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCCGACCGCA
251 CGGTACATAT CGACCACTAC AGCGGCAAAA TCCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT CTGGGCTGGT GGAGCGTGTG GCGCAACGTC TTGTTCTGCC
401 TTGCCGTCAT TTTTATCGGT ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGACCG GAGCGGTGGG CATCGTTCCG CCGGCGCAGA AAGTCAAGCT
501 GCCGGTTTGG TGGATGATGG CATTGCCGCT ATTGGCAATC GCACGTCTCT
551 TCCCGACCTC ACTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTTCG GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

```
m219.pep
1   MTARLRKCRG FWSLRLCLFQ GRXWAKTALT LTRXHWKPS TALRGEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLNV LFCLAVIFIG ISGCVMWKR
151 RPTGAVGIVP PAQVKLPVW WMMALPLLLI ALLEPTSLLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

m219/g219

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRLCLFQGRXWAKTALTLSRXHWKPS TALRGEIGFKGRYQLNLPKG					
g219	MTARLRKCRGFWSLCLCLSQGRLWVKALTTPSPITLETVDRFAREIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
g219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFMAASIALHMG					



505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMMWKRPTGAVGIVPPAQKVKLPVWMMALPLLAI					
	:     :     :     :     :					
g219	LGWWSVLANVVFCLAVIFIGISGCVMMWKRPSGAVGIVPPAQKIKLPVWWMALPLLII					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	:     :     :					
g219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRKWKX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219.seq
1  ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTCG GCGG.GAAAT CCGTTTCAAA
151 GGGCGTTATC AGCTGAATT GCGCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CGGTGCATAT CGACCAGTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTT GGCGAACGTT TTGTCTGCCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGTCCG GCGCGGTGGG CATGGTCCG CCGGCGCAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CGGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219.pep
1  MTARLRKCRG FWSLRCLFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG LGWWSVLANV LFCLAVIFIG ISGCVMMWKR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRW WFK*

```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
	:     :     :     :					
a219	MTARLRKCRGFWSLRCLFQGRWAKTVLTLSRXHWKPSTVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	:     :     :     :					
a219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMMWKRPTGAVGIVPPAQKVKLPVWMMALPLLAI					
	:     :     :     :					
a219	LGWWSVLANVLFCLAVIFIGISGCVMMWKRPSGAVGMVPPAQKIKLPVWWMAMAVPLLI					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	:     :     :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```
g221.seq
1  atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
51  gatgcggcga gccgtaaatc adatcgacgc tgacggattt gaaccctgcc
101 tcacgggcgg catcgatgac ttctttgggt tcttcgtagc tttggatgcy
151 gttgactgcc gcctgcactt tggggtcgaa atcctgaatg ccgacgtca
201 tgcggttgaa gccgagtcctg ccgagcatga ggacggtgtc gcggtgact
251 ttgcgcgggt cgatttcgat ggaatattcg ccggacggta tcagttcgaa
301 atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351 aggtcggcgt gccgccgccg aagtgcagtt gggcaagctg gtgccgtccg
401 ttcagatgtg gagcgaagcag ttccatttct ttttcaagat attcgatgta
451 ggtatcgccg cggcttttgt ctttgggtgat gattttgttg cagccgcagt
501 agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag ggaaagcgg
551 ttgtttaa
```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```
g221.pep
1  MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FGFVVALDA
51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101 MFADHAEDTF DLFVAQKGRR AAEEVQLGKL VPSVQMWSEQ FHFFFKIFDV
151 GIGAAVFVGD DFVAAAVVAD GVAERNVNVK GKRFV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```
m221.seq
1  ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAA
51  CGACGCTGAC GGATTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGGGAAGAC
301 ACGTTCGATC TGTTCTGCGC TCAAAAAGGt GCGTGCCCG CCGAAGTGCA
351 GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCATT
401 TCTTTTTCAA GATATTCGAT GTAGGCATCG GCGCGGCTTT TGTCTTTGGT
451 GATGATTTTG TTGCAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501 TGTGAATGTA AAGGGAAAGC GGTTCGTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```
m221.pep
1  MXVLMXRSLV RQAVNQIDAD GFEPFRFARRI DDFGFFVTL DAVDRRLHFG
51  VEILNADAH VEAESAHEH GVAADFARVD FDGVFAGGDX LEMFAYHAED
101 TFDLFVAQKG ACPAEVQLGK LVPSVQMWSE QFHFFFKIFD VGIGAAVFVGD
151 DDFVAAAVVA DGVAERNVNV KGKRFV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng)

from *N. gonorrhoeae*:

m221/g221

	10	20	30	40	50
m221.pep	MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDAVDRRLHFGVE				
g221	MHDHGAMDRRLPAFGSLMRRAVNXIDADGFEPCLTGGIDDFFGFFVALDAVDCRLHFGVE				
	10	20	30	40	50
	60	70	80	90	100
m221.pep	ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLFVAQKGA-				
g221	ILNADAHAVEAESAEHEDGVAADFARVDFDGI FAGRYQFEMFADHAEDTFDLFVAQKGRR				
	70	80	90	100	110
	120	130	140	150	160
	170				

507

```

m221.pep    CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAFVFGDDFVAAAVVADGVAERNVNVK
              |||||
g221        AAAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAFVFGDDFVAAAVVADGVAERNVNVK
              130      140      150      160      170      180

m221.pep    GKRFVX
              |||||
g221        GKRFVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 785>:

```

a221.seq
1  ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTGGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TGC GGAAGAC
301 ACGTTCGATT TGGTCGTCGC TCAAAAAGGT CGGCGTGCCG CCGCCGAAGT
351 GCAGTTGGGC AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTCC
401 ATTTCTTTTT CAAGAAATTC GATGTAGGCA TCGGCGCGGC TTTTGTCTTT
451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGAACC
501 GAATGTGAAT GTAAAGGGAA AGCGGTTTGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 786; ORF 221.a>:

```

a221.pep
1  MVVLMRLSLV RQAVNQIDAD GFEPFRFARRI DDFFGFFVTL DAVDRRLHFG
51  VEILNADAHA VEAESAHEHD GVAADFARVD FDGVFAGGD* LEMFAYHAED
101 TFDLVVAQKG RRAAAEVQLG KLVPSVQMWS EQFHFFFKKF DVGIGAAFVF
151 GDDFVAAAVV ADGVAERNVN VKGKRFV*

```

m221/a221 95.5% identity in 177 aa overlap

```

              10      20      30      40      50      60
m221.pep    MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFFGFFVTLDAVDRRLHFGVEILNADAHA
              |||||
a221        MVVLMRLSLVRQAVNQIDADGFEPFRFARRIDDFFGFFVTLDAVDRRLHFGVEILNADAHA
              10      20      30      40      50      60

              70      80      90      100     110     119
m221.pep    VEAESAHEHDGVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLFVAQKGA-CPAEVQLG
              |||||
a221        VEAESAHEHDGVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLVVQAQKGRRAAAEVQLG
              70      80      90      100     110     120

120      130      140      150      160      170
m221.pep    KLVPSVQMWSEQFHFFFKIFDVGIGAAFVFGDDFVAAAVVADGVAERNVNVKGKRFVX
              |||||
a221        KLVPSVQMWSEQFHFFFKIFDVGIGAAFVFGDDFVAAAVVADGVAERNVNVKGKRFVX
              130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 787>:

```

g223.seq
1  atggaattca ggcaccaggt agtggtagtt ggtgtcgaac catttggtca
51  tttcgatggc gaattggtct ttgttgccgc gcgccagttg gaagaattgt
101 tccaaaggca ggttttggtc atcgaagccg aaacgggagg gaatcgcgcc
151 cgtggatact tgcaggtcga ggatgtgatg gtagaaagtg aaatcacgta
201 cagcaacgta atcagcgtaa ggagcagctt ggtgtttcca gtttttctcg
251 cgcaggtctt tggcaacgtc gagcagctct tgttactga tctctttgcg
301 ccagtatatt tcttgggcga atttcaattc acggaaggcg cgcacacgcg
351 ggaagcctga

```

This corresponds to the amino acid sequence <SEQ ID 788; ORF 223.ng>:

g223.pep..

1 MEFRHQVVVV GVEPFGHFDG ELVFVAARQL EELFQRQVLA IEAETGGNRA  
 51 RGYLQVEDVM VESEITYSNV ISVRSSLVFP VFLAQVFGNV EQLLFTDLFA  
 101 PVFFLGEFQF TEGADTREAA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 789>:

m223.seq  
 1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTGGTCA  
 51 TTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT  
 101 TCCAAAGACA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC  
 151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCCTAC  
 201 GGCAACGAAA TCGGCGTTGG CAGCGACCTG GTGTTCCAG TTTTCTCGC  
 251 GCAAGTCTTT AGCAACAGCC AGCAATTCTT GCTCGCTGAT TTCTTTGCGC  
 301 CAGTATTTT CTTGTGCGAA TTTCAATTCG CGGAAGGCGC CGACACGCGG  
 351 GAAGCCTGA

This corresponds to the amino acid sequence <SEQ ID 790; ORF 223>:

m223.pep  
 1 VEFRHQVVVV GVEPFGHFDS ELVFVTARQL EELFQRQVLA VEAEGGNRA  
 51 GGDQVEDV VVESEIXYGN IGVGSDLVFP VFLAQVFSNS QQFLADFFA  
 101 PVFFLGEFQF AEGADTREAA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 223 shows 80.7% identity over a 119 aa overlap with a predicted ORF (ORF 223.ng) from *N. gonorrhoeae*:

m223/g223

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV					
g223	MEFRHQVVVVGVEPFGHFDGELVFVAARQLEELFQRQVLAIEAETGGNRARGYLQVEDVM					
	10	20	30	40	50	60
m223.pep	VESEIXYGNIEIGVGSGLVFPVFLAQVFSNSQQFLADFFAPVFFLGEFQFAEGADTREAX					
g223	VESEITYSNVISVRSSLVFPVFLAQVFGNVEQLLFTDLFAPVFFLGEFQFTEGADTREAX					
	70	80	90	100	110	120
m223.pep	VESEIXYGNIEIGVGSGLVFPVFLAQVFSNSQQFLADFFAPVFFLGEFQFAEGADTREAX					
g223	VESEITYSNVISVRSSLVFPVFLAQVFGNVEQLLFTDLFAPVFFLGEFQFTEGADTREAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 791>:

a223.seq  
 1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTGGTCA  
 51 TTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT  
 101 TCCAAAGATA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC  
 151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCGCCTA  
 201 CGGCAACGTA ATCGGCGTTG GCAGCGGCCT GGTGTTTCCA GTTTTCTCG  
 251 CGCAAGTCTT TAGCAACAGC CAGCAATTCT TGCTCGCTGA TTTCTTTGCG  
 301 CCAGTATTTT TCTTGTGCGA ATTCAATTC GCGGAAGGCA CCGACACGCG  
 351 GGAAGCCTGA

This corresponds to the amino acid sequence <SEQ ID 792; ORF 223.a>:

a223.pep  
 1 VEFRHQVVVV GVEPFGHFDS ELVFVTARQL EELFQR\*VLA VEAEGGNRA  
 51 GGDQVEDV VVESEIAYGN IGVGSGLVFP VFLAQVFSNS QQFLADFFA  
 101 PVFFLGEFQF AEGTDTREAA\*

m223/a223 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV					
a223	VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV					
	10	20	30	40	50	60
m223.pep	VESEIXYGNIEIGVGSGLVFPVFLAQVFSNSQQFLADFFAPVFFLGEFQFAEGADTREAX					
a223	VESEIAYGNVIGVGSGLVFPVFLAQVFSNSQQFLADFFAPVFFLGEFQFAEGTDTREAX					
	70	80	90	100	110	120
m223.pep	VESEIXYGNIEIGVGSGLVFPVFLAQVFSNSQQFLADFFAPVFFLGEFQFAEGADTREAX					
a223	VESEIAYGNVIGVGSGLVFPVFLAQVFSNSQQFLADFFAPVFFLGEFQFAEGTDTREAX					

70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcggtccgc cccgcccttg cgcagcagtt gaccaacctg ctcagcagcc
101 gcgagcagat tctcagacag tttgccgaag acgaacagcc cgttttaccc
151 gtcaaccgag ccccgcccg ggcggcgggc aatgccgacg aactcatcgg
201 cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251 ccgcccggcg ggcgggcaat gccgacaaac tcacggcag cgcgatgcgg
301 cttttgggta ttgctaccg ctacggcggc acatcggtgt ctaccggtt
351 tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401 acctgccgcg cacgtcggcg gaacaggcgc ggatgggcgc acccgttgcc
451 cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501 cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551 acgcgccgcg cacggggaaa aatatcgaaa tcaccagcct gagccacaaa
601 tattggagcg gcaaatatgc gttcgccgc cgggtcaaga aaaacgaccc
651 gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201 YWSGKYAFAR RVKNDPSRF LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1  ..TTTTCAAACC CGGCAGTTTG GCGGTTTGTG TGGCTGAWGT TTGCCGTCCG
51  CCCC GCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101 TTCTCAGACA GTTTGCCGAA GACGAACAGC CCGTTTACC CATCAACCGA
151 GCCCCGCCCC GCGGGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201 GGGGCTTAAC GAACAGCCCC TTTTACCCGT CAACCGAGTC CCGCCCCGGC
251 GGGCGGCGAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAACGAA
301 CAGCCCGTTT TACCCGTCAA CCGAGCCCC GCGGCGGG CGGGCAATGC
351 CGACGAACTC ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCGCT
401 ACGGCGGCAC ATCGGTTTCT ACCGTTTGT ACTGCAGCGG CTTATGCAG
451 CACATCTTCA AACGCGCCAT GGGCATCAAC CTGCCGCGCA CGTCGGCAGA
501 ACAGGCACGG ATGGGTACGC CGGTTGCCCG AAGCGAATTG CAGCCCGGAG
551 ATATGGTGTT TTTCCGACG CTCGGCGGCA GCCGCATTTC CCATGTGCGA
601 CTTTATATCG GCAACAACCG CTTATCCAC GCGCCGCGCA CGGGGAAAAA
651 TATCGAAATC ACCAGCCTGA GCCACAAATA TTGGAGCGGC AAATACGCGT
701 TCGCCCGCCG GGTCAAGAAA AACGACCCGT CCCGCTTCT GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1  ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQVLPINR
51  APARRAGNAD ELIGSAMGLN EQVLPVNRV PARRAGNADE LIGNAMGLNE
101 QPVLVNRAP ARRAGNADEL IGNAMGLLGI AYRYGGTSVS TGFDCSGFMQ
151 HIFKRAMGIN LPRTSAEQAR MGTTPVARSEL QPGDMVFFRT LGGSRISHVG
201 LYIGNNRFIH APRTGKNIEI TSLSHKYWSG KYAFARRVKK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

m225/g225

```

              10      20      30      40      50
m225.pep      FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
              | : ||||| | | | | | | | | | | | | | | | | | | | | | | | |
g225           MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPVNRAPARRAG
```

510

	10	20	30	40	50	60
m225.pep	60	70	80	90	100	110
	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
	:       :					
g225	NADELIG-----			GAMGLNEQPVVRVNRAXARRAGNA		
		70	80	90		
m225.pep	120	130	140	150	160	170
	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
	:     :  :					
g225	DKLIGSAMRLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225.pep	180	190	200	210	220	230
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225.pep	240	249				
	VKKN DPSRFLNX					
g225	VKKN DPSRFLN					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225.seq
1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTACCC
151 ATCAACCGAN CCCCCGCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAATCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCGCCGCCCC GCGGGCGGG CAATGCCGAC
451 GAACATCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTTGA CTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCAGCTCG GCGGCAGCCG CATTCCC CAT GTCGGA TTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC GCGGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVAR S ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKN DPSRFLN *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225.pep	FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG				
	:				
a225	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG				
	10	20	30	40	50
	60	70	79	80	
m225.pep	NADELIGSAMGLNEQPVLPVNR-----VPARRAGNA				

```

|||||
a225  NADELIGSAMGLNEQPVLVPVNRXPARRAGNADXLIGNAMGLNEQPVLVPVNRVPARRAGNA
      70      80      90      100     110     120

      90      100     110     120     130     140
m225.pep DELIGNAMGLNEQPVLVPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
|||||
a225  DELIGNAMGLNEQPVLVPVNRAPARRAGNADDELIGNAMGLLGIAYRYGGTSISTGFDCSGF
      130     140     150     160     170     180

      150     160     170     180     190     200
m225.pep MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
|||||
a225  MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
      190     200     210     220     230     240

      210     220     230     240     249
m225.pep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNPDSRFLNX
|||||
a225  IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNPDSRFLNX
      250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

g225-1.seq

```

1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgccgtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag ttgcccgaag acgaacagcc cgttttacc
151  gtcaaccgag ccccgcccg gcggcggggc aatgccgagc aactcatcgg
201  cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251  ccgcccggcg ggcgggcaat gccgacaaac tcacgcgcag cgcgatgcgg
301  cttttgggta ttgcctaccg ctacggcgcg acatcggtgt ctaccggttt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401  acctgccgcg cagctcggcg gaacaggcgc ggatgggcgc acccgttgcc
451  cgaagcgaat tgcagcccg ggatatggtg ttttccgca cgctcggcgg
501  cagccgcatt tcccattgct gactttatat cggcaacaac cgcttcatcc
551  acgcgcgcgc caggggaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gttcgcccgc cgggtcaaga aaaacgaccc
651  gtcacgcttt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

g225-1.pep

```

1  MDSFFKPAVM AVLWLMFAVR PALADELTNL LSSREQILRQ PAEDEQPVLP
51  VNRAFPARRAG NADELIGGAM GLNEQPVVVR NRAXARRAGN ADKLIGSAMR
101  LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNPDSRF LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

m225-1.seq

```

1  ATGGATTCTT TTTCAAACC GGCAGTTTGG GCGGTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101  GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTACCC
151  ATCAACCGAG CCCC GCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201  CAGCGCGATG GGGCTTAACG AACAGCCCCT TTTACCCGTC AACCGAGTCC
251  CCGCCCGGCG GCGGGGCAAT GCCGACGAAC TCATCGGCAA CGCGATGGGG
301  CTTAACGAAC AGCCCGTTT ACCCGTCAAC CGAGCCCCCG CCCGGCGGGC
351  GGGCAATGCC GACGAACTCA TCGGCAACGC GATGGGACTT TTGGGTATTG
401  CCTACCGCTA CGGCGGCACA TCGGTTTCTA CCGGTTTGA CTGCAAGCGC
451  TTCATGCAGC ACATCTTCAA ACGCGCCATG GGCATCAACC TGCCGCGCAC
501  GTCCGCAGAA CAGGCACGGA TGGGTACGCC GGTGCCCGCA AGCGAATTGC
551  AGCCCGGAGC TATGGTGT TCCGCACGC TCGGGCGCAG CGGCATTTC
601  CATGTCGGAC TTTATATCGG CAACAACCGC TTCATCCACG CGCCGCGCAC
651  GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGGAGCGGCA
701  AATACGCGTT CGCCCGCGG GTCAAGAAAA ACGACCCGTC CCGCTTCTG
751  AACTGA

```

**m225-1/g225-1** 84.9% identity in 251 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pap

1	MDSFFKPAVW	AVLWLMFAVR	PALADELTNL	LSSREQILRQ	FAEDEQPVLP
51	INRXPPRRAG	NADELIGSAM	GLNEQPVLPV	NRXPARRRAG	ADXLIGNAMG
101	LNEQPVLPVN	RVPARRAGNA	DELIGNAMGL	NEQPVLPVNR	APARRAGNAD
151	ELIGNAMGLL	GIAYRYGGTS	ISTGDCSGF	MQHIFKRAMG	INLPR TSAEQ
201	ARMGTPVAR	ELQPGDMVXF	RTLGGSSRI	VGLYIGNNRF	IHPARTSGKNI
251	EITSLSHKYW	SGKYAFARRV	KKNDPSRFLN	*	



a225-1/m225-1 88.6% identity in 280 aa overlap

```

      10      20      30      40      50      60
a225-1.pep MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG
          |||
m225-1     MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
          |||

      70      80      90     100     110     120
a225-1.pep NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
          |||
m225-1     NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA
          70                        80      90

     130     140     150     160     170     180
a225-1.pep DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
          |||
m225-1     DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
          |||

     190     200     210     220     230     240
a225-1.pep MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
          |||
m225-1     MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
          |||

     250     260     270     280
a225-1.pep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKNDPSRFLNX
          |||
m225-1     IHAPRTGKNIEITSLSHKYWSGKYAFARRVKNDPSRFLNX
          |||
          220     230     240     250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51 CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGcgtCG TCGTGCTTGC CGTGCCGCTC TACCAAACCC
251 GCCGTAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccgataacc caattctcct tcccgctcgc tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcggtg tctcccgcca
451 tttctgttgc ctccgcctct cctgcgcgcg ctcggcccgcc atacattgcg
501 ccggttcaca ataacttcaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggt cctttctcct Cgggcctcgc cccctccctc cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

g226.pep

```

1  MSEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
51 LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
101 GSVTGIVTGM YFAAWLGPDT QSFPPRLQY LLFTPSGIPI HTLYARVLP
151 FLLPPPLLPR LGPHTLRRFT ILPKLRRPFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51 CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCCGCGCTCG TCGTGCTTGC CGTGCCGCTC TACCAAACCC
251 GCCGTAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACAGGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTCG CGGTCTGGTC GGACAGATTG CCGGTTACAA

```

501 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCCGTGGGT ATGTCGCTCG  
 551 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC  
 601 CGTATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC  
 651 CGCGCTGATT GCGCCGCTGC TCATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

m226.pep  
 1 MNEILRQPSV LLFLTLAVYA LAIVRTRTG NIFCNPVLVS TIVLIAYLKI  
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA  
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT  
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR  
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

	10	20	30	40	50	60
m226.pep	MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	:					
g226	MSEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m226.pep	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGM YFAKWLGAER					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGM YFAAWLGPDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m226.pep	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG					
	:					
g226	QFSFPRLQYLLFTPSGIPHTLYARVLPFLLPPLLPRLGPHTLRRFTILPKKLRPFK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

a226.seq  
 1 ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC  
 51 CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGT AATATCTTCT  
 101 GCAACCCCGT ACTGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC  
 151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATTT  
 201 CTGGCTCAAG CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAACCC  
 251 GCCGTAAAT CTTCAACCAA TGGCTGCCCG TCATCGTTTC GCAGCTTGCG  
 301 GGCAGCGTTA CGGGCATTGT TACGGGGATG TATTTTGCCA AATGGCTGGG  
 351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAATC  
 401 CTATCGCCAT CGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC  
 451 GCCGCCACCG TCATCATTGC CGGCTGGTC GGACAGATTG CCGGTTACAA  
 501 AATGTTGAAA AACACGGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG  
 551 GCACGGCTTC GCACGCGATG GGCATTGCCG CCTCGCTCGA ACGCAGCCGC  
 601 CGCATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC  
 651 CGCGCTGATT GCGCCGCTGC TTATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

a226.pep  
 1 MNEILRQPSI LLFLTLAVYA LAIVRTRTG NIFCNPVLVS TIVLIAYLKI  
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA  
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT  
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR  
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF \*

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

515

```

m226.pep  MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
a226      MNEILRQPSILFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
           10      20      30      40      50      60

           70      80      90      100     110     120
m226.pep  AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
a226      AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
           70      80      90      100     110     120

           130     140     150     160     170     180
m226.pep  EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG
a226      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG
           130     140     150     160     170     180

           190     200     210     220     230
m226.pep  MSLGTASHAMGIAASLERSRRMAAYAGLGTfNGVLTALIAPLLIPVLGFX
a226      MSLGTASHAMGIAASLERSRRMAAYAGLGTfNGVLTALIAPLLIPVLGFX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1  atgaacatca tccgcgcgct cctcatcatc ctccggtgcc tcgccgccgg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccggc agcatcgtcg
101 gcatggcgct gctgtttgcg cttttgcagg cgggttggtc caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgctgttcct
201 cgtgccgccc tgcgtggcgg tcatcagcta tttggatttg attgccgacg
251 attggttttc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1  MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLF LQAGWLKTS
51  WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1  ..ACGTCTTKGC TGCAACAGCT TACCGACGCG CTGATGTCGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTG GATTTGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCCG CCTCCGCCAG cACTTTGTGC
151 GTA CTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1  ..TSXLQQLTDA LMSNLTFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

```

m227/g227

           10      20      30
m227.pep  TSXLQQLTDALMSNLTFLVPPCVAVISYL
           || |||||:|||||
g227      TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTLFLVPPCVAVISYL
           20      30      40      50      60      70

           40      50      60

```

516

```

m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
                |||||
g227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
                80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51 CGAAACCGCC GTTTCCTAG CAGGCATCAA ACTGCCCCGC AGCATCGTCG
101 GCATGGGCGT ACTGTTTGC CTTTTCAGG CGGGTGGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCC TCGTGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATTGTTTTTC GATACTGGTT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGGTTACAG GCAAGGTTCA CCGCTGGATA CGGAGCATT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLEA LLQAGWVKTS
51 WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep      TSXLQQLTDALMSNLTFLVPPCVAVISYL
                || |||||:|||||
a227          TAVFLAGIKLPGSIVGMGVLEALLQAGWVKTSWLQQLTDALMANLTFLVPPCVAVISYL
                20      30      40      50      60      70

m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
                |||||
a227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
                80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
1  MKLLIIAAMM AAALACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

517

a228.pep  
 1 MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA  
 51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD  
 101 KMKDAAK\*

m228/a228 100.0% identity in 107 aa overlap

	10	20	30	40	50	60
m228.pep	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
a228	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
	10	20	30	40	50	60
	70	80	90	100		
m228.pep	AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
a228	AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

g229.seq  
 1 atggctgccg tatcgggcgg cggtgccgtc ttcctgataa tgcttcacaa  
 51 tattgcccgc gttcagcgtc agccgccagc gttcgcccaa gcgtcgggag  
 101 aaatcgccat tgaagccgcc ggcgaaattg tatcggtctc cgcccaagag  
 151 gttttgcccc acaaacggca cggtgccgaa cgagcgcgtt accgaacggt  
 201 tttgatggcc gaacgacagg cgcaggttct gttcgtgtaa atctttgtta  
 251 tccaataat gcacgccgcg gctgatgccg ccgtagagga aatgatgccc  
 301 gccgcattg atttcgcgcg acacgcccaa gccgtagcgc aaaccgtgtg  
 351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaaat  
 401 tcaatcgttt tttcggacga agcgttggtt atagcggatt acaaaaaatc  
 451 aggacaagc ggccggccgc aggcagtagc gatggtacg aaccggttcg  
 501 cccggtgctt ggacgcctta gggaaaccgt ccctttgagc cggggcgggg  
 551 caaccgtac cggttttgt tcatccgcca tattgtgttg a

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

g229.pep  
 1 MAAVSGGGAV FLIMLPHIAR VQRQPPAFAQ ASGEIGIEAA GEIVSAAAEQ  
 51 VLPDKRHGAE RARYRTLMA EROAQVLF AE IFVIPIMHAA ADAAVEEMMP  
 101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFFGR SVVYSGLTKE  
 151 RTRRRAGST DGTEPVRPVL GRLREFFPLS RGGATRTGFC SSAILC\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

m229.seq (partial)  
 1 ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC  
 51 GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG  
 101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC  
 151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCGC CTGATGCCGC  
 201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTGCGCGCA CACGCCTAAG  
 251 CCCTAGCGCA AACCGTGTGC CTTTTCGCGC AGGCTGTGCG CGGTTTTTCGT  
 301 CCAGCTTCTG CCCGCAAATT CAATCGTTTT TTCGGACGAA GCGTTGTTTA  
 351 TAGCGGATTA ACAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA  
 401 AATAGTACGG AACCGATTCA CTGGGTGCTT CAGCACCTTA GAGAATCGTT  
 451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

m229.pep (partial)  
 1 ..AQALGEIGIE AADEIVSAAA XEVLDDKRHD AERARYRTVF IAERQAQALF  
 51 AEIFVIPIMH AAAADA AVEE MPPARIDFAR HAXALAQTV LRLQAVGGFR  
 101 PASARKFNRF FGRSVVYSGL TKIRTRQSA DSTNSTEPIH LVLQHLRESR  
 151 SLFCSSAILC \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 229 shows 80.5% identity over a 169 aa overlap with a predicted ORF (ORF 229.ng) from *N. gonorrhoeae*:

m229/g209

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAAE
                                ||| ||||| ||||| ||||| ||||| ||
g229      MAAVSGGGAVFLIMLPHIARVQRQPPAFAQASGEIGIEAAAGEIVSAAAEVLDPKRRHGA
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFIPIIMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
g229      RARYRTVLMARQAQVLF AEIVFIPIIMHAAA-DA AVEEMMPARIDFARHAQAVAQTVCLL
                                70      80      90      100     110

                                100     110     120     130     140
m229.pep      RQAVGGFRPASARKFNRFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRE----
                ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
g229      RQAVGGFRPASARKFNRFGRSVVYSGLTKIRTRRRRAAGSTDGTEFVRPVLGRLREPFPL
                120     130     140     150     160     170

                                150     160
m229.pep      -----SRSLFCSSAILCX
                :||| :||| :||| :||| :|||
g229      SRGGATRTGFCSSAILC
                180     190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

```

a229.seq (partial)
1  ATGGCTGTCTG TATCGGGCGG CGGTGCGGTC TTCCTGATAA CGCTTCCACA
51 TATTGCCCAC GTTCAGCGTC AGCCGCCA.. GTTCGCTCAA GCGTCGGGAG
101 AAATCGGCAT TGAAGCCGCC GACGAAATTG TATCGGCTGC CGCCTAAGAG
151 GTTTTGCTCG ATAAACGGCA CGATGCCGAA TGAGCGCGTT ACTGAACGGT
201 TTTTATAGCC GAGCGACAGG CGCAGGCTCT GTTCGCTGAA ATCTTTGTTA
251 TCCTAATAGT GCACGCCGCC GCCGCTGATG TCTCCGTAGA GGAAATGATG
301 CCCGCCCGCA TTGATTTCGC GCGACACGCC CAAGCCGTAG CGCAAACCGT
351 GTGCCTTTTG CGGCAGGCTG TCGGCGGTTT TCGTCCAGCT TCTGCCTGCA
401 AATTCAATCG TTTTTCGGA CGAAGCGTTG TTTATAGCGG ATTAACAAAA
451 ATCAGGACAA GGCACGAAG CGCAGACAGT ACAGATAGTA CGGAACCGAT
501 TCACTTGGTG CTTAGCACC TTAGAGAATC GTCTCTTTGA GCTAAGGCGA
551 GGCAACGCCG TACTGGTTT TGTTATCCA CTATA

```

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

```

a229.pep (partial)
1  MAVVSGGGAV FLITLPHIAH VQRQPPXFAQ ASGEIGIEAA DEIVSAAA*E
51  VLLDKRHDAA *ARY*TVFIA ERQAQALFAE IFVILIVHAA AADVSVEEMM
101 PARIDFARHA QAVAQTVCLL RQAVGGFRPA SACKFNRFEG RSVVYSGLTK
151 ITRRRRSADS TDSTEPIHLV LQHLRESSL* AKARQRTGF CSSTI

```

m229/a229 85.6% identity in 167 aa overlap

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAAE
                                ||| ||||| ||||| ||||| ||||| ||
a229      MAVVSGGGAVFLITLPHIAHVQRQPPXFAQASGEIGIEAADEIVSAAAXEVLLDKRHDAAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFIPIIMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
a229      XARYXTVFIAERQAQALFAEIVFVILIVHAAAADVSVEEMMPARIDFARHAQAVAQTVCLL
                70      80      90      100     110     120

```

	100	110	120	130	140	149
m229.pep	RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---					
a229	RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX					
	130	140	150	160	170	180
	150	160				
m229.pep	-----RSLFCSSAILCX					
a229	AKARQRRTGFCSTI					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

```

g230.seq
1  atgttccatt ccatcgaaaa atacagaaca cccgcccagg tcttattagg
51  cctgattgca ttaacttttg tcggcttcgg cgtcagcacg gtttcccatc
101 cgggcgccga ctacatcgtc caagtgggcg acgaaaaaat cagcgagcac
151 tcaatcaaca acgccatgca gaacgagcag gcggacggcg gcagcccttg
201 gcgcgacgcg gtgttccaat ccctgctgca acgcgcctac ctgaaacagg
251 gcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtcacgc
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtttg
401 tcgaagaaat ccgcgatcag tttgccttgc agaatttggg aagcctcgtc
451 caaaacggcg tattggtcgg cgacgcgcag gcggaacagc tgatcagggt
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcatcgccca agtcaaagcg tctgaagccg atttgagaaa attttataat
601 gcgaacaaaa aagactatct gctgccgcag gcggtcaaat tggaaatagt
651 cgccttgaat ctgaaggatt ttgcagacaa gcagaccgtc agtgaacagg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgtttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaaa gcggttgccg acttcaacaa ggcaaaagaa aagctgggcg
851 acgatgcgtt caatcatccc tcctcgcttg ccgaagccgc caaaaaacagc
901 gggttgaaag tggaaaccca agaaacttgg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaaa acctaataca tgccgtattc agcgacgacg
1001 tattgaagaa aaaacacaaat tccgaagtgc tgaccatcaa cagcgaaacc
1051 gcgtgggtcg tccgcgccaa agaagtccgc gaagaaaaaa acctactggt
1101 tgaagaagcc aaagatgcgg tgcgctcaggc ctatatccgt accgaagccg
1151 ccaaactttt gaaaacaatg taa

```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

```

g230.pep
1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGA KLMI SVSSEIKQM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMSE DQFVEEIRDQ FALQNLVSLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEK AAVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINA VF SDDVLKKKHN SEVL TINSET
351 AWWVRAKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLLKTM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

```

m230.seq (partial)
1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCC.GACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCAACG
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC

```

```

451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTGTCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAAATATG
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGg
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CCGGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAGAA AAATTGGGCG
851 ACGATGC.GT CAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCCGAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTGC TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCT.. ...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSDA VFQSLQRAY LKQGAALMI SVSSEIQKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQKA AVENELKMKK AVADFNKAKE KLGDVAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRAKEVR EEKTLPFMEA KDAVRQAYIR TEAAKL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

m230/g230

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHINNAIQNEQ					
g230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230.pep	ADGGGPSDAVFQSLQRAYLKQGAALMISVSSEIQKIIVDDPNFHDANGKFDHALLN					
g230	ADGGSPWRDAVFQSLQRAYLKQGAALMISVSSEIQKQIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230.pep	RYLSQRHMSEDQFVEEIRDQFALQNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN					
g230	QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN					
	130	140	150	160	170	180
m230.pep	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230	PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
m230.pep	ERVARLPANEAKPSFEQKA AVENELKMKKAVADFNKAKEKLGDVAVNHPSSLAEAAKNS					
g230	ERVARLPAHEAKPSFEQKA AVENELKMKKAVADFNKAKEKLGDVAFNHPSSLAEAAKNS					
	250	260	270	280	290	300



521

	310	320	330	340	350	360
m230 . pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDVLKKKHNSEVLTINSETAWVVRakevr					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDVLKKKHNSEVLTINSETAWVVRakevr					
	310	320	330	340	350	360
	370	380				
m230 . pep	EEKTLPPFAEAKDAVRQAYIRTEAAKL					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230 . seq (partial)

```

1   ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTACGACAG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGTCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTGCGA CACTTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAAA AAGACTACCT GCTTCCCAAA GCGGTCAAAT TGGAAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TGCCTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GTTTGAAGAG TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTG AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACTT

```

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230 . pep (partial)

```

1   MFHSIEKYRT PAQVLLGLIA LTFVGFVSTV VSHPGADYIV QVGDEKISDH
51  SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAQLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEK AAVENELMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWWVRAKEVR EEKTLPPFAE KDAVRQAYIR TEAAKL

```

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230 . pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230 . pep	ADGGGPSRDAVFQSLQRAYLKQGAQLMGISVSSEQIKQIIIVDDPNFHDANGKFDHALN					
a230	ADGGGPSRDAVFQSLQRAYLKQGAQLMGISVSSEQIKQIIIVDDPNFHDANGKFDHALN					
	70	80	90	100	110	120
	130	140	150	160	170	180

m230.pep	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
a230	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
	130 140 150 160 170 180
m230.pep	190 200 210 220 230 240
	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
a230	PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE
	190 200 210 220 230 240
m230.pep	250 260 270 280 290 300
	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAVNHPS SLAEAAKNS
a230	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPS SLAEAAKNS
	250 260 270 280 290 300
m230.pep	310 320 330 340 350 360
	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHSEVLTINSETAWVVRKEVR
a230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHSEVLTINSETAWVVRKEVR
	310 320 330 340 350 360
m230.pep	370 380
	EEKTLPF AEAKDAVRQAYIRTEAAKL
a230	EEKTLPF AEAKDAVRQAYIRTEAAKL
	370 380

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT  CCATCGAAAA  ATACAGAACA  CCCGCCCAAG  TCTTATTAGG
51  CCTGATTGCA  TTAACCTTTG  TCGGCTTCGG  CGTCAGCAGC  GTTTCCTATC
101 CGGGCGCCGA  CTACATCGTC  CAAGTGGGCG  ACGAAAAAAT  CAGCGAGCAC
151 TCAATCAACA  ACGCCATGCA  GAACGAGCAG  GCGGACGGCG  GCAGCCCTTG
201 GCGCGACGCG  GTGTTCCAAT  CCCTGCTGCA  ACGCGCCTAC  CTGAAACAGG
251 GCGCGAAGCT  GATGGGCATT  TCGGTTTCTT  CCGAACAAAT  CAAGCAGATG
301 ATTGTGGACG  ATCCCAATT  CCACGACGCA  AACGGCAAAT  TCAGTCACGC
351 GTCCTTTGAGT  CAATACCTGT  CGCAACGCCA  TATGTCTGAA  GACCAGTTTG
401 TCGAAGAAAT  CCGCGATCAG  TTTGCCTTGC  AGAATTGGT  AAGCCTCGTC
451 CAAAACGGCG  TATTGGTCGG  CGACGCGCAG  CGGGAACAGC  TGATCAGGCT
501 GACGCAGGTC  AACCGCACCA  TCCGTTTCGA  CACTTTC AAC  CCCGACGAGT
551 TCATCGCCCA  AGTCAAAGCG  TCTGAAGCCG  ATTTGCAGAA  ATTTTATAAT
601 GCGAACAAAA  AAGACTATCT  GCTGCCGCG  GCGGTCAAAT  TGGAAATATG
651 CGCCTTGAAT  CTGAAGGATT  TTGCAGACAA  GCAGACCGTC  AGTGAAACGG
701 AAGTGAAAAA  TGCCTTTGAA  GAGCGCGTGG  CGCGTTTGCC  GGCACATGAA
751 GCCAAACCTT  CTTTCGAGCA  GGAAAAAGCC  GCCGTCGAAA  ACGAATTGAA
801 AATGAAAAAG  GCGGTTGCCG  ACTTCAACAA  GGCAAAAGAA  AAGCTGGGCG
851 ACGATGCGTT  CAATCATCCC  TCCTCGCTTG  CCGAAGCCGC  CAAAAACAGC
901 GGTTTGAAAG  TGGAAACCCA  AGAACTTGG  CTGAGCAGGC  AGGACGCACA
951 AATGTCCGGC  ATGCCCGAAA  ACCTAATCAA  TGCCGTATTC  AGCGACGACG
1001 TATTGAAGAA  AAAACACAAT  TCCGAAGTGC  TGACCATCAA  CAGCGAAACC
1051 GCGTGGGTGC  TCCGCGCCAA  AGAAGTCCGC  GAAGAAAAAA  ACCTACTGTT
1101 TGAAGAAGCC  AAAGATGCGG  TGGCTCAGGC  CTATATCCGT  ACCGAAGCCG
1151 CCAAACCTGC  CGAAAACAAG  GCAAAAGAAG  TGCTTACCCA  ACTGAACGGC
1201 GGCAAGGCAG  TTGACGTGAA  ATGGTTCGG  GTGTCCGTTT  TGGGCGCGCA
1251 GCAGGCAAGG  CAGTCCATGC  CGCCGAGGCG  TTATGCGGAA  CTGCTGAAAG
1301 CAAAACCGGC  AAACGGCAAA  CCCGCCTATG  TCAGACTGAC  CGGTCTGCCG
1351 GCACCCGTGA  TTGTCGAGGC  GCAGGCAGTC  ACGCCTCCGG  AGGATATTGC
1401 CGCACAGCTT  CCTCCTGCGA  AACAGGCTTT  GGCGCAACAG  CAGTCTGCCA
1451 ATACTTTCGA  CCTGCTGATC  CGCTATTTC  ACGGAAAAAT  CAAACAGACT
1501 AAAGGAGCAC  AATCGGTTGA  CAACGGCGAT  GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pep

```

1  MFHSIEKYRT  PAQVLLGLIA  LTFVGVGVST  VSHPGADYIV  QVGDEKISEH
51  SINNAMQNEQ  ADGGSPWRDA  VFQSLQRAY  LKQGAKLMI  SVSSEQIKQM
101  IVDDPNFHDA  NGKFSHALLS  QYLSQRHMSE  DQFVEEIRDQ  FALQNLVSLV

```

```
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRakeVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWSE VSVLGAQQAR QSMPPPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TFPEDIAAQL PPAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNG GQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```
1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTACGACAG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG CGCGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCTTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAAGTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 CACACAGGTC AACCGCACCA TCCGTTTCGA CACTTTCAC CCACGACGAGT
551 TCATCGCCCA AGTCAAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACCGG
701 AAGTGAAAAA TGCATTTTGA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTTGGCG
851 ACGATGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCGCG CAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTACGGC TTATATCCGT ACCGAAGCGG
1151 CCAAACCTGC CGAAACAAG GCAAAGACG TGCTTACCCA ACTGAACGGC
1201 GCGAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACGGGC AAACGGCAAA CCCGCCCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTGCAAGT ACAGGCTGTA ACCCCGCCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GCGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CTTGTTGATA CGTTATTTCA ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTCAAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVSTV VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAALMGI SVSSEQIKQI
101 IVDPNFHDA NGKFDHALLN RYLSQRHMS E DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRakeVR EEKTLPPAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWSE VSVLGAQQAR QSMPPPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TFPDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNG GQ*
```

m230-1/g230-1 96.3% identity in 512 aa overlap

```
10 20 30 40 50 60
m230-1.pep MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ
|||||
g230-1 MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ
10 20 30 40 50 60

70 80 90 100 110 120
m230-1.pep ADGGGPSRDAVFQSLQRAYLKQGAALMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN
|||||
g230-1 ADGGSPWRDAVFQSLQRAYLKQGAALMGISVSSEQIKQMIIVDDPNFHDANGKFSHALLS
70 80 90 100 110 120

130 140 150 160 170 180
m230-1.pep RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
```

g230-1	QYLSQRHMSDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVWRTIRSHTFN
	130 140 150 160 170 180
m230-1.pep	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
g230-1	PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
	190 200 210 220 230 240
m230-1.pep	ERVARLPANEAKPSFEQEKAAVENELMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
g230-1	ERVARLPAHEAKPSFEQEKAAVENELMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
	250 260 270 280 290 300
m230-1.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR
g230-1	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR
	310 320 330 340 350 360
m230-1.pep	EEKTLPPFAEAKDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVKWSEVSVLGAQQAR
g230-1	EEKNLLFEEAKDAVRQAYIRTEAAKLAENKAKEVLTQNGGKAVDVKWSEVSVLGAQQAR
	370 380 390 400 410 420
m230-1.pep	QSMPEEAYAEALLKAKPANGKPAYVRLTGLPAPVIVEAQAVTPPDIDIAAQLPLAKQALAAQ
g230-1	QSMPEEAYAEALLKAKPANGKPAYVRLTGLPAPVIVEAQAVTPPDIDIAAQLPPAKQALAAQ
	430 440 450 460 470 480
m230-1.pep	QSANTFDLLIRYFNGKIKQTKGAQSVNDNGDGQX
g230-1	QSANTFDLLIRYFNGKIKQTKGAQSVNDNGDGQX
	490 500 510

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 837>:

a230-1.seq

1	ATGTTCCATT	CCATCGAAAA	ATACAGAACG	CCGCCCAAG	TCCTTTTGGG
51	CCTGATTGCA	TTAACTTCCT	TCGGTTTCGG	GGTCAGCAGC	GTATCCCATC
101	CGGGTGGCGA	CTACATCTCG	CAGTGGGCG	ACGAAAAAT	CAGCGACCAC
151	TCCATCAACA	ACGCCATACA	GAACGACACG	CGGCAGCGCG	CGGGCCCTTC
201	CGCGCAGCGG	GTGTTTCCAA	CCCTGCTGTA	ACGCGCCTAC	CTGAAACAGG
251	GCGCAGACTC	GATGGGCATT	TCGGTTCTCT	CCGAACAAAT	CAAGCAGATT
301	ATCGTGGACG	ATCCCAATTT	CCACGACGCA	ACCGGCAAA	TGACCACGCG
351	GCTTTTAAAC	CGCTACCTTT	CCCAACGCTA	TATGCTGAA	GACCAGTTTG
401	TGCAAGAAAT	CCGCGACTCAG	TTTGGCTTGC	AGAATTTGGT	AAACCTCTGC
451	CAAAACGGCG	TATTGCTCGG	CGACGCGCAG	CGGGAACAG	GATCAGGCTC
501	GACGCAGGTC	AACCGCACCA	TCGTTTCGCA	CACTTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAGTG	CTGAAGCCCG	ATTTGCGAAG	GTTTATATAC
601	GCAAAACAAA	AGAGTACCTT	GCTTCCCAA	CGGGTCAAA	TGGAATTAAT
651	CGCCTTGAAT	CTGAAAGACT	TTGCAAGACA	ACAGACCTTG	AGCGAAACAG
701	AAGTAAAAAA	TGCGTTTGAA	GAGCGCGTGG	CGCGCTTTGCC	GGCAATATGAA
751	CGCAACCTTT	CTTTCGAGCA	GGAAAAAGCC	CGCGTCGAAA	ACGAATTGAA
801	AATGAAAAAG	CGGGTTGCCG	ACTTCAATA	GGCAAAAGAA	AAGCTGGGCG
851	ATGACGCGTT	CAACCATCTT	TCCTCGCTTG	CCGAAGCCGC	CAAAAACAGC
901	GGTTTGAAAG	TCGAAACCCA	AGAAACTTGG	CTGAGCAGCG	AGGATCGCGA
951	AATGTCGGGT	ATGCCCGAAA	ACCTGATCA	TGCCGTATTC	AGCGACGACG
1001	TATTTGAAGA	AAAAACATA	TCCGAAGTGC	TGACCATCAA	CAGCGAAAAACC
1051	CGGTGGGGTC	TCGCGCCCAA	AGAAGTCCGC	GAAAGAAAAA	CCCTGCGGTT
1101	TGCCGAAGCC	AAAGACGCGG	TACGTGACGC	TTATATCCGT	ACCGAAGCCG
1151	CCAAACTTGC	CGAAAAACAG	GCAAAAGACG	TGCTTACCCA	ACTGAACGGC
1201	GGCAAGGCTG	TTGACGTGAA	ATGGTCGGAA	GTGTCGGTT	TGGCGCGACA
1251	GCAGGCAAGG	CAGTCCATCG	CGCCCGAGGC	TTATGCGGAA	CTGCTGAAAG
1301	CAAAACCGGC	AAAGCGCAAA	CCCCCCTACG	TACAGCTGAT	CGGCTCTGCC
1351	GCACCGGTGA	TTGTGCAAGT	ACAGGCTGTA	ACCCCGCGGT	ATGATATGCT
1401	CGCACAGCTT	CGCGTTGCA	AACAGGTTT	GGCGCAACAG	CAGTCTGCCA
1451	ATACTTTTCA	CTTGTTGATA	CGTTATTTCA	ACGGCAAAAT	CAAACAGACC
1501	AAAGGAGCGC	AATCGGTCGA	C AACGCGAC	GGTCAGTA	

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGFSRDA VFQSLQRAY LKQGAKLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKHNN SEVLTINSET
351 AWVVRAKEVR EEKTLPPFAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKKSE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPDDIAAQL PLAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDGD GQ*
```

a230-1/m230-1 99.8% identity in 512 aa overlap

a230-1.pep	10	20	30	40	50	60
m230-1	10	20	30	40	50	60
a230-1.pep	70	80	90	100	110	120
m230-1	70	80	90	100	110	120
a230-1.pep	130	140	150	160	170	180
m230-1	130	140	150	160	170	180
a230-1.pep	190	200	210	220	230	240
m230-1	190	200	210	220	230	240
a230-1.pep	250	260	270	280	290	300
m230-1	250	260	270	280	290	300
a230-1.pep	310	320	330	340	350	360
m230-1	310	320	330	340	350	360
a230-1.pep	370	380	390	400	410	420
m230-1	370	380	390	400	410	420
a230-1.pep	430	440	450	460	470	480
m230-1	430	440	450	460	470	480
a230-1.pep	490	500	510			
m230-1	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

```

g231.seq
1  atgtcaaaac gaaaatccat aaaccgtccg tatcaaaaac cggcggaact
51  gccgccgttg caaaataatc cgccatttta ccgtaaaaac cgccgcctga
101 acttttttat cgcggcagac gccggttgcg cgtctccgca aaaatgcagg
151 gcgcgcggtt ttcagacggc atttgccgtt caaggccgtg cgggtgtctt
201 accaaatgcc caaccattcg cccacggaat ccatccaatc cttattgccc
251 ccgccgctcc tgcctgcccg gcggtacgcc caccggcgctt gcggattttt
301 agctttccac aatcctttgc gttcccttcc cgctgaatt tgagcgctcg
351 catagtcggc aaaatccgcc ttatcctgct gttcttttag ataactttta
401 taatgccacg ccgcccgtc ctgcacctgc atcagggtca aatcggtttt
451 gccggcggat acctgcgcca cttcgcgctg atagcggctg gtttcaaaca
501 cactacact gactttccta ccctccgccg ccgcgcgcag gttgtcgcgc
551 gaacgtgtac cgtaacgctg tttcatctcc ggtgcgtcga tatacgccat
601 ccgaatttta tgtttcgcgc cgtcgcgctc gatgacgtga agggatatcg
651 cgtcatagac tttggacacc gtgctgtgt agctgtggcc ggatttcgcc
701 gatgcccgtc gccgaacggg cgcgtcgaaa cccacgtccc ctgcagtgcc
751 gagtacgtcg agtacggcaa ccgccgtccg caccgcctca ctgtcatatc
801 ccgtataacc caacgcgccc aaaagcgaca ggcgcacggg aagccatttc
851 atgatttttt taatctgcat atttttcaaa tgccgatgcc gtctgaacat
901 ctctga

```

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

```

g231.pep
1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSVIGV KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 AGGYLRHFAV IAVGFKHTYT DFPTLRRAQ VVARTCTVSL FHLRCVDIRH
201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFRRCPSANG RVETHVPCSA
251 EYVEYGNRRP HRLTVISRIT ORAQKROGDG KPFHDFNLH IFQMPMPSEH
301 L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

```

m231.seq (partial)
1  ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAAC
51  GCCGCCGTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCCGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTGC GC...

```

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

```

m231.pep (partial)
1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV QGRAVSLPNA QPFG.....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng) from *N. gonorrhoeae*:

```

m231/g231
          10      20      30      40      50      60
m231.pep  MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
          |||||
g231      MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
          10      20      30      40      50      60

          70
m231.pep  QGRAVSLPNAQPFG
          |:|||||:
g231      QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVSVIGV
          70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

527

**a231.seq** (partial)

```

1  ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
51  GCCGCCGTTG CAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCC GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCGGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTGTCGAACA
501 CCGGACGCT GACTTTCCTG CCTTCGCGC CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GCGCGCTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGCTC GATAACGTGA AGGTGTGCGC
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGGCGGG CGGTCGGAA CCGCGCTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTT
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

**a231.pep** (partial)

```

1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPOKCR
51  ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAACP AVRPRLRIF
101 SFQSFAPFP RLNLVGLIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRAVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 I

```

**m231/a231** 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
a231						
	10	20	30	40	50	60
	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
	70					
m231.pep	QSRVSLPNAQPFQ					
a231						
	70	80	90	100	110	120
	QSRVSLPNAQPFQAHGIHPILIAPAACPAPVRPRLRIFSFQSFAPFPRLNLVGLIG					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

**g231-1.seq**

```

1  ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
51  GCCGCCGTTG CAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCC GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTCGCGCTG ATAGCGGTCG GTTTCAAACa
501 CaCgTaCaat gagtttcgta ccctccGCCG ccgcgcgCAG GTTgtcgcGC
551 GAACgtGTAC CGTAagcgtg TTtcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTTta tGTTtcgcgc cgtcgcCgtc gATGACGTGA AGGgtatcGC
651 CgtcATAGAC TTTGGACACC Gtgcctgcgt AGctGTGGCC GGATTtcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

**g231-1.pep**

```

1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR
51  ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAACP AVRPRLRIF

```

101 SFPQSFAFPF RLNLVGVIG KIRLILLEFS ITFIMPRRPV LHLHQVQIGF  
151 AGGYLRHFAL IAVGFKHTYN EFRTLRRRAQ VVARTCTVSV FHLRCVDIRH  
201 PNMFRVAVV DDVKGIAVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq  
1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC  
51 GCCGCCCTTG CAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA  
101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG  
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT  
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCC  
251 CCGCCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTTT  
301 AGCTTTCCAC AATCCTTTCG GTTCCCTTTC CGCTGAATT TGAGCGTCGG  
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA  
401 TAATGCCACG CCGCCCGTTC CTGCACCTGC ATCAGGTTC AATCGGTTTT  
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTG GTATCGAACA  
501 CGCGCAGCT GACTTTCCTG CCTCCGCGC CCGCGCGCAG GTTGTGCGC  
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GCGCGCTCGA TATACGCCAT  
601 CCGGATTTG TGTTCGCGC CGTCGCCGTC GATAACGTGA AGGTGTGCG  
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC  
701 GATGCTCGGC GCGGGGCGG CGCGTCGGAA CCGCGTCCC CTGCCGCGCC  
751 GAGTACGTCG AGTACGGCAA CCGCGTCCG CACCGCTCG CTGCCGTACC  
801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC  
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT  
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep  
1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR  
51 ARGFQTAFV QSRAVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF  
101 SFPQSFAFPF RLNLVGVIG KIRLILLEFS ITFIMPRRPV LHLHQVQIGF  
151 ADRNLRHFAL VAVGIEHAHA DFPFRRAQ VVARTRAVSL FHLRRVDIRH  
201 PDFVFRVAV DNVKGVAVD FGHRACVAVA GFRCSAAG RVGTRVPCRA  
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH  
301 IGIQFTAS\*

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPFAGHIHPILIAAPACPAVRPRRLRIFSFPQSFAFFRLNLVGVIG					
m231-1	QSRAVSLPNAQPFAGHIHPILIAAPACSAVRPRRLRIFSFPQSFAFFRLNLVGVIG					
	70	80	90	100	110	120
g231-1.pep	KIRLILLEFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFRTLRRRAQ					
m231-1	KIRLILLEFSITFIMPRRPVLHLHQVQIGFADRNLRFALVAVGIEHAHADFPFRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSVFHLRCVDIRHPNFMFRVAVDDVKGIAVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRCSAAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq  
1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC  
51 GCCGCCCTTG CAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA  
101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG



529

```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGCGCTT GCGGATTTT
301 AGCTTTCAC AATCCTTTC GTTCCCTTTC CGCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTGTCGAACA
501 CCGGACGCT GACTTTCCTG CCTTCGCCCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GCGCGCTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCCGTC GATAACGTA AGGGTGTCGC
651 CGTCATAGAC TTTGGACACC GTGCGTGTGT AGCGGTGGCC GGATTCGCC
701 GATGCTCGGC GCGGGCGGG CGCGTCGGAA CCCGCTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLSVGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRLNRHFAL VAVGVEHADA DFPAFERRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQDGG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
a231-1.pep	70	80	90	100	110	120
	QSRVSLPNAQPFAHGIHPILIAAPACPAVRPRRLRIFSFQSFAPFRLNLSVGIIG					
m231-1	QSRVSLPNAQPFAHGIHPILIAAPACSAVRPRRLRIFSFQSFAPFRLNLSVGIIG					
	70	80	90	100	110	120
a231-1.pep	130	140	150	160	170	180
	KIRLILFFSITFIMPRRPVHLHLQVQIGFADRLNRHFALVAVGVEHADADFFAFRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVHLHLQVQIGFADRLNRHFALVAVGIEHADADFFAFRRRAQ					
	130	140	150	160	170	180
a231-1.pep	190	200	210	220	230	240
	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDENVKGVAVIDFGHRACVAVAGFRRCSAAGG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDENVKGVAVIDFGHRACVAVAGFRRCSAAGG					
	190	200	210	220	230	240
a231-1.pep	250	260	270	280	290	300
	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQDGGKPFHDFNLHIFQMPMPSEH					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQDGGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300
a231-1.pep	310					
	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatacctgtt
51 tggtcagatt ttgggaacgg cggttgccgg cgcgccgct tatattgtcg
101 ggatactggt tttgctggtc gccgtcggag gaacggccgg cagcctgttt

```

```

151 atgccgtccg taccgcgcaa ggctgccgat acccaaatcg agtgggaatat
201 tgtccgtggt acaaaatccc tgctgctga aacggtgcgg cacaatcccc
251 tttttaccgc cattatcggc atctcgtggt tttggtttgt cggcgcggtt
301 tataccacgc aactgcccac ctttacccaa atccatttgg gcggcaacga
351 taatgttttt aacctgatgc ttgctttgtt ttccatcggg attgccgcgg
401 gtccggtact gtgtgccaaag ttcggcaggg aacggctgat gttggcttgg
451 gtaacgggtg gtgcgttggg ttcgacgggt tgcggcctgg ttttgggtgtg
501 gctgacgcac ggacaccgtt ttgaagggtt gaacggcatt ttttggtttt
551 tatcgcaagg atgggcatac cccgtgatgg cggtgatgac gctgatcggc
601 tttttcggcg gattttttctc cgttccgctc tatacctggc tgcaaacgcg
651 cagcagcgag actttccgcy cccgcgcgtt tgcgcgcaac aatatcggtta
701 acggcatctt tatgggtttcc gccgcgctt tgagcgcggg attgctgttt
751 ttgtttgaca gcattttcct gctgtatctg attgtcgcct tgggcaatat
801 tccgttgccg gtatttttga ttaagcgca aaggcggttt ttaggcgcgg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HNPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGLNGI FWFLSQGWAY PVMAVMTLIG
201 FFGGFFSVPL YTNLQTASSE TFRARAVAN NIWNGIFMVS AAVLSAVLLF
251 LFDSISLILYL IVALGNIPLA VFLIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m232.seq

```

1 ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTGC CCATCCTGTT
51 CGGTCAGATT TTGGGAACGG CGGTGGCAGG TGTACGCCT TATATTGTGC
101 GGATACTGGT TTGCTGGTGC GCCGTCGGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATG AGTGAATAT
201 TGTCCTGGC ACAAATCCC TGCTGCGTGA AACGGTGGG CACAAGCCCG
251 TTTTACC GC CATTATCGGT ATTTCGTGGT TTTGGTTTGT CCGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTC AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAKGG AACGCCTGAT GTTGGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGTT TGCGGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CCGTGATGAC GCTGATCGGC
601 TTTTTCGGCG GATTTTCTC CGTTCGCTC TATACCT(g)TG CAAACGCCCA
651 TAGCGAGATT TCCGCGCCG GCCGTTGCCG CCAACAATAT CGTTAACGGT
701 ATTTTATG TTTCCGCTGC CGTTTGTAGC GCGGTGTGTC TGTTTTGTG
751 TGACAGCATT TCCTGTGTGT ATCTGATTGT CGCTTTGGGC AATATTCCGT
801 TGTCGGTATT TTGATTAAAG CGCGAAAGGC GGTTTTTAGG CGCGCGGCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HKPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGLNGI FXFLSQGWAY PVMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLILYLIV ALGNIPLSVF LIKRERRFLG AAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

	10	20	30	40	50	60
m232.pep	MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD					
	:     :     :     :     :					
g232	MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD					

531

	10	20	30	40	50	60
	70	80	90	100	110	120
m232.pep	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m232.pep	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFGRRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	130	140	150	160	170	180
	190	200	210	220	230	
m232.pep	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMV					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAVAANNIVNGIFMV					
	190	200	210	220	230	240
	240	250	260	270	280	289
m232.pep	AAVLSAVLLFLFDSISLLYLIVLALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLIVLALGNIPLAFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```
a232.seq
1  ATGTACGCTA AAAAAGGCGG TTTGGGACTG GTTAAAGCC GCCGTTTCGC
51  ACCTCTTTTC GCTACGCAGT TTCTCGGCGC GTTCAACGAC AATGTGTTCA
101 AAACCGCGCT GTTGTGATG ATTGGGTTT ACGGTTTGGG GCAAAACGGC
151 TTCCTGCCTG CCGGACAGAT GTTGAAC TTG GCGCGTTGC TGTATTATT
201 GCCGTATTC CTGTTTTCCT CGCTGTCGGG GCAGTTGGGT AACAAATTCG
251 ACAAGGCCGT TTTGGCGCGT TGGGCCAAGG TGCTGGAAT GATCATTATG
301 GCGGTGGCGG CATACGGGT TTATATCCGG TCTGCCCGC TGCTTTTGGC
351 GTGTCTGTTT TGCATGGGCG CGCAATCGAC GCTGTTTCGG CCGTGAAAT
401 ACGCCATCCT GCCCGATTAT CTCGACGACA AAGAGTTGAT GATGGGCAAC
451 AGCCTGATTG AATCGGGTAC GTTGTGCGC ATCCTGTTCC GTGAGATACT
501 GGGGACTGCG GTGGCAGGTG TACCGCCTTA TATTGTCGGG ATACTGGTTT
551 TGCTGGTCGC CGTAGGAGGC ACGGTCGGCA GCCTGTTTAT GCCGTCCGTA
601 CCCGCCAAGG CTGCCGATAC ACAAATTGAG TGAATATTG TCCGGGGTAC
651 AAAATCCCTG CTGCGTGAAA CGGTGCGGCA CAAGCCCGTT TTTACCGCCA
701 TTATCGGTAT TCGTGTTT TGTTTGTGCG GCGCGGTTA TACCACGCAA
751 CTGCCGACCT TTACCCAAAT CCATCTAGGC GGCAACGACA ATGTTTTCAA
801 CCTGATGCTT GCCCTGTTT CCATCGGTAT TGCCGCCGGT TCGGTACTGT
851 GTGCCAAGTT CAGCAGGAA CGGCTGAGGT TGGCTTGGT AACGGTTGGT
901 GCGTTGGGTT TGACGGTTG CGGCTTGGT TTGGTGTGGC TGACGCACGG
951 ACACCGTTTT GAAGGGCTGA ACGGCATTTT TTGGTTTTTA TCGAAGGAT
1001 GGGCATATCC CGTGATGGCG GTGATGACGC TGATCGGCTT TTCGGCGGA
1051 TTTTCTCCG TTCCGCTCTA TACCTGGCTG CAAACCGCCA GTAGCGAGAC
1101 TTTCCGCGCC CGCGCGGTTG CCGCCAACAA TATCGTTAAC GGTATTTTTA
1151 TGTTTCCCG TGCCGTTT AGCGCGGTG TGCTGTTTT GTTTGACAGC
1201 ATTTCTTGT TGTATCTGAT TGTGCTTTG GGCAATATTC CGTTGTCGGT
1251 ATTTTGTATT AAGCGCGAAA GCGGTTTTT AGCGCGGCG GCAATCAGGA
1301 AAAACCTTG A
```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```
a232.pep
1  MYAKKGGLGL VKSRRFAPLF ATQFLGAFND NVFKTALFVM IGFYGLGQNG
51  FLPAGQMLNL GALLFILPYF LFSSLSGQLG NKFDKAVLAR WAKVLEMIIM
101 AVAAYGFYIR SAPLLLACLF CMGAQSTLFG PLKYAILPDY LDDKELMMGN
151 SLIESGTFVA ILFGQILGTA VAGVPPYIVG ILVLLVAVGG TVGSLFMPSV
201 PAKAADTQIE WNIVRGTKSL LRETVRHKPV FTAIIGISWF WFGAVYTTQ
251 LPTFTQIHLG GNDNVFNLM ALFSIGIAAG SVLCAKFSRE RLRLAWVTVG
```

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPUMA VMTLIGFFGG  
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAVL SAVLLFLFDS  
 401 ISLLYLIVAL GNIPLSVFLI KRERRFLGAA AIRKKP\*

m232/a232 95.9% identity in 290 aa overlap

m232.pep					10	20	30
					MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLFCMGAQSTLFGPLKYAILPDYLDKELMMGNSLIESGTFVAILFGQILGTAVAGVPP						
	120	130	140	150	160	170	
m232.pep		40	50	60	70	80	90
		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
a232		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
		180	190	200	210	220	230
m232.pep		100	110	120	130	140	150
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMALFSIGIAAGSVLCAKFSXERLMLAW					
a232		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMALFSIGIAAGSVLCAKFSRERLRLAW					
		240	250	260	270	280	290
m232.pep		160	170	180	190	200	210
		VTVGALGLTVCGLVLVWLTHGHRFEGNLGIFXFLSQGWAYPVMAMVMTLIGFFGGFFSVPL					
a232		VTVGALGLTVCGLVLVWLTHGHRFEGNLGIFWFLSQGWAYPVMAMVMTLIGFFGGFFSVPL					
		300	310	320	330	340	350
m232.pep		220	230	240	250	260	
		YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
a232		YTWLQTASSETFRARAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
		360	370	380	390	400	410
m232.pep		270	280	289			
		VFLIKRERREFLGAAAIRKKPX					
a232		VFLIKRERREFLGAAAIRKKPX					
		420	430				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq

```

1  atgaaacgca aaaatatcgc gctgattccc gccgccggca tcgggggtgcg
51  ttctcgtgcg gacaaaacca agcaatatgt cgaaatcgga agcaaaaccg
101 ttttagaaca tgtacttggg atttttgaac ggcattgaggc cgtcgatttg
151 accgtcgttg tcgtctcgcc cgaagacacg tttgccgata aggttcagac
201 ggcatttcca caggttcggg tgtggaaaaa cgggtggacag acccgcgccg
251 aaactgtccg caacgggtgtg gcaaaactgt tggaaaaccg tttggcggcg
301 gaaaccgaca atattctggt acacgatgcc gcccgctgct gcctgccgtc
351 tgaagctctg gcgcggttga tagaacaggc gggcaacgcc gccgaaggcg
401 ggattttggc agttcccggt gccgatacgc tcaagcgcgc agaaagcgga
451 caaatcagtg caactgtcga ccgttcgggg ctttggcagg cgcaaacgcc
501 gcagcttttt caagcggggt tgctgcaccg cgcattggct gcggaaaact
551 tgggcggcat taccgatgaa gcgtccgccg tggaaaaact ggggtgtgct
601 ccgctactga tacaggcgga gcgcgcgaat ttgaaactga cgcagccgca
651 ggacgcatac atcgtcaggc tgctgctcaa tgccgtctga
```

This corresponds to the amino acid sequence <SEQ ID 858; ORF 233.ng>:

g233.pep

```

1  MKRKNIALIP AAGIGVRFGA DKPKQYVEIG SKTVLEHVLG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFP QVRVWKNGGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL ARLIEQAGNA AEGGILAVPV ADTLKRAESG
```

533

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR  
 201 PLLIQGDARN LKLTQPDAY IVRLLLNAV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)  
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG  
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG  
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG  
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC  
 201 GGCATTTCCTA CAGGTTTCGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG  
 251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGGCGGCG  
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC  
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGGCG  
 401 GGATTTTGGC AATTCCCAT TCCGATACGC TCAAGTGC GCACGGTGGG  
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)  
 1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL  
 51 TVVVVSPEDT FADKVQTAFF QVRVWKNNGGQ TRAETVRNGV AKLLETGLAA  
 101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG  
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

m233.pep	10	20	30	40	50	60
	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
g233	MKRKNIALIP AAGIGVRFGADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
m233.pep	70	80	90	100	110	120
	FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
g233	FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
m233.pep	130	140	150			
	TRLIEQAGNAAEGGILAIPIADTLKCADGGNI					
g233	ARLIEQAGNAAEGGILAVPVADTLKRAESGQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq  
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG  
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG  
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG  
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC  
 201 GGCATTTCCTA CAGGTTTCGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG  
 251 AAACGTGTCG CAACGGTGTG GCAAAATTGT TGGAAACCGG TTTGGCGGCG  
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC  
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG  
 401 GGATTTTGGC AATTCCCGTT GCCGATACGC TCAAGTGC GCACGGTGGG  
 451 AACATTAGTG CAACCGTCGA GCGGACGAGC CTTTGGCAGG CGCAAACGCC  
 501 GCAGCTTTTC CGCGCCGGGC TGCTGCACCG CGCATTGGCT GCGGAAAACT  
 551 TGGACGGCAT TACCGATGAA GCGTCCGCCG TGGAAAAATT GGGCATCCGC  
 601 CCTTTGCTGG TGCAGGGCGA CGCGCGCAAT TTGAACTGA CGCAGCCGCA  
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1  MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAIPIV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDVAV*
```

m233/a233 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
a233	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m233.pep	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
a233	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
	130	140	150			
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
a233	TRLIEQAGNA AEGGILAI PVADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA					
	130	140	150	160	170	180
a233	AENLDGITDEASAVEKLGIRPLLQGDARNLKLTPQDAYIVRLLLDVAVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1  atgaaaaccg tttccgccgc catcgctttt gccgccgctg ccgtttcact
51  gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat cacggtgttc gcaccccgat ttccgtcgga
151 acattcgaca accgctccag cttccaaaaa ggcattttct ccgacagtga
201 agaccgtctg ggcagccagg caaaaacccat cctggtaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccctag cgattgaaa
301 caggaatccg gcatttccgg caaagcgag aacctgaaag ggcgagatta
351 tgtcgttacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggtcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctattc
501 cacacagggc gcggggcgaat acgcacttcc caaccgcgaa atcatcggtt
551 tcggcggcac ttccggctac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaaccg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1  MKTVSAAIAF AAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
51  TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRFNV LNRNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSNRE IIGFGTSGY DATLNGKVL
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1  ...GGCGCGGGCG AATACGCACT TTCCAACCGt GAAATCATCG GTTTCGGCGG
51  CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTGA GACTTGCCAA
101 TCCGCGAAGC .gTCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

Computer analysis of this amino acid sequence gave the following results:

**Homology with a predicted ORF from *N. gonorrhoeae***

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng) from *N. gonorrhoeae*:

m234/g234

m234.pep  
 GAGEYALSNREIIIGFGGTSGYDATLNGKVL  
 g234  
 LGRGKSQIAYAKVALNIVNVNTSEIVYSTQGAGEYALSNREIIIGFGGTSGYDATLNGKVL  
 140 150 160 170 180 190  
 40 50  
 m234.pep  
 DLAIREAVNSLVQAVDNGAWQPNRX  
 |||||:|||||||  
 g234  
 DLAIREAVDNLVQAVDNGAWQSNRX  
 200 210 220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)

1	AACCGCACCT	ATTTGAACGC	ATTA AACAG	GAATCCGGCA	TTCGGCAA
51	AGCGCATAAC	CTGAAAGGCG	CAAATTATGT	CGNNACCGGC	GATGTAACCG
101	AATTCGACG	CANAGATGTC	GGCGATCATC	AGCTCTTCGG	CATTTTGGGT
151	CGCGGCAAAT	CGCAAATCGC	CTATGCAAAA	GTGGCTCTGA	ATATCGTCAA
201	CGTCAATACT	TCCGAAATCG	TCTATTCGCG	ACAGGGCGCG	GGCGAATACG
251	CACTTTCCAA	CCGTGAAATC	ATCGGTTTCG	GCGCACTTC	CGGCTACGAT
301	GCGACTTTGA	ACGGCAAAGT	TTTAGACTTG	GCAATCCGCG	AAGCCGTCAA
351	CAGCCTGGTT	CAGGCTGTTG	ACAACGGCGC	ATGGCAACCC	AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)

1	NRTYLNALKQ	ESGISGKAHN	LKGANYVXTG	DVTEFGRXDV	GDHQLFGILG
51	RGKSQIAYAK	VALNIVNVNT	SEIVYSAQGA	GEYALSNREI	IGFGGTSGYD
101	ATLNGKVLDL	AIREAVNSLV	QAVDNGAWOP	NR*	

**m234/a234** 100.0% identity in 54 aa overlap

```

30                                     10                                20
m234.pep
GAGEYALSNREIIGFGGTSGYDATLNGKVL

|||||||||||||||||||||||||||||
a234
LGRGKSQIAYAKVALNIVNVNTSEIVYSAQGAGEYALSNREIIGFGGTSGYDATLNGKVL
      50      60      70      80      90      100

          40      50
m234.pep      DLAIREAVNSLVQAVDNGAWQPNRX
              |||||||||||||||||||
a234          DLAIREAVNSLVQAVDNGAWQPNRX
      110      120      130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq

1	atgaaacctt	tgattttag	gcttgccgc	gtgttggtc	tgtctgctg
51	ccaagtcga	aaagctccc	acctcgacta	cacgtcattc	aaagaaagca
101	aaccggcttc	aatttttggt	gttccgcgc	tgaacgagtc	gctctgatgc
151	aacggcactt	gggggatgct	ggcttcgcac	gcgcgcgcga	ttcccgaaac
201	cggctattac	gtctttcccg	cccgactcgt	ggaggaaacc	ttcaagaaaa
251	acggcttgac	caatgccgcc	gatattcacg	ccgtccggcc	ggaaaaactg
301	catcaaat	tcggcaatga	tcgggttttg	tacattacga	ttaccgaata
351	cggcacttca	tatcaaat	tagacagctg	gacgacccta	tcgcgcaaac
401	cacggctggt	cgattcccgc	aacgggaaag	agtgtggtg	ggtctcggcc
451	agcatccgcg	aaggcagcaa	caacagcaac	agcggcctgt	tgggggcttt
501	ggtcggcgca	gtggtaaatc	agattgccaa	caccctgacc	gacctccgcc
551	atcaggtttc	caaaacccgc	gcatacaaac	tactgtcgcc	ctattcccg
601	aacggttatc	tgaagggtcc	gaatttcctc	qaagaqaac	ccaaataa

This corresponds to the amino acid sequence <SEQ ID 870; ORF 235.ng>:

g235.pep

1	<u>MKPLILGLAA</u>	VLALSACQVR	KAPDLDYTSF	KESKPASILV	VPPLNESPDV
51	NGTWGMLAST	AAPISEAGYY	VFPAAVVEET	FKENGLTNAA	DIHAVRPEKL
101	HQIFGNDAVL	YITVTYGTG	YQILDSVTVV	SAKARLVDSR	NGKELWSGSA
151	SIREGSNNNS	SGLLGALVGR	VVNQIANSLT	DRGYQVSKTA	AYNLLSPYSR
201	NGILKGRPNV	EEOPK*			

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 871>:

m235.seq

1	ATGAAACCTT	TGATTTTAGG	GCTTGCCGCC	GTGTTGGCGC	TGTCTGCCTG
51	CCAAGTTCAA	AAAGCGCCCG	ATTTCGACTA	CACGTCATTC	AAGGAAAGCA
101	AACCGGCTCT	AATTTTGGTG	GTTCGCCGCA	TGAACGAATC	GCCCGATGTC
151	AACGGAACAT	GGGGTGTACT	GGCTTCGACC	CGCGCGCCGC	TTTCCGAAGC
201	CGGCTATTAC	GTCTTCCCCG	CCGCAGTCGT	GGAGGAAACC	TTCAAAACAA
251	ACGGCTTGAC	CAATGCCGCC	GATATTCACG	CCGTCGGGCC	GGAAAAACTG
301	CATCAGATTT	TCGGCAATGA	TGCGGTTTGT	TACATTACGG	TTACCGAATA
351	CGGCATCTCA	TATCAAATTT	TAGACAGCGT	GACGACCGTA	TCCGCCAAAG
401	CACGGCTGGT	CGATTCCCGC	AACGGAAAGT	AGTTGTGGTG	TGGTCTCGGC
451	AGCATCCGCG	AAGGCAGCAA	CAACAGCAAC	AGCGGCCTGT	TGGGGGCTTT
501	GGTCACGCGA	GTGGTCAATC	AGATTGCCAA	CAGCCTGACC	GACCCGCGGT
551	ATCAGGTCTT	CAAAACGCCC	GCATACAACC	TGCTGTGCGC	GATTCTCTAC
601	AACCGCATCT	TGAAAGGTCC	GAGATTCTGT	GAAGAGCAGC	CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 872; ORF 235>:

m235 . pep

1	MKPLILGLAA	VLALSACQVQ	KAPDFDYTSF	KESKPASILV	VPPLNESPDV
51	NGTWGVLAST	AAPLSEAGYY	VFPAAVVEET	FKQGLTNAA	DIHAVRPEKL
101	HQIFGNDAVL	YITVTVEGTS	YQILDSVTVT	SAKARLVDSR	NGKELWSGSA
151	SIREGSNNNS	SGLLGALVSA	VVNQIANSLT	DRGYQVSKTA	AYNLLSPYSH
201	NGILKGPRFV	EEOP*			

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/q235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTGWGLAST					
g235	MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTGWMLAST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVAVLYITVTEYGTS					
	:					
g235	AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVAVLYITVTEYGTS					
	70	80	90	100	110	120
	130	140	150	160	170	180



537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          130      140      150      160      170      180

          190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g235      DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPKX
          190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTCGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCGAAGC
201 CGGCTATTAC GTCTTCCCCG CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGGTTTGT TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAG
401 CACGGCTGGT CGATTCGCCG AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

          10      20      30      40      50      60
m235.pep  MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          10      20      30      40      50      60

          70      80      90      100     110     120
m235.pep  AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
          70      80      90      100     110     120

          130     140     150     160     170     180
m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          130     140     150     160     170     180

          190     200     210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq

```

1 ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51 CGGTTTCATA ACCTGCAACC GCGCCACAT CGCGGGTGTA ATGCCAGCAG
101 CGTTCGCATT TTTCGCCGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATT CTCCGGCGC GGTAAATTCG
251 GCTTCCGCCT GCAAaggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtageggcg gTTACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAAGTC GGCTTCGGCT TTTCGTTGA TGGCCGGGAA CTGGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGCCCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTGC CGCGC TGCGGCGGGC GCGGCTGTGC
551 GCTTTGGTGG TGTAGAGGCG GTCTTTCAGG ATGTGCGAGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGAAGG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTCTTGAG CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCCACC ATATCCGCCT GTTGACCGC
751 ATCTTCAATC GGATTAAGT CGCTCAAATT GGCAAacag AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTCGGTAA CGCGTTTGAG GATTTCTTTG
851 GAAatcgCCA ATtcgcccgt gTAATCGGTG GATGCCGCCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCTG TATAGACTTC CTGCGGCGCG ACGACGTGTC
951 CGATGGATTT CGACATTTTG CGGCCGTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TCGCGTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1 MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAFAFFAV AGFGNGKFI
51 TDFHFCFRHQ QGKAQFFAQS IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFVVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGGRLAAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNV FHEVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAG
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1 ..TTGCACGGAC GAACCGACGG TTTTGTCCGC GCGCAAAGGC TCGATGGCGG
51 CGGTTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATTT TTTCACCAGT
101 TCGGCTTCGG TTTTTCGTT GATGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCTCTTCGC CGCCCGCGWT GAYGTCCAC GCTTCTTCGC
201 CCGTGAAGCA CAAATCGGT GCAATCAAGA GAACCAAACT CCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CCGTCTTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACATG TCTTTTACGG CAAAGTGGaA kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG AACTCTTGC AGCTGACGTG CCAATACCAC
451 GCGTAGCGG TCGATTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTT AGGATTTCTT TGGAAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCG CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCAGT CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCCTTC GCCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GGCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1 ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGGFFV DGRELVPMSME
51 EDAVXFAAAX DVPRFFAGEA QNRCNQENQT ACDVIQGS LC AAACMAVCFG
101 GVEAVFQDVE VERTQVFAE RNXFYQKVE XITRIVIAQ TLLQLTCQYH
151 GVAVDFFHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMQQ
251 LFIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

```

a236.seq
1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCTGCACAG CGTTTGCAGA
51  CGGTTTCATG GCCTGCAACC GCGCCACAT  CGCGGGTGTA GTGCCAGCAG
101 CGTTCGCATT TTTCACCATT ACTGGCTTTA GCGGCAACGG CAAGTTCGCT
151 GCGTACTTTC ACTTCTGCTT TAGACACCAG CAAGCAAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CGGGCCATTT TCTCCGGCGC GGTAATTTCG
251 GCTTCGGCTT GCAAGGACGA ACCGACGGTT TTGTCGGCGC GCAAAGGCTC
301 GATGGCGGCG GTTACGCTT  CGCGGCTTC  GCGGATTGCC GTCCATTTTT
351 TCACCAGTTC GGCTTCGGCT TTTTCGTTGA TGGTCGGGAA CTCGTGCCAA
401 TTCTGAAAA GCACGCTGTC TTCTGCGCCG CGCCCGATGA TGTCCACGCG
451 TCTTTCGCGG GTACAGCACA AAATCGGTGC AATCAAGAGA ACAGCGCTCG
501 GCGTGATGTG GTACAGGGCG GTTTCGCGCG TCGCGCGGGC GCGGCTTCG
551 GCTTTGTGG TATAGAGGCG GTCTTTCAGG ATATCGAGGT AGAACCGGCC
601 CAAGTCTTCC GAGCAGAAAG AAACCATTTC TTTACGGCA  AAGTGGAAAG
651 CATAACGCGG ATAAAAATCA CCGGCAACGC GTTCTTGCA  CCGCCTTGCC
701 AACACCAAGC CATTGCGGTC GATTCCACC  ATATCCGCCT GTTGCACGGC
751 ATCTTCAATA GGATTGAAGT CGTCCAAGT  GGCAACAARA AAGCTCAAGG
801 TATTGCGGAT ACGGCGGTAG CTTTCGGTTA CGCGCTTGAG GATTTCTTTG
851 GAAATCGCCA ATTCGCGGCT GTAATCGGTG GATGCCGCC  ACAGGCGCAG
901 GATGTCCGCG CCGAACTCGT TATACACTTC TTGCGCGCGG ACGACGTTGC
951 CGATGGATT  CGACATTTTG CGCCCGTTTT GATCCACCAC GAAACCATGG
1001 GTCAGCAGCT GTTTGTGTCG CGCGCGACCC ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

```
a236.pep
1 MARFAFSADI LCTAFADGFM ACNRAHIAGV VPAAFAFFTI TGFSGNGKFA
51 AYFHF CFRHQ QSKAQFFAQ IGIAGHFFRR GNGFGFLQGR TDFGVGAQRL
101 DGGGYREAGF ADCRPFFHQF QFGFVFDGRE LVPSMEKHAV FCAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGGRLAAAG AAVGFGGIEA VFQDIEVERA
201 QVFRARNRHF FHKQVEGIR IKITGNAFLQ PPCQHQGIAR DPHHIRLLHG
251 IFNRIEVAQV GKQKQGIAD TAVAFGYALE DFFGNRQFAA VIGGCRPQAO
301 DVRAELVIHF LRRDDVADGF RHFAFVLIHH ETMGOLFVR RATH*
```

m236/a236 81.0% identity in 258 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

g237.seq	1	atgcgggaca	aggttggcgg	taatatcgca	ctccccgcc	cacgaatatt
51	cgattctaac	atcggaacgc	tgcggaaaaa	ctttaagcat	atcttggcgg	
101	acaagctcgg	tcatacgcgc	aggattgtcg	ataaaatcgt	tatccctacc	
151	gccgaaaagc	agcctgcggt	ccgcgctgag	gcggtataaa	tccaaaatat	
201	ggcggttgtc	gcatactgcc	atattgtgtg	ggataagccc	ttttgtgcgc	
251	gcgcccaagg	gttcggtggc	aataataaag	gtgctgacgg	caatcgcctt	
301	gcgttccaaa	ggccggaata	tcgggttcaa	accgacataa	gtattgcagg	
351	catagaccac	atttttacac	tgacgcgtgc	cttcgggggt	gtaaacacgc	
401	caaccgtttt	gatacgggtc	catgcgcgtc	atcggcgatt	ctgcgaaaat	
451	ctgcgcgcgc	gcttcggcag	cggcgctggc	aacacccaac	gtgtaattga	
501	gcg gatgaag	atgcccgga	aagggatcga	actgtgcgcc	ttggtacata	
551	tcgctgtcaa	gctgctgttt	caactcgggt	ttatcccaaa	gttgataatg	
601	atctgcaccg	taatgcggtt	ggcgctgttc	atgccactgc	tgcacactct	
651	cccaatgctg	cggacggagc	gcacccgtag	cataaccgcg	ctgccaactc	
701	caatcgatgg	catgtttgcg	gacgcgttcg	tccaccagtt	cgaccgcctg	
751	caaagactgt	tgccaaaacc	attgcgcctg	ctcaaggcgc	acctgttttt	
801	caattttccc	catacccgag	gcgtagtcgc	tgataaacctg	cccgccactc	
851	ctgccggacg	cgccgaagcc	gatacgtgcg	gctttccaaa	cgagcgcctc	
901	atgtccgtgt	tccgcagcgc	gcaatgcggt	acacaaacgc	ctcaaacgcg	
951	cgccgataat	gcagggtttc	gctttcagac	ggcattggag	tttcggataa	
1001	acagtatcgg	gattaaccca	actaaaataa	taagaaggca	gatattcttg	
1051	aaaatcaggg	cgaatcattg	tgtttgcttt	atcgggtata	ttttcggag	
1101	gaatgataca	gactgtcggg	ccatatcgtc	caacacaaaa	atcggttgca	

This corresponds to the amino acid sequence <SEQ ID 882; ORF 237.ng>:

g237.pep  
1 MRDKVGGNIA LPAPRIFDSN IGKLRKQFKH ILADKLGHTR RIVDKFVILT  
51 AEQPAVRAE AVIIQNMAVV AYCHIVADKP FCARAQGGFG NNGKADGNRL

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN  
 151 LRAGFGSGAG NTQRVIERMK MPQGIELCA LVHIAVKLLF QLGFI PKLIM  
 201 TRTVMPLGVF MPLLQLFPML RTDGNRGITA LPIAIDGMFA DAFVHQFDRLL  
 251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTCGFQNDGF  
 301 MSVFRQRQCG TQTAQTAADN AGFGFQTALE FRINSMRINR TKIIRRQIFL  
 351 KIRANHCVCF IGYIFGRNDT DCRAISSKQK IG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m237.seq  
 1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCGCCGCC CACGAATATT  
 51 CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTAAGCAT ATCTGGCGG  
 101 ACAAGCTCGG TCATaCGCTC AGGATTGTCG ATAAACTCGT TATCCTTACC  
 151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT  
 201 GGCGGTTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTGCGCGC  
 251 GCCCCAAGG GTTCGGTCGC AATAATAAAG GTGCTGACAG CAATCGCCTT  
 301 GCGTTCCAAA GGCCGGAATA TCGGGTTCAA ACCTGCATAA GTATTGACAG  
 351 CATAGACCAC ATTTTTGCAC TCGACGCTGC CTTCGGGCGT GTAAACCAGC  
 401 CAACCGTTT GATGCGGTTT GATGCACGTC ATCGGGGATT GCTCGAAAAT  
 451 CTGCGCACCG GCTTCGGCAG CGGCACGAGC GATGCCCAAA GTGTAAGTGA  
 501 GCGGATGCAG GTGTCCGAT AAGGGGTCGA ATTGTGCCCC TTGGTACATA  
 551 TCGCTGTCAA GCTGCTGTTT CACTCGGCT TTATCCCAA GTTGATAATG  
 601 ACTCGCACCG TAATGCCGTT GGGCGTGTTC ATGCCACTGC TGCAACTCTT  
 651 CCCAATGCTG CGGACGACG GCAACCGTGG CATAACCGCG CTGCCAATCA  
 701 CAATCGACGG CATGTTTGCG GACGCGTTCG TCCACCAGTT CGACCGCCTG  
 751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT  
 801 CAATTTCCCC CATAACCGAG nCGTAATCGC TGATAACCTG CCCGCCACTC  
 851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC  
 901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCAATCCGC  
 951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTtCGGATAA  
 1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG  
 1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCAGGTGTA TTTTCGGACG  
 1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAWACAGAAA ATCGGTTGA

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m237.pep  
 1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGHTL RIVDKLVILT  
 51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNGGADSNRL  
 101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN  
 151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFI PKLIM  
 201 TRTVMPLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRLL  
 251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRRAET DTRGFQHNRF  
 301 MSLLRQGQCS AQTTQSAADD TGIGFQTALK FRINSMRINR TEIIRRQIFL  
 351 KIRANHCVCF IRCIFGRNDT GCRAISSXQK IG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m237/g237

m237.pep	10	20	30	40	50	60
	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE					
g237	MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGHTRIVDKFVILTAEQPAVRAE					
	10	20	30	40	50	60
m237.pep	70	80	90	100	110	120
	AVIIQNMAVVAYCHIVTDKPF CARPQGFGRNNGGADSNRLAFQRPEYRVQTCISIDSIDH					
g237	AVIIQNMAVVAYCHIVADKPF CARAQGFGRNNGGADGNRLAFQRPEYRVQTDISIDGIDH					
	70	80	90	100	110	120
m237.pep	130	140	150	160	170	180
	IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					

**g237**

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 885>:

a237

This corresponds to the amino acid sequence <SEQ ID 886; ORF 237.a>:

a237.

## m237/a237 85.6% identity in 382 aa overlap

m237.pep	10	20	30	40	50	60
	MRDKVGGNVALPAPRIFDFDIGKLRNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE					
a237	10	20	30	40	50	60
	MRDKVGGNVALPAPRIFDFDIGKLRNFKHILADKLGHTRGIVDKLVILTAEKQSAVRAE					
m237.pep	70	80	90	100	110	120
	AVIIQNMVAVYCHIVTDKPFPCARPQGFGRNNKGADSNRLAFQRPYRVQTCISIDSIDH					
a237	70	80	90	100	110	120
	AVIIQNMVAVYCHIVADKPFCTRAQGFGRNNKGADSNRLALQRLRYRIQTGISIDGVHQ					
m237.pep	130	140	150	160	170	180
	IFALDAAFGRVNQPTVLMRFDARHRLLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					
a237	130	140	150	160	170	180
	IFAFDAAFGGVNQPTVLIRFNAYHGRMLKNLRTSFGSGAGDAQRVIERMEMPGQGIELCA					
m237.pep	190	200	210	220	230	240
	LVHIAVKLLFQLGFIPKLMTRTVMPLGVFMPLQLFFMLRTDGNRGITALPITIDGMFA					
a237	190	200	210	220	230	240
	LVHIAVKLLQLQFSVIPELIMSCTVIFLGVLMPLQLFFMLRTDGNRGITALPIAINGMFA					
m237.pep	250	260	270	280	290	300
	DAFVHQFDRLQRLLPKPLRLQADLFFNFPHTAXVIADNLPATPSRRAETDTRGFQHNRF					
a237	250	260	270	280	290	300
	DAFVHQFDRLQRLLPKPLRLQTDLFFNFLTAGVIADNLPATPSRRAETDTRGFQHNRF					
m237.pep	310	320	330	340	350	360
	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCF					
a237	310	320	330	340	350	360
	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCF					
m237.pep	370	380				
	IRCIFGRNDTGCRAISSXQKIGX					
a237	370	380				
	IGYIFGRNDTGCRAISSXQKIGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctgttggcag cggcaatatc
51  gatgctgcat atccccatta gtcatgcgaa cggtttggat gcccgtttgc
101 gcgatgatat gcaggcaaaa cactacgaac cgggtggcaa ataccatctg
151 tttggtaatg ctgcgcggcag tgtaaaaaat cgggtttgcy ccgtccaaac
201 atttgatgca actgcggtcg gcccataact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtcggtt cgataatcat gattcaaaaa gcacttctga
351 tttcagcggc ggcgtagacg gcggttttac cgtttacca cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacgggc tcaaggcggc
451 ggttatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaacaa agataaacac tgttccgcaa gccctttttt
551 cagaccgctg gctaaaagaa aatgccggtg ccgcttccgg ttttctcagc
601 cgtgcggatg aagcaggaaa actgatattg gaaaacgacc ccgataaaaa
651 ttgdcgggct aaccgtatgg atgatattcg cggcatcgtc caaggcgagg
701 ttaatccctt ttaacgggtt tttcaagggt tagggattgg ggcaattaca
751 gacagtgcgg taagcccgtt cacagataca gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtcc ggaagcacia cttgccgcgg

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851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgcccttgcc gtagcagagg ccgcagggtac ggtttggcgc ggtaaaaaag
1001 tagaacttaa cccgacccaa tgggattggg ttaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcggg aggaaaagct aatgctgcaa
1151 cctatcctaa gttggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacaatt
1401 tgcaactaca ggtattcaag caaattttga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1 MNLPIQKFM LLAALISMLH IPISHANGLD ARLRDMQAK HYEPGGKYHL
51 FGNARGSVKN RVCVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGTG TKTKINTVPQ APFSDRWLKE NAGAASGFLS
201 RADEAGKLIW ENDPKNWRA NRMDDIRGIV QGAVNPFLTG FQGVGIGAIT
251 DSAVSPVTDI AAQQTLLQGIN DLGNLSPEAQ LAAASLLQDS AFVAVKDGINS
301 ARQWADAHPN ITATAQTALA VAEAAGTVWR GKKVELNPTK WDWVKNTRYK
351 KPAARHMQTV DGEMAGGNRP PKSITSEGKA NAATYKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYT IDSNEKRNKI KNHGLNLR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CAcTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAG CGGGTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGTTTGA AGGTGTTATC GGTATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAAA GCATTCTGA
351 TTTGAGCGGC GGTGTAGACG GCGGTTTAC TGTTTACCAA CTTTCATCGAA
401 CAGGTCGCGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGAGG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACTTCA ACAAAAACAA AGACTAATAT TGTCCCTCAA GCCCATTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTTC GGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTTCAAGGAG TAGGGATTGG GCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTAGGAA AATTAAGTCC GGAAGCACA CTTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTGCGG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCAAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TAAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAATCTT TACCAAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAAGTGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAATTTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTACAAC AACAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1 MNLPIQKFM LFAAAILLQ IPISHANGLD ARLRDMQAK HYEPGGKYHL
51 FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDHH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

```



```

151 DYPPPGGARD IYSYYVKGTS TKTKTNIVPQ APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDVRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTTT AAQOTLQGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS
301 AKQWADAHPN ITATAQTALS AAEAAGTVWR GKKVELNPTK WDWVKNTGYK
351 KPAARHMQTL DGEMAGGNKP IKSLPNSAAE KRKQNFEFN SNWSSASFDS
401 VHKTLPNAP GILSPDKVKT RYTSLDGKIT IIKDNENNYF RIHDNSRKQY
451 LDSNGNAVKT GNLQKQAKD YLQQQTHIRN LDK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 238 shows 86.0% identity over a 401 aa overlap with a predicted ORF (ORF 238.ng) from *N. gonorrhoeae*:

m238/g238

m238.pep	10	20	30	40	50	60
	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
g238	MNLPIQKFMMLLAAAI SMLHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
m238.pep	70	80	90	100	110	120
	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHHD SKSTSDFSG					
g238	RVCAVQTFDATAVGPILPITHERTGFEGVIGYETHFSGHGHEVHSPFDNHDSKSTSDFSG					
	70	80	90	100	110	120
m238.pep	130	140	150	160	170	180
	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYYVKGTSTKTKTNIVPQ					
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGYEPQGGARDIYSYHIKGTSTKTKINTVPQ					
	130	140	150	160	170	180
m238.pep	190	200	210	220	230	240
	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDDVRGIVQGAVNPFLMG					
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPKNWRANRMDDIRGIVQGAVNPFLTG					
	190	200	210	220	230	240
m238.pep	250	260	270	280	290	300
	FQGVGIGAITDSAVSPVTTTAAQOTLQGINDLGKLSPEAQ LAAASLLQDS AFAVKDGINS					
g238	FQGVGIGAITDSAVSPVTTTAAQOTLQGINDLGNLSPEAQ LAAASLLQDS AFAVKDGINS					
	250	260	270	280	290	300
m238.pep	310	320	330	340	350	360
	AKQWADAHPNITATAQTALSAAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL					
g238	ARQWADAHPNITATAQTALAVAEAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTV					
	310	320	330	340	350	360
m238.pep	370	380	390	400	410	420
	DGEMAGGNKPIKSLPNSAAEKRKQNFEFNSNWSSASFDSVHKTLPNAPGILSPDKVKT					
g238	DGEMAGGNRPPKSI-TSEGKANAATYPKLVNQLNEQNLNNIAAQDPRLSLAIHEGKKNFP					
	370	380	390	400	410	
m238.pep	430	440	450	460	470	480
	RYTSLDGKITIIKDNENNYFRIHDNSRKQYLD SNGNAVKTGNLQKQAKDYLQQQTHIRN					
g238	IGTATYEEADRLGKIWVGEGARQTSGGGWLSRDGTRQYRPPTEKKSQFATTGIQANFETY					
	420	430	440	450	460	470

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

**a238.seq** (partial)

```

1 ATGAATTGCG CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAT CGGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTTCG GCCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTGA AGGCATTATC GGTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACCTTCTGA
351 TTTAGCGGC GCGGTAGACG GTGGTTTAC CGTTTACCAA CTTATCCGGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGGAGG AGCAAGGGAT ATATACAGCT ACTATGTCAA
501 AGGAACTTCA ACAAAAACAA AGAGTAATAT TGTTCCTCGA GCCCATTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATATTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTTGCAG TAAAAGACGG TATCAATTCC
901 GCCAGACAAT GGGCTGATGC CCATCCGAAT ATAAGTCAA CAGCCCCAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAAAAAAG
1001 TAGAACTTAA CCCGACCAAA TGGGATTGGG TTTAAAATAC CGGCTATAAA
1051 ACACCTGCTG TTCGCACCAT GCATACTTTG GATGGGGAAA TGCCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA

```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

**a238.pep** (partial)

```

1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPGGKYHL
51 FGNARGSVKN RVYAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD AAQQTQGIN HLGNSPEAQ LAAATALQDS AFAVKDGIN
301 ARQWADAHFN ITATAQTALA VAEAATTWVG GKKVELNPTK WDVVKNITGYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ

```

**m238/a238** 91.9% identity in 385 aa overlap

	10	20	30	40	50	60
m238.pep	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYEPGGKYHL	FGNARGSVKK
a238	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYEPGGKYHL	FGNARGSVKN
	70	80	90	100	110	120
m238.pep	RVYAVQTFDA	TAVSPVLPIT	HERTGFEGV	IGYETHFSGH	GEVHSPFDH	DSKSTSDFSG
a238	RVYAVQTFDA	TAVGPILPIT	HERTGFEGV	IGYETHFSGH	GEVHSPFDH	DSKSTSDFSG
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYVKGTS	TKTKTNIVPQ
a238	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYVKGTS	TKTKSNIVPR
	190	200	210	220	230	240
m238.pep	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDVRGIV	QGAVNPFLMG
a238	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDIRGIV	QGAVNPFLMG
	250	260	270	280	290	300
m238.pep	FQGVGIGAIT	DSAVSPVTD	AAQQTQGIN	DLGKLSPEAQ	LAAASLLQDS	AFAVKDGIN

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```

|||||
a238      FQGVGIGAITDSAVSPVTDTAQQTLQGINHLGNLSPEAQLAAATAIQDSFAVKDGIN
           250      260      270      280      290      300
           310      320      330      340      350      360
m238.pep  AKQWADAHFNITATAQTALSAEEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL
           |||||
a238      ARQWADAHFNITATAQTALAVAEAAATTVWGGKKVELNPTKWDWVKNTGYKTPAVRTMHTL
           310      320      330      340      350      360
           370      380      390      400      410      419
m238.pep  DGEMAGGNPKIKSLP-NSAAEKRKQNFEEKFNSNWSSASFDSVHKTLTPNAPGILSPDKVK
           |||||
a238      DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1  atgttccacc ataaaggatg tgcccgaaac cggcggatgg aggttttgtt
51  tttctgccgc cgccctgatc gcttcgtgat tcgccaaacg cgcctgttgc
101 agcctcattt gcgcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctggttttgc tgcatacaca
201 cggaaaaagc ggaaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcatgccc ttcatgacgtt tttctctgtt attattccgg tatcggaccg
301 gcagtcgcgt ccgccacacg caaaactgcg ctccctcgcc tcgggttggc
351 ggcaatttcc gcttaccaccg gctttaatgc cctgccacg attttcaggg
401 gcggatcggg caaatccgct tctctgaccg ccgccagct cggcaggggc
451 tcgtgttgcg aatatttttt gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaactgcc gccctcttcc agacggcaca
551 tgacctgcgg caataccgcc cctacttctt caagctcgcg gttataaaag
601 atgctggattg cctggaaggt gcgcgtcgca ggatcctgcc ccgcgtcgcg
651 agtacggacg ttttgtgcca cgatctgcgc cagcttgcgg gttgtatcga
701 ttggactttc cgcccgttgc gcgacaatgg cgcgcacaat ctggcggcta
751 aaccgctctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1  MFHHKGIARN RRMEVLFFCR RPDRFVIRQT RLLQPHLRRI LLQGDPLFFR
51  LVQSCVEPV LVLLHHNGKS GNAHRKQOKE IRFVHCRSDV FLCYYSGIGP
101 AVRSATRKA LALGLAAIS ASPGFNALPT IFRGSGKSA SLTAAQLGRG
151 SCCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSRLLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMTIWRLL
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1  ATGCTCCACC ATAAAGGTmy kGCCCCGAAAC CGGCKGATGG AGGTTTGTGT
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATT TCGCATTAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTCG TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTACCCG GCTTTAATGC CCTGCCACG ATTTTCAGGG
401 GCAGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCACGCG CGGCAGGGGC
451 GCGTGTGCG AATATTTTTT GACAACTGC TTCACAATGC GATCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTTACTTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTTGTGCCA CGATCTGCGC CAGCTTGCAG GTTGTATCGA
701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CCGGCGGCTA
751 AACCCTCTT CACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

## m239.pep

```

1  MLHHKGXARN RXMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
51  LIQSCEIEPV LVLLHHNGKS GNAHRKQQKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRTAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIRRL
251 NRSSP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng) from *N. gonorrhoeae*:

## m239/g239

m239.pep	10	20	30	40	50	60
	MLHHKGXARNRXMEVLFFCRPDRFVVRQTRLLQPHLRRIILLQGDFLFFRLIQSCEIEPV					
g239	MFHHKGIARNRRMEVLFFCRPDRFVIRQTRLLQPHLRRIILLQGDFLFFRLVQSCEIEPV					
	10	20	30	40	50	60
m239.pep	70	80	90	100	110	120
	LVLLHHNGKSGNAHRKQQKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTAALLALGLAAIS					
g239	LVLLHHNGKSGNAHRKQQKEIRFVHCRSDVFLCYYSIGIGPAVRSATRKTAALLALGLAAIS					
	70	80	90	100	110	120
m239.pep	130	140	150	160	170	180
	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
g239	ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
m239.pep	190	200	210	220	230	240
	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
g239	RRHMTGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
m239.pep	250					
	ATMARAIRRLNRSSPX					
g239	ATMARTIWRNLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

## a239.seq

```

1  ATGCTCCACC ATAAAGGTAT TGCCCGAAAC CGGCGGATGG AGGTTTTGTT
51  TTTCTGCCGC CGCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCTT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAGT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCG GCCTCACCCG GCTTTAATGC CCTGCCCGCG ATTTTCAGGG
401 GCGGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCCAGCG CGGCAGGGGC
451 GCGTGTGCGG AATATTTTTT GACAACTGCG TTCACAATGC GGTCTTCCAA
501 CGAATGAAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTAATTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGATTG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTTGTGCCA CGATCTGCGC CAGCTTGGCG GTTGATCGA
701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CTGGCGGCTA
751 AACCGCTCTT CACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
  1 MLHHKGIARN RRMEVLFFCR RPDRFVVRQT RLLQPHLR II LLQGDFLFFR
  51 LIQSCEVEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
 101 AVRSATRKTA LLALGLAAIS ASPGFNALPA IFRGGSGKSA SLTAAQRGRG
 151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
 201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIWRL
 251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

	10	20	30	40	50	60
m239.pep	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLR IILLQGDFLFFRLIQSCEIEPV					
a239	MLHHKGIARNRRMEVLFFCRRPDRFVVRQTRLLQPHLR IILLQGDFLFFRLIQSCEVEPV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRK TALLALGLAAIS					
a239	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRK TALLALGLAAIS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
a239	ASPGFNALPAIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMTCGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
a239	RRHMTCGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
	250					
m239.pep	ATMARAIIRLNRSSPX					
a239	ATMARAIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
  1 atgatagaag tcatacat ttcggcgcc gaaacgcgca gacagtttgc
  51 ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
 101 gggtaaacat gggatcatc gcgcacggga gacggtccga ttttataagg
 151 ctgcgtattc agccggttcgt tcaaatacgg tttgcccgc tccaatgcct
 201 tcgcaatcac gaacggtttg attgccgaac cagggttcgat catatcggtt
 251 acggcacggt tgcgcgcgtg ttcgctgtct gcccgcccg gtctgttggg
 301 atcgtaggcg ggcgtattgg ccaaggcgag gatttcccc gtgcgggcat
 351 ccaaaaccac caccgttcg gcttttgctt gatggtattc gaccgccttg
 401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
 451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagctgt
 501 ccacaatatt gccctgccgg tcccgcacaa caacttccgc gccgtcttcg
 551 ccatacaggc tgtcttcaag cgaaagtcc aaaccttctt gacctttgcc
 601 gtcaatatcg gtaaatccga tgacgtgtgc aaacaggttg cccatcgggt
 651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
  1 MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
  51 LRIQPFVQIG FARIQCLRNH ERFDCRTRFD HIGYGTVA PL FAVCPAGSVG
 101 IVGGRIQQGE DFPRAGIQNH HRSGFCLMV F DRLVQLFIGO GLNPLIEGKD
 151 DVFAVLRCFI ARGVQAVHNI ALPVPQNNFR AVFAIQAVFK RKFQTFLTFA
```

201 VNIGKSDDVC KOVAHRVMAF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

```
m240.beq
1  ATGATAGAAG TCATACATTT CTTCCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGTAAACAT GGGTATCGCG CACGGGAGAC GGTCGGATT TATAAGGCTG
151 CGTATTCAGT CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCCGTGTTC GCTGTCTGCC CGGCCGGGCC TGTGTTGGATC
301 GTAGGCGGGC GTATTGCCCC AGGCGAGGAT TTCCCCCGTG CCGGCATCCA
351 AaACCACCAT CGTTCGGGCT TTGCGCTGAT GGTATTTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGATC
451 GTCCTTGCCG TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTGCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCACAA CCTTCTGAC CTTTGCGGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 902: ORF 240>:

m240.pep

1	MIEVIHFFGT	ETRRQFACAD	VGRFLHDAAH	IQRGVNMGIA	HGRRSDFIRL
51	RIQPFVQIGF	ARIQCLRNHK	RFCDCRTGFDH	IGYGTVA <del>PLF</del>	AVCPAGPVGI
101	<u>VGGRIGQGG</u>	FPRAGIQXHH	RSGPCLMVFD	RLVQLFIQGG	LNPLIEGKDD
151	VFAVFRGFEXA	RGVQAVHNIA	LPVPQNDFRA	VFAMQAVFKR	KQOTFLTFAV
201	NIGKSDDVCK	OV <del>AHR</del> VMF <del>AF</del>			

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

```

m240/g240
      10          20          30          40          50          59
m240.pep MIEVIHFPGTETRRQFACADVGRFLHDAAHIQRGVNMGI-AHGRRSDFIRLRIQPFVQIG
|||:::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g240      MIEVIHFPGAETRROFACADVGRFLHNAAHIQRGVNMGIIAHGRRSDFIRLRIQPFVQIG
      10          20          30          40          50          60
m240.pep 60          70          80          90          100         110        119
FARIQCLRNHKRFD CRTGFDPHIGYGT VAPLF AVCPAGVPVGIVGG RIGQGEDFP PRAGIQXH
|||:::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g240      FARIQCLRNHERFD CRTRFDPHIGYGT VAPLF AVCPAGSVGIVGG RIGQGEDFP PRAGIQNH
      70          80          90          100         110        120
m240.pep 120         130         140         150         160         170        179
HRSGFCMLMVFDRLVQLFIGOGLNPLIEGKDDVF AVFRGF XARGVQAVHNIALPVPQNDFR
|||:::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g240      HRSGFCMLMVFDRLVQLFIGOGLNPLIEGKDDVF AVLRCFIARGVQAVHNIALPVPQNNFR
      130         140         150         160         170        180
m240.pep 180         190         200         210         220
AVFAMQAVFKRKFTFLTFAVNIGKSDDVCKQVAHRVMAFX
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g240      AVFAIQAVFKRKFTFLTFAVNIGKSDDVCKQVAHRVMAF
      190         200         210         220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 903>:

a240.seq

```
1 ATGATAGAAG TCATACATTT CTTCCGCCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCGGATT TATAAGGCTG
151 CGGTAATCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
```

551

```

251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCTGC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51 RIQPFVQIGF ARIQCLRNHK RFDCRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFIA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTFLTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH	IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF				
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH	IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF				
	10	20	30	40	50	60
	70	80	90	100	110	120
m240.pep	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLF	AVCPAGPVGIVGGRIGQGEDFPRAGIQXHH				
a240	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLF	AVCPAGPVGIVGGRIGQGEDFPRAGIQNH				
	70	80	90	100	110	120
	130	140	150	160	170	180
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDD	VFAVFRGFARGVQAVHNIALPVPQNDFRA				
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDD	VFAVFRGFARGVQAVHNIALPVPQNDFRA				
	130	140	150	160	170	180
	190	200	210	220		
m240.pep	VFAMQAVFKRKFTFLTFAVNIGKSDDVCK	QVAHRVMAFX				
a240	VFAMQAVFKRKFTFLTFAVNIGKSDDVCK	QVAHRVMAFX				
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTICA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCTGC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
1 MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS

```

```

51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPS C RQSVVMTVR
101 TVDMTVCDL IGCIAHAFNR SPKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)

```

1  ..CGGCAATCAG TGGTGGTGAT GACCGTGCGG GCCGTGGACA TGACCGTGTG
51  CGATTCCTC ATCGGATGCA TCGCGCACGC TTTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCCGGATCC TGCTCGCCGA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGCAACG
351 CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT AACCGCCGTG CAGATACGCA
401 ATCGGTTCTT CGGTTTGTG CAAAAGCTGA TTGTTGGCAT CACATCTCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGCTCTTT
501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)

```

1  ..RQSVVMTVR AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA
51  VGNIGYTIDD NIAGFRIVGF KHADDFDNR EHARIFDQ LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

m241/g241

m241.pep				10	20	30
				RQSVVMTVR	AVDMTVCDL	IGCIAHAFNC
g241	QPTYLLHPSN	KMPSETEQTL	FRRHQIPPS	CRQSVVMTVR	TVDMTVCDL	IGCIAHAFNR
	70	80	90	100	110	120
m241.pep		40	50	60	70	80
		SLKADFHACQ	RMVAVVHRLA	VGNIGYTIDD	NIAGFRIVGF	KHADDFDNR
g241		SFKADFHACQ	RMVAVVHRLA	VGNIGYTIDD	NIAGFRIVRF	KHHTDLDFNR
		130	140	150	160	170
m241.pep		100	110	120	130	140
		LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFV
g241		LRIMLTERIV	GRKRHFDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFI
		190	200	210	220	230
m241.pep		160	170			
		IMQRNHGIFH	DSHICPFRNS	RLITGAFX		
g241		IMQRNHGIFC	NSHICPFRNS	RLITGAFX		
		250	260			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq

```

1  ATGCCAACAC GTCCAACCTG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC

```



```

251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACGGTGGACA TGACCGTGTG CGATTTCTCTC ATCGGATGCA TCGCGCACAC
351 TTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAAG GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

```

a241.pep
1  MPTRPTRAAK HPTPPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDLF IGICIAHTFNR SLKADFHACQ RMVAVHHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDENR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241/a241 96.0% identity in 177 aa overlap

```

                                10      20      30
m241.pep                                RQSVVMTVRVAVDMTVCDFLIGICIAHAFNC
                                |||||:|||||:|||||:|||||:
a241      QPTYLLHPSNKMPSMEQTLFRRHQIPPSQSVVMTVRTVDMTVCDFLIGICIAHTFNR
                                70      80      90      100     110     120

                                40      50      60      70      80      90
m241.pep      SLKADFHACQRMVAVHHRLAVGNIGYTIDDNIAGFRIVGFKHHADFDENREHARIFDTDQ
                                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a241      SLKADFHACQRMVAVHHRLTVGNIGYTIDDNIAGFRIVGFKHHADFDENREHARIFNTDQ
                                130     140     150     160     170     180

                                100     110     120     130     140     150
m241.pep      LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
                                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a241      LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
                                190     200     210     220     230     240

                                160     170
m241.pep      IMQRNHGIFHDSHICPFRNSRLITGAFX
                                |||||:|||||:|||||:|||||:
a241      IMQRNHGILHDSHICPFRNSRLITGAFX
                                250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 911>:

```

g241-1.seq
1  ATGATAGAAG TCATACATTT CTTCCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTCA AATCGGTTTT GCCCGCATCC AATGCCCTCG
201 CAATCAGAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGG GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACCCAC CGTTCGGCT TTTGCCGTAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGCTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

## g241-1.pep

```
1  MPTRPTRAAN PPTFTTWLQT AYCPRPYPYR PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPS RQSVVMTVR
101 TVDMTVCDFL IGCIAHAFNR SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

## m241-1.seq

```
1  ATGCCAACAC GTCCAACCTCG CGCTGCAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCAGC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAACCCCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCGGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTGT
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCG GCATCTTCGA TACGGACCAA CTCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCCTT CAGGAACAGC AGATTAATA CAGCGCATT
801 CTAA
```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

## m241-1.pep

```
1  MPTRPTRAAN PPTPPTWLQT AYCPRPYPYR PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPS RQSVVMTVR
101 AVDMTVCDFL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVGF KHADDFDFNR EHARIFDQDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFH
251 DSHICPFRNS RLITGAF*
```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPPTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPPTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSNKMPSETEQLFRRHQIPPSRQSVVMTVRVDMTVCDFLIGCIAHAFNC					
g241	QPTYLLHPSNKMPSETEQLFRRHQIPPSRQSVVMTVRTVDMTVCDFLIGCIAHAFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQRMVAVVHRLAVGNIGYTIDDDNIAGFRIVGFKHADDFDNREHARIFDQDQ					
g241	SFKADFHACQRMVAVVHRLAVGNIGYTIDDDNIAGFRIVRFKHHTDLDFNRERARIFNTDQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFIQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

## a241-1.seq

```
1  ATGCCAACAC GTCCAACCTCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
```

```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGGTGT CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1. pep

```

1 MPTRPTRA AK HPTPPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51 ANRRENFHNA OPTYLLHPSN KMPSEMEQTL FRRHQIPPS RQSVVMTVR
101 TVDMTVCDFL IGCIAHTFNR SLKADFACQ RMVAVHHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADDFNR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNREFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1. pep	MPTRPTRA	ANPPTPPTWLQT	AYCPRPPYRP	PSVQTHTPHE	PASSTCAAKS	ANRRENFHNA
a241	MPTRPTRA	AKHPTPPTWLQT	AYCPRPPYRP	PSVQTHTPHE	PASSTCAAKS	ANRRENFHNA
	10	20	30	40	50	60
	70	80	90	100	110	120
m241-1. pep	OPTYLLHPSN	KMPSETEQTL	FRRHQIPPS	CRQSVVMTVR	AVDMTVCDFL	IGCIAHAFNC
a241	OPTYLLHPSN	KMPSETEQTL	FRRHQIPPS	CRQSVVMTVR	TVDMTVCDFL	IGCIAHTFNR
	70	80	90	100	110	120
	130	140	150	160	170	180
m241-1. pep	SLKADFACQ	RMVAVHHRL	AVGNIGYTIDD	NIAGFRIVGF	KHHADDFNR	EHARIFNTDQ
a241	SLKADFACQ	RMVAVHHRL	TVGNIGYTIDD	NIAGFRIVGF	KHHADDFNR	EHARIFNTDQ
	130	140	150	160	170	180
	190	200	210	220	230	240
m241-1. pep	LRILLAERIV	GRKRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNREFGFV	QKLIVGIIHL
a241	LRILLAERIV	GRKRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNREFGFV	QKLIVGIIHL
	190	200	210	220	230	240
	250	260				
m241-1. pep	IMQRNHGIFH	DSHICPFRNS	RLITGAFX			
a241	IMQRNHGILH	DSHICPFRNS	RLITGAFX			
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242. seq

```

1 atgatacggcg aacttggtgt tttgttcgtg atcgagcact tcaagcaacg
51 cgctggcggg atcgcccgga aagtcgctgc ccaattgtgc gatttcgtcg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccc cggtattcgc
201 tttcgtcgcg cagcccgccc aaggccatac ggacatatat ccgccccgtt
251 gctttggcga tggattcgcc caaagaggtt ttgcccacgc ccggagggcc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt ttttgacggt
351 cgaggtattc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtcgggc tttggcgatg tctttgctga cgcgggattt
451 tttcttccac ggcagtcgga gcagggtgct gatgtagttg cgtacgacgg

```

501 tggattcggc agacatcggc ggcattcattt tgagtttttt cagttcggac  
551 aggcattttt ctccgccttc tttggtcata cccgcctttt tgatgcctgc  
601 ctccaaggca tccagttcgc cgttttcgtc ttcttcgccc aattctttgt  
651 gtatcgcttt aatctgttcg ttcagataat attcgcgttg ggatttttcc  
701 atttgcgctt tgacgcgctc gcgtatgcgt ttttcggcct gcataatgtc  
751 gagttcggat tccagctttg ccagcaggaa ttccatccgt ttgccgattt  
801 cgggaatctc caaaattctgt tggcgttcgc ccagtttcaa ctgcaaatgc  
851 gctgcgaccg tatcggttag

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

g242.pcp

1	MIGELVVLVF	IEHFKQRAGG	IAPKVAAQFV	DFVEQEQRVS	YACFCHILQN
51	LAGHRADIGT	AVPADFAFVA	HAAQGHTDIF	PPRCFGDGFA	QRGFAHARRA
101	DQTQNRTFEL	VHTFLDGEVF	QNPFFDFFQA	VVVGIQHSGS	FGDVVFADAGF
151	FLPRQSEQGV	DVVAYDGGFG	RHRRHHFEFF	QFGQAFFFRF	FGHTRLFDAC
201	LQIQIEFAVVF	FFAQFFVYRF	NLFVQIIFAL	GFHHLAFDAS	AYAFFGLHNHV
251	EFQFQLCQQE	FHPFDADFNL	ONLLALROFO	LOMRCDRIG*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

m242.seq

1	ATGATCGGCA	AAC TTGTTGT	TTTGTTCCGG	ATCGAGCACT	TCGAGCAACG
51	CGCTGCGGG	ATCGCCTCGG	AAGTCGTTAC	CCAATTTGTC	GATTTTCGTCG
101	AGCAGGAACA	AGGGGTTTTT	CACGCCGGCT	TTTGCCATAT	TC TGCAAAAT
151	CTTACCGGG	ATAGAGCCGA	TATAGGTGCG	GCGGTGTCCC	CTGATTTTCGC
201	TTTTCGTCGC	CACGCGGCC	AAAGCCATGC	GGACATATTT	CCGCGCCGGT
251	GCTTTGGCGA	TGGAATTCGCC	CAAGAGGTT	TGTCCCAACG	CCGGAGGCC
301	GACCAGGCAC	AGAATCGGGC	CTTTGAGTTT	GTCCATACGT	TTTTGGACGG
351	CGAGGTATTC	CAAAATCCGT	TCTTTGACTT	TTTCCAGGCC	GTAGTGGTCG
401	GCATCCAGCA	CCAGTCCGGC	TTTGGCGATG	TC TTTGCTGA	CGCGGGATTT
451	TTTCTTCCAC	GGCAGCTCGA	GCAAAGTGTC	GATGTAGTTG	CGTACGACGG
501	TGGATTCCGC	AGACATCGGT	GGCATCATTT	TGAGCTTTTT	CAGTTCCGACG
551	AGGCATTTTT	CTTCGCGTTC	TTTGGTCATA	CCGCGCTTTT	TGATATCTGC
601	TTCCAAGGCA	TCCAGTTCGC	CGTTTTCGTC	TTCTTCGCCC	AGTTCTTTGT
651	GTATCGCTTT	AATCTGTTCG	TTCAGATAAT	ATTTCGCGCTG	GGATTTTTTCC
701	ATTTGCGGTT	TGACGCGTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
751	GAGTTCGGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TTGCCGATTT
801	CGGGAATTTT	CAAAATCTGT	TGGCGTTGCG	CCAGTTTCAA	CTGCAAATGC
851	GCTGCGACCG	TATCGGTTAG			

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

m242.pap

1	MIGKLVVLF	IEHFQQRAGG	IASEVVTFQV	DFVEQEQGVF	HAGFCHILQN
51	LTGHRADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHARRA
101	DQAQNRAFEF	VHTPLDGEVF	QNPFDFDQFA	VVVGIQHSGS	FGDVFDADAGF
151	FLPRQLEQSV	DVVAYDGGFR	RHRWHHPELF	QFGQAFFFRF	FGHTRLFDIC
201	FQIQEQFAVF	FFAQFVYRFE	NLFVQIIFAL	GFHHLAFDAS	AYAFFGLHNH
251	EFQFGLCQOE	FHPADFNGNF	QNLALRQFO	LMQRCDRIG*	

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

m242/g24290.3% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVVLF	GIIEHFEQ	RAGGIASE	VVTQFVD	FVEQEQQ	VVFHAGFCHILQNL
	:	:	:		:	:
g242	MIGELVVLF	VIIEHFKQ	RAGGIAPK	VAAQFVD	FVEQEQR	VSACFCHILQNL
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAF	VAHAAQ	SHADIF	PPRCFGD	GFGFAQ	RGFHAHARRADQAQ
			: :			: : : :
g242	AVPADFAF	VAHAAQ	GHTDIF	PPRCFGD	GFGFAQ	RGFHAHARRADQTQ
	70	80	90	100	110	120

557

	130	140	150	160	170	180
m242.pep	QNPFDFDFFQAVVVGIIHQSGFGDVFDAGFFLPRQLEQSVDDVAYDGGFRRHRWHHFELF					
g242	QNPFDFDFFQAVVVGIIHQSGFGDVFDAGFFLPRQSEQGVDDVAYDGGFGRHRRHHFBFF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m242.pep	QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS					
g242	QFGQAFFFRFFGHTRLFDACLOGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS					
	190	200	210	220	230	240
	250	260	270	280	290	
m242.pep	AYAFFGLHNVEFGFQLCQQEFHFPADFGNFNLLALRQFQLQMRCDRIGX					
g242	AYAFFGLHNVEFGFQLCQQEFHFPADFGNQLNLLALRQFQLQMRCDRIGX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 921>:

a242.seq

```

1  ATGATCGGCG  AACTTGTGTG  TTTGCTCGGG  ATCAAGCACT  TCGAGCAACG
51  CGCTGGCGGG  ATCGCCCGGG  AAGTCGCTAN  CCAATTTGTC  GATTTCGTCG
101 AGCAGGAACA  ATGGGTTTTT  TACGCCGGCT  TTTGCCATAT  TCTGCAAAAT
151 CTTACCGGGC  ATGGAGCCGA  TATAGGTGCG  GCGGTGTCCC  CGGATTTTCG
201 TTTGCTCGCG  CACGCCGGCC  AAAGCCATGC  GGACATATT  CCGCCCGGTT
251 GCTTTGGCGA  TGGATTCGCC  CAAAGAGGTT  TTGCCACGC  CTGGAGGGCC
301 GACCAGGCAC  AGAATCGGGC  CTTTGAGTTT  GTCCATACGT  TTTTGGACGG
351 CGAGGTATTC  CAAAATCCGT  TCTTTGACTT  TTTCCAGGCC  GTAGTGGTCG
401 GTATCCAGCA  CCAATCCGCG  TTTGGCGATG  TCTTTGCTGA  CGCGGGATTT
451 TTTCTCCAC  GGCAGTTCGA  GCAGGGTGTC  GATGTAGTTG  CGTACGACGG
501 TGGATTCGCG  AGACATCGGC  GGCATCATT  TGAGCTTTT  CAGTTCGGAC
551 AGGCATTTT  CTCCGCTTC  TTTGGTCATA  CCCGCCTTT  TGATATCTGC
601 TTCCAAGCA  TCCAGTTCGC  CGTTTTCGTC  TTCTTCGCCC  AGTTCTTTGT
651 GTATCGCTT  AATCTGTTCG  TTCAGATAAT  ATTCGCGCTG  GGATTTTTC
701 ATTTGGCGTT  TGACGCGTCC  GCGTATGCGT  TTTTCGGCCT  GCATAATGTC
751 GAGTTCGGAT  TCCAGCTGTG  CCAGCAGGAA  TTCCATCCGT  TTGCCGATTT
801 CGGGAATTC  CAAAATCTGT  TGGCGTTGCG  CCAGTTTCAA  CTGCAAATGC
851 GCTGCGACCG  TATCGGTTAG

```

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

a242.pep

```

1  MIGELVLLG  IKHFEQRAGG  IAPEVAXQFV  DFVEQEQWVF  YAGFCHILQN
51  LTGHGADIGA  AVSPDFAFVA  HAAQSHADIF  PPRCFDGF  QRGFAHAWRA
101 DQAQNRAFEF  VHTFLDGEVF  QNPFDFDFFQ  VVVGIIHQSG  FGDVFADAGF
151 FLPRQFEQGV  DVVAYDGGFG  RHRHRRHFELF  QFGQAFFFRF  FGHTRLFDIC
201 FQGIQFAVFV  FFAQFFVYRF  NLFVQIIFAL  GFFHLAFDAS  AYAFFGLHNV
251 EFGFQLCQOE  FHPFADFGNF  QNLLALRQFQ  LQMRCDRIG*

```

m242/a242 95.2% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVVLFGLIEHFEQRAGGIASEVVTFVDFVEQEQQGVFHAGFCHILQNLTGHRADIGA					
a242	MIGELVLLGIIKHFEQRAGGIAPEVAXQFVDFVEQEQQWVFYAGFCHILQNLTGHGADIGA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGFQARGFAHARRADQAQNRAFEFVHTFLDGEVF					
a242	AVSPDFAFVAHAAQSHADIFPPRCFGDGFQARGFAHAWRADQAQNRAFEFVHTFLDGEVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m242.pep	QNPFDFDFFQAVVVGIIHQSGFGDVFDAGFFLPRQLEQSVDDVAYDGGFRRHRWHHFELF					

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```

a242      QNPFFDFFQAVVVGIIHQSGFGDVFADAGFFLPRQFEQGVDDVAYDGGFGRHRRHHFELF
           130      140      150      160      170      180
           190      200      210      220      230      240
m242.pep  QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRENLFVQIIFALGFFHLAFDAS
           |||||
a242      QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRENLFVQIIFALGFFHLAFDAS
           190      200      210      220      230      240
           250      260      270      280      290
m242.pep  AYAFFGLHNVEFGFQLCQQEFHFPADFNGFNLLALRQFQLQMRCDRIGX
           |||||
a242      AYAFFGLHNVEFGFQLCQQEFHFPADFNGFNLLALRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243.seq
1  ATGGTaatcg tctGGTTGcc cgAGTTaccg CCGATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GCGGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGCGGAACA GGTCTTCCTC
201 TTCCTGCAAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCc tgCCGATGAG CTTTTTGTTT
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51  IQRFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGGCGAGG AAGGCGGTGC AGAGGTTGAC GCGGAGCCAC
151 ATCCAGyGGT TTTTCACCGA ATCCCACACG GGGCGGAaYa GGTCTTCCTC
201 TTCCTGCAAA CCCGCCATAT TCAGCATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243.pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

```

m243/g243
           10      20      30      40      50      60
m243.pep  MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
           |||||
g243      MVIVWLPELPPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT
           10      20      30      40      50      60
           70      80      90      100     110
m243.pep  GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
           |||||
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```

70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GCGGAGCCAC
151 ATCCAGCGGT TTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTCGTCA ACGGTCACCC TGCCGATGAG CTTTTGTGTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSFLF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSISASDSSRITSTISSMVLPMSEFLFSSTTGAVTKSX					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSVTLPMSFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1  atgccgcctg aagcccggcc ggcgggttca gacggcattg ccgctttact
51  tcgatcggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggett cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcacgcctg atggatattc
251 ggatcgagct tatcgcccg cttaggattg atttccttga ttgctgtggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcatcgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acatttcac ggcaaaattc tgtccggcga acttgtgcgt
451 atcggcaatt tcctgctggt ggcggcgccg caggttttgc tcgtttgcca
501 aagcgcgag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcgccg gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacggtttc caccgcctcc acattttcaa
651 ccgctttctt actgttttgc tgctgtgtct gttcgctcat atcgatatcc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgcgcgc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1  MPPEARPAGS DGIAALLRSV YTONALQEQIN QIIPQTPSGF LPCHRNHSRA
51  QHTVQGQITL LHHTNHGIGF LLTGHRHLRL MDIRIELIAR FRIDFLDLRG
101 IKRLLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNEFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRLQILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLLCFLAH IVSLKTNWKS KSGYYPKIR
251 TFSRNFQQRQ EISHPPPNTL PQPKYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

m244.seq

1	ATGCCGTC	TGG	AAGCCGACA	GGCGGTTCA	GACGGCATTG	CCGCTTTACT
51	TCGATCGGT	TATACGCAA	ACGCGCTTCA	GGAAATAAAT	CAGATTATTC	
101	CCCAGACGCC	TTCAGGCTTC	CTTCTGCGCC	ACCGTAACCA	TAGCCGGGCG	
151	CAACACGCGG	TCGGACAGCT	TATAACCCCT	CTTCATCACA	CCCACACCGG	
201	TATTCGGCTC	CTGTTCGCT	GCCACCGCCT	GCATCGCCTG	ATGGATATTC	
251	GGATCGAGCT	TATCGCCCGC	TTTAGGGTTG	ATTTCCTTGA	TTTGCGTAGC	
301	ATCAAATGCT	TTCTGCAACT	CGTTCAAAGT	CATCTGCACG	CCCATTTTCA	
351	GCGCATCGAA	ATTGCCGCTC	TGATCCAAAA	GCGCCATTTC	CAGATAATCC	
401	TTGACCCGGCA	GCATTTCAC	GGCAAACTAT	TGTCGGGCGA	ACTTGTGCGT	
451	ATCCGCAATT	TyCTGCTGGT	GGCGGCGGCG	CAGGTTTTGC	TCGTTTGCCA	
501	AAGCGCGCTG	CTCGTCTTTC	AACTCGCTTT	CCAGCTCGGC	AATCCGCGCC	
551	TGCAAATCCT	CATAAGCCGG	CTCTGCGGCA	GCCTGTTCCT	GCACACCGTC	
601	CGCATTTCT	ACTGTTTCGA	CGGTTTCAC	CGCTCCACA	TTTTCAACCG	
651	CTTCTTCACT	GTTTGTCTGC	TGTGTCTGTT	CGTTCATATC	GTATCCCTTA	
701	AAACAAATTG	GAAATCAAAA	TCCAGTTATT	ACCCGCGCAA	GATAAGGACA	
751	TTTTCAAGAA	ACTTCAAKCA	AAACAGCAGA	ATTTCAAATT	CATTTTCAAA	
801	TCCCCTACCG	AAAAATAAAT	ATAGACGGTA	A		

This corresponds to the amino acid sequence <SEQ ID 932: ORF 244>:

m244 . pep

```

1  MPSEARQAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LLRHRNHSRA
51  QHAVGQRITL  LHHTHHGIRL  LFACHRLHRL  MDIRIELIAR  FRVDFDLRS
101  ICFQLQVQS  HLHAHFQRIE  IAAALQKRHF  QIILDRQHFH  GKLLSGELVR
151  IRNFFLLVAA  QVLLVQCSAL  LVFQLRFQLG  NPRLQILISR  LCGSLFLHTV
201  RISYCEGRFH  RLHIFNRFET  VLLLCLFAHI  VS�KTNWKS  SSYPYRKIRT
251  FSRNFQXQOR  ISNSFSNPLP  KKYR*

```

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 244 shows 86.3% identity over a 277 aa overlap with a predicted ORF (ORF 244.ng) from *N. gonorrhoeae*:

M244/G244

	10	20	30	40	50	60
m244 . pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
	:					
g244	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLPCRHNHSRAQHTVGQGITT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLSIKCFLQLVQSHLHAHFQRIE					
	:       :   :                     :           :         :					
g244	LHHTNHGIGFLTGHRLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m244 . pep	IAALIQRKRFQIILDRQHFHGKLLSGELVRIRNFLLVAAQAQVLLVCQSAAALLVFQLRFQL					
	:   :					
g244	ITALIQRKRFQIILDRQHFHGKLLSGELVRIGNFLLVAAQAQVLLVCQSAQLFVFQLRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244 . pep	GNPRLQILISRLCGSLFLHTVIRISYCFDGFHRLHIFNRFFTULLCLFAHIVSLKTNWKS					
	:           :					
g244	GNPRLQILISRLGGSLFLYTIVIRISYCLDGFHRLHIFNRFFTULLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244 . pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKXYRRX					
	:                       :     :           :					
g244	KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQPKYKRX					
	250	260	270			



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1  ATGCCGTCTG AAGCCCGACA GCGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCTT CTTTCATCAG CCCACCACGG
201 TATTGGGTTT CTGTTCTGCT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAACTTC TGTCCGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGCGGCG CAGGTTTGC TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCAATT CCTACTGTCT CGACGGTTTC CACCGCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTGC TGCTGTGTCT GTTCGTCAT ATCGTATCCC
701 TTAAACAAA TTGAAATCA AAATCCAGT ATTACCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTCAA ATTCATTTC
801 AAATCCCTA CCGAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1  MPSEARQAGS DGIAALLRSV YTONALQEI QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQH FH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAO LLVFQLRFQL GNPRQLILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQKRO RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTONALQEI QIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
a244	MPSEARQAGSDGIAALLRSVYTONALQEI QIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244.pep	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSA-LLVFQLRFQL					
a244	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	230
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
a244	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	240	250	260	270		
m244.pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
a244	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKXYRRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1  atgccgctg aagcccgcc gccgggttca gacggcattg ccgctttact
```

51	tcgatcggtt	tatacgcaaa	acgcgcttca	ggaaataaat	cagattatttc
101	cccagacgcc	ttcaggcttc	cttcgcgtcc	accgtaacca	tagccgcggcg
151	caacacacgg	tcggacaggg	tataaccttt	cttcatacga	ccaaccacgg
201	tattgggttc	ctgctcactg	ggaccgcctt	gcctgcgtct	atggatattc
251	ggatcgagct	tatcgcccgc	tttaggattg	atttccttga	tttgctgtgc
301	atcaaacgcc	ttctgcaact	cattcaaaat	catctgcaca	cccattttgc
351	gcgcatcgaa	attaccgttc	tgatccaaaa	gcgcctattc	cagataatcc
401	ttgacgggca	acattttcac	ggcaaaactc	tgctcggcga	acttgtgcgt
451	atcgggcaat	tctctgctgt	ggcgcgggcg	caggttttgc	tcggtttgcc
501	aagcgcgcag	ttgttctgtt	ttcaactcgc	cttcagcttc	ggcaatccgc
551	gcttcgcaat	cctcataaagc	cggtctcgcg	gcagcctgtt	cctgtacacc
601	gtccgcattt	cctactgtct	cgacggtttc	cacgcctctc	acattttcaa
651	ccgctcttct	actgttttgc	tgctgtgtct	gttcgctcat	atcgatatcc
701	tcaaaaacaa	tggaaattca	aaatccggtt	attaccggag	caagataagg
751	acattttcaa	gtgaatttcaa	gcaaaggcag	gaaattttac	atccgcgcgc
801	gaatacccta	ccgcaaaaac	catataaacg	gtaa	

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

**g244-1.pep**

1	MPPEARPAGS	DGIAALLRSV	YTQNALQEIN	QIIPQTPSGF	LPCHRNHSRA
51	QHTVQGQGIT	LHHTNHGTFE	LLTGHRLHRL	MDIRELTAR	FRIDPLDLRG
101	IKRLLQLQTS	LHHTHFGRIE	ITGALQKHFH	QIILDRQHFF	GKLLSGELVR
151	<u>IGNELLVAAA</u>	<u>QVLVVCQSAQ</u>	LFVFQLRFQL	GNPRLQILIS	RLGGSFLFLYT
201	VRISYQCDGF	HRHLIFNRFI	<u>TVLLCLCPAH</u>	IVSLKTNWKS	KSGYYPSKIR
251	TFSRNFQKQD	EISHPPNTL	PQPKYK*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

**m244-1.seq**

1	ATGCCGTCGT	AAGCCCGACA	GGCGGGTTCA	GACGGCATTG	CCGCTTTACT
51	TCGATCGGTT	TATACGCAAA	ACGCGCTTCA	GGAAATAAAT	CAGATTATTG
101	CCACAGACGC	TTACGGCTTT	CTTCTGCGCC	ACCGTAAACA	TACCGCGGCG
151	CAACACGCGG	TCGGACAGCG	TATTAACCTT	CTTCATCAAC	CCACAGACGC
201	TATTCGCGTC	CTGTTCGTCT	GCCACGCGCT	GCATCGCCCTG	ATGGATATTC
251	GGATCGAGTG	TATCGCCCGC	TTTAGGGTTG	ATTTCTCTGA	TTTGCGTATG
301	ATCAAAATGCT	TTCTGCAACT	CGTTCAAAGT	CATCTGCACG	CCCATTTTCA
351	GCGCATCGAA	ATTGCCGCTC	TGATCCAAAA	GCGCCATTTC	CAGATAATCC
401	TTGACCGCGA	CGATTTCGAC	GGCAAACTTC	TGTCGCGGCA	ACTTTGCGGT
451	ATTCGCGAAT	TyCTGTGCGT	GGCGCGCGCG	CAGGTTTTFG	TCGTTTGCCA
501	AAGCGCGCTG	CTCGTCTTTC	AACTGCGTTT	CCAGCTCGGC	AATCCGCGCC
551	TGCAAAATCT	CATAAGCCGG	CTCTGCGGCA	GCCTGTTCTT	GCACACCGCT
601	CGCAATTCTT	ACTGTTTTCG	CGGTTCCGAC	CGCTCTCCAC	TTTTCACCGC
651	CTTCTTCACT	GTTTGTGTGC	TGTGTCTGTT	CGCTCAIATC	GATACCTCTTA
701	AAACAAATTG	GAAATCAAAA	TCCAGTTATT	ACCGCGCAA	GATAAGGACA
751	TTTTCAGAA	ACTTCAAKCA	AAAKCAGAGA	ATTTCAAATT	CATTTTCAAA
801	TCCCTTACCG	AAAAATAAA			

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1.pgp

```

1 MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LLRHRNHSRA
51 QHAVQQRILT LHHTHHGRIE LFACHARLRL MDIRIELTAR FRVDFDLRS
101 IKCFLQILVQS LLHHAHQRIE IAAILQKRHF QIILDRQHFF GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAL LVFQLRFQLG NPLRLQILIS LCGSLFLHTV
201 RISYCFDGFH RLHIFRNFET VLLLCFLFAH VSLKTNWKSX SSYYPRKIRT
251 FSNYFXOKOR INSFSNPLP KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQII	PQTPSGFLLRHRNHSRAQH	AVGQRITL			
g244-1	MPPEARQAGSDGIAALLRSVYTQNALQEINQII	PQTPSGFLPCRNHSRAQHTV	GQGITL			
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRV	DFDLRSIKCFQLVQSHLHAHFQRIE				
g244-1	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFR	IDFLDLRGIKRLLQLIQSHLHTHFQRIE				
	70	80	90	100	110	120

	130	140	150	160	170	180
m244-1.pep	IAALIQKRHFQIILDRQHFGKLLSGELVRI	RNFLLVAAQVLLVCQSAALLVVFQLR	FQ			
	:				: :	
g244-1	ITALIQKRHFQIILDRQHFGKLLSGELVRI	GNFLLVAAQVLLVCQSAQLFVFQLR	FQ			
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRI	SYCFDGFHRLHIFNRF	FTVLLLC	FAHIVSLKT	NWKS	
g244-1	GNPRLQILISRLGGSFLFYTVRI	SYCLDGFHRLHIFNRF	FTVLLLC	FAHIVSLKT	NWKS	
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTF	SRNFXQXQRIS	NFSNPLPKKX			
	:		: :	:		
g244-1	KSGYYPSKIRTF	SRNFKQRQEI	SHPPNTLPQKPYKRX			
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

```
a244-1.seq
1  ATGCCGCTCTG AAGCCCGCACA GCGGGGTTCAC GACGGCATTG CCGCTTTACT
51  TCGATCGGGTT TATACGCAGAA AGCGCGTTCA GGAATAAAAT CAGATTATTC
101 CCCAGACGCC   TTCAGGCTTC  CTTCTGTGCC ACCGTAACCA TAGCGGGGCG
151 CAACACGCGG   TCGGACAGCG TATAACCCTT CTTCATCACG CCCACCACGG
201 TATTGGGTTC   CTGTTCTGTT GCCACCGCCT GCATCGCTCG ATTGATATTC
251 GGATCGAGCT   TATCGCCCGC TTTAGGATTG ATTTCCCTGA TTTGCGTAGC
301 ATCAAAATGCT TCTCGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA   ATTGCGCGTC TGATCCAAAA CGCGCAATTTC CAGATAATCC
401 TTGACCGGCA   GCATTTCCAC GCGAAACATTC TGTCGGGCGA ACTTGTGCGT
451 ATCCGCAATT   TCTGCTGGT  GCGCGCGCGC CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG   TCCTCGCTCT TTCAACTGCG TCTTCAGGTC GCGAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCGTGTT CCTGCACACG
601 GTCCGCAATT   CTTACTGTCT GCACGGTTTC CACGCGCTCC ACATTTTCAA
651 CGGCTTCTTC   ACTGTTTTCG TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTTAAACAAA   TTGAAATCA  AAATCCAGTT ATTACCCGAT CAAGATAAGG
751 ACATTTTCAA   GAAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCTTA   CCGAAAAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pap

1	MPSEARQAGS	DGIAALLRSV	YTONALQEIN	QIIPQTPSGF	LLCHRNHSRA
51	QHAVGQRITL	HLHAHHGIGF	LFACHRLRL	MDIRIELIAR	FRIDFLDELRS
101	IKCFQLQVQS	LLHAHFQRIE	IAALLQKRHF	QIILDQRQHF	GKLLSGELVR
151	IRNFLLVAAA	<u>QVLVLCQSAQ</u>	<u>LLVFLQLRFL</u>	GNPRLQILIS	RLCGSLFLHT
201	VRISYCLDGF	HLRHILFNRF	<u>TKVLLCLFAH</u>	IVSLKTNWKS	KSSYYPRKIR
251	TFSRNFKORO	RHSNFSNPL	PQL*		

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQII	PQTPSGFLLRHRNHSRAQHAVGQRITL				
a244-1	MPSEARQAGSDGIAALLRSVYTQNALQEINQII	PQTPSGFLLCHRNHSRAQHAVGQRITL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHGGIRLLFACHRLHRLMDIRIELIARFRVDF	LDLRSIKCFQLQVLVQSHLHAHFQRIE				
a244-1	LHHAHGGIGFLFACHRLHRLMDIRIELIARFRIDF	LDLRSIKCFQLQVLVQSHLHAHFQRIE				
	70	80	90	100	110	120
	130	140	150	160	170	179
m244-1.pep	IAALIQRHFQIILDRQHFGKLLSGELVRIRNFFL	VAAQVLLVCQSA-LLVFQLRFLQ				
a244-1	IAALIQRHFQIILDRQHFGKLLSGELVRIRNFFL	VAAQVLLVCQSAQLLVFQLRFLQ				
	130	140	150	160	170	180
	180	190	200	210	220	239
m244-1.pep	GNPRLQILISRLCGSLFLHTVRIISYCDG	FHRLHIFNRFFT	VLLCLFAHIVSLKTNWKS			
a244-1	GNPRLQILISRLCGSLFLHTVRIISYCDG	FHRLHIFNRFFT	VLLCLFAHIVSLKTNWKS			
	190	200	210	220	230	240

```

      240      250      260      270
m244-1.pep  KSSYYPRKIRTF SRNFXQXQRISNSFSNPLPKXX
             |||||
a244-1      KSSYYPRKIRTF SRNFKQRQRISNSFSNPLPKXX
             250      260      270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 941>:

```

g246.seq
1  atgtacgggc ggaacggtag tactcaagcg gccgttgctt tcgttttcga
51  ccagacacag cgtgcccgtt tcggcaacgg cgaagtttac gccgctcaag
101 ccgacatcgg cagtgtctga aatatcgcg agggctttgc gggcgaaatcc
151 ggtcagttgg tccacgtcgt ctgtaagcgg tgtgcccagg ttttggtgga
201 acagttcgct gacctgttct ttggttttat ggattgcggg catcacgata
251 tgggtcgggt tttcgctgc catttggaag ataaactcgc ccaagtcgct
301 ttccaccgcc ttaatgcctt ttgcttcaag ataatggttc agctcgattt
351 cttcgctgac catggatttg cctttgacca tcagcttgcc gtttttggct
401 gtgatgatgt cgtggataat ttggcaggct tcggcagggg tttccgcccc
451 gtgtactttc acgcccaact tagtcagggt ttcttccaac tgctccagca
501 gcgcgggtaa

```

This corresponds to the amino acid sequence <SEQ ID 942; ORF 246.ng>:

```

g246.pep
1  MYGRNGSTQA AVAFVFDQTO RARFGNGEVY AAQADIGSAV NIAQGFAGES
51  GQLVHVVCCKR CAEVLVEQFA DLFFGFMDCG HHD MGRFFAC HLDDKLAQVA
101 FHRLNAFCFK IMVQLDFFAD HGFAFDHQLA VFGCDVVDN LAGFGRGFRP
151 VYFHAQLSQV FFQLLQQRG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 943>:

```

m246.seq (partial)
1  ATGCACGGGC GGTACGGTGG TACTCAAGCG ACCGTTgCTT CGTTTTCCAC
51  CAGACACAGC GTACCTGTTT CAGCAACGGC AAAGTTTACG CCACTCAAAC
101 CGACATCGGC AGTGCTGTAA ATATCGCGCA GTGCTTTACG GGCGAAGCCG
151 GTCAGTTGGT CTACATCGTC TGTCAGCGGC GTACCGAGGT TTTGGTGGA
201 CAGTTCGCTA ACCTGTTCTT TGGTTTGTG GATAGCAGGC ATCAGGATAT
251 GGGTCGGTTT TTCGCCTGCC ATTTGGACGA TGAACTCGCC CAAGTCGCTT
301 TCTACCGCTT TAATGcyTTT TGCTTCAAGA TAATG-TTCA GCTCGATTTC
351 CTCGCTGACC ATCGATTGTC CTTTGACCAT CAGCTTGCCG TTTTGGCTG
401 TGATGATGTC GTGGATAATT TGGCAGGCTT CGGTCGGGGT TTCTGCCCG...

```

This corresponds to the amino acid sequence <SEQ ID 944; ORF 246>:

```

m246.pep (partial)
1  MHGRYGGTQA TVAFVFHQTO RTCFSNGKVY ATQTDIGSAV NIAQCFTEGA
51  GQLVYIVCQR RTEVLVEQFA NLFFGFVDSR HHD MGRFFAC HLDDELAQVA
101 FYRFNAFCFK IMXQLDFLAD HRFAFDHQLA VFGCDVVDN LAGFGRGFCP...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 246 shows 80.0% identity over a 150 aa overlap with a predicted ORF (ORF 246.ng) from *N. gonorrhoeae*:

```

m246/g246
      10      20      30      40      50      60
m246.pep  MHGRYGGTQATVAFVFHQTO RTCFSNGKVYATQTDIGSAVNIAQCFTEAGQLVYIVCQR
           |||  |||:|||||  |||:  |||:||||:|||||  |||:||||:|
g246      MYGRNGSTQA AVAFVFDQTORARFGNGEVYAAQADIGSAVNIAQGFAGESGQLVHVVCCKR
           10      20      30      40      50      60

      70      80      90      100     110     120
m246.pep  RTEVLVEQFANLFFGFVDSRHHD MGRFFACHLDDELAQVAFYRFNAFCFKIMXQLDFLAD
           :|||||:||||:|  |||:|||||:||||:|  |||:|  |||:|
g246      CAEVLVEQFADLFFGFMDCGHHD MGRFFACHLDDKLAQVAFHRLNAFCFKIMVQLDFFAD

```

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	70	80	90	100	110	120
m246 . pep	130	140	150			
	HRFAFDHQLAVFGCDDVVDNLAFGRGFCP					
g246	HGFAFDHQLAVFGCDDVVDNLAFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246 . seq (partial)

```

1  ATGCACGGGC  GGAACGGTGG  TACTCAAGCG  ACCGTTGCCT  TCGTTTTCCA
51  CCAGACACAG  CGTACCTGTT  TCAGCAACGG  CGAAGTTCAC  GCCACTCAAA
101 CCGACATCGG  CAGTGTCTGT  AATATCGCGC  AGTGCTTTAC  GGGCGAAGCC
151 GGTCAGTTGG  TCTACGTCGT  CCGTTAACGG  TGTGCCGAGG  TTTGGTGGGA
201 ACAGTTCGCT  AACCTGTTCT  TTGGTTTTAT  GGATTGCGGG  CATCACGATA
251 TGGGTCGGTT  TTTCACCTGC  CATTGAGCG  ATGAAGTCGC  CCAAGTCGCT
301 TTCCACCGCT  TTAATGCCTT  TTGCTTCAAG  ATAATGGTTC  AGCTCGATT
351 CCTCGCTGAC  CATCGATTG  CCTTTGACCA  TCAGCTTGCC  GTTTTGGCT
401 GTGATGATGT  CGTGGATGAT  TTCGCAGGCT  TCGGCCGGTG  TTCCGCCCA
451 GTGTACTTTT  ACGCCCAACT  TGTCAGGTT  TTCTTCAGC  TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246 . pep (partial)

```

1  MHGRNNGTQA  TVAFVFHQQT  RTCFSNGEVH  ATQTDIGSAV  NIAQCFTGEA
51  GQLVYVVR*R  CAEVLVEQFA  NLFFGFMDCG  HHDMGRFFTC  HLDDELAQVA
101 FHRFNAFCFK  IMVQLDFLAD  HRFAFDHQLA  VFGCDDVDD  FAGFGRCFRP
151 VYFYAQLGQV  FFQLLQQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246 . pep	MHGRYGGTQATVAFVFHQQTQRTCFNSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNNGTQATVAFVFHQQTQRTCFNSNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
m246 . pep	70	80	90	100	110	120
	RTEVLVEQFANLFFGFVDSRHDMGRFFACHLDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFACHLDELAQVAFHRFNAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
m246 . pep	130	140	150			
	HRFAFDHQLAVFGCDDVVDNLAFGRGFCP					
a246	HRFAFDHQLAVFGCDDVDDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247 . seq

```

1  atgaaacgta  aaatgctaaa  cgtaccaaag  ggcgggttatg  atggtatgaa
51  ggggtttacc  attggtgaat  ttctggttgc  gggcctgctc  agtataattg
101 tcctgatagc  ggtcgatcgc  agttacttta  catcccgga  attaaatgat
151 gtggcaaacg  agcgtcttgc  cattcaacag  gatttgcgga  atgcggcaac
201 attaattgtc  cgcgatgcaa  gaatggcggg  gagcttcggt  tgtttcaata
251 tgtccgagca  tactaaagac  gatattgttg  attcaagtaa  tcaaactcaa
301 tctaaccctg  caaaaccggg  tgccaaacaa  gaaaatcccc  ttttttcctt
351 aaaaaggagc  ggcattggata  aacaactgat  tcccgttgct  gaatccatag
401 atattaaata  tccgggtttt  atccagcgcc  ttaacgcatt  ggttttccaa
451 tacggtatcg  atgatcttga  tgcgagtgc  gagactgttg  tagtcagcag
501 ctggtccaaa  atagcaaaac  cgggtaagaa  aatatctacc  ttgcaagaag
551 caaagagtgc  attacagatt  actaatgatg  ataaacaaaa  tggaaatatc

```

```

601 accgcgcaga aacatgtggt caatgcctat gcggtcgcca ggtttggcaa
651 taatgaggaa agtttggtcc gcttccaatt ggatgataag ggcaagtggg
701 gtaatcctca gttgctcgtg aaaaaggtta aacgtatgga tgtgcggtat
751 atttatgttt ccggttgctc tgaagatgaa gatgccggca aagaggaaaa
801 attcagatat acgaataaat tcgacaaatc caaaaatgct gttacgcctg
851 ccggggtgga ggttttattg tgatgcggcc ttaatgccaa gattgccgct
901 tcttcagaca atagtattta tgctaccgtt atcaatgcga caatacgcgg
951 gggaaatgta tgcgcaaaaca qaacactttg a

```

This corresponds to the amino acid sequence <SEQ ID 948; ORF 247.ng>:

g247.pap

1	MKRKMLNVPK	GGYDGMKGFT	IVEFLVAGLL	SIIVLIAVVS	SYFSTRKLND
51	VANERLAIQQ	DLRNAATLIV	RDARMAGSFG	CFNMSEHTKD	DIVDSSNQQT
101	SNLAKPGAQK	ENPLFSLKRS	GMDKQLIPVA	ESIDIKYPGF	IQRLNALVFQ
151	YGIDDLDASA	ETVVVSSCSK	IAKPGKKIST	LQEAKSALQI	TNDDKQNGNI
201	TRQKHVVNAY	AVGRFGNNEY	SLFRFQLDDK	GKWGNPQLLV	KKVKRMDVRY
251	IYVSGCFEDE	DAGKEEFRY	TNKFDSKSKNA	VTPAGVEVLL	DSGLNAKIAA
301	SSDNSIYAYR	INATIEGRGNV	KANRTL*		

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 949>:

m247.seq (partial)

1	ATsAGACGTA	AAATGCTAAA	CGTwsyArAA	GGCAGTTATG	ATGGTATGAA
51	AGGTTTATACC	ATTATGAAT	TTTtGGTTGC	GGGCTGTCTC	AGTATGATTG
101	TCCTGATTGGC	GGTCGGATCG	AGTtACTTCA	CATCCCGGAA	ATTAAATGAT
151	CGGGCAAACG	AGCGCTTTGC	CGCGCAACAG	GATTtGCGGA	ATGCCCGCAAC
201	ATTGATTGTCT	CGCGATGCGA	GAATtGGCAGG	CGGCTtCCGT	TGTTTCAATA
251	TGTCCGAGCA	TCCTGCAACT	GATGTTATTC	CCGATACGAC	GCAACAAAAT
301	TCTCCTTTTT	CCTTAAAAAG	GAACGGTATA	GATAAACTTA	TCCCATAGC
351	GGAACTCTTCA	AATATCAATT	ATCAGAATTt	TTTCCAGGTT	GGTAGCGCAT
401	TGATTTTTCAT	ATACGGAAATC	GATCATGTTA	ATGCAAGCAC	CGCGACTACC
451	GTCGTACGCA	GCTGTGCCGC	AATATCGAAA	CCGGGCAAGC	AAATCCCTAC
501	TTTAGAAGAT	GCAAAAAAAG	AATTGAAGAT	TCCGGATCAG	GATAAGGAGC
551	AAAATGGCAA	TATAGCGCGT	CAAAGGCTATG	TGGTCAATGC	CTATGCCGTC
601	GGCAGGATTG	CCGATGAGGA	AGGTTTGTTT	CGCTTCCAAT	TGGATGATAA
651	GGGCAAGTGG	GGTAATCCTC	AGTTGC...		

This corresponds to the amino acid sequence <SEO ID 950; ORF 247>:

m247.pep (partial)

1	XRRKMLNVXX	GSYDGMKGFT	IIIEFLVAGLL	SMIVLMVGS	SYFTSRKLND
51	AANERLAAQQ	DLRNRATLIV	RDARMAGGFG	CFNMSEHPAT	DVIPDTTQON
101	SPFSLKRNGI	DKLPIAESS	NINYQNFFQV	GSALIFQYGI	DDVNASATT
151	VVSSCAAISK	PGKIPTLED	AKKELKIPDQ	DKEQNGNIAR	QRHVVNAYAV
201	GRIADEESLF	RFQLDDKGKW	GNPOL...		

**Computer analysis of this amino acid sequence gave the following results:**

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng) from *N. gonorrhoeae*:

m247/q247

	10	20	30	40	50	60
m247.pep	XRRKMLNVXGSGYDGMKGFTIIIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAANERLAAQQ					
	: : : :	: : : : : : : : :	: : : : : : : : :	: : : :	: : : : : : : : :	: : : :
g247	MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSIIVLIAVVSSTSRKLNVDVANERLAIQQ					
	10	20	30	40	50	60
	70	80	90		100	
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNSPFSLKRN					
	: : : : : : : : : : : :	: : : : : : :	: :	: : : :	: : : :	: : : :
g247	DLRNAATLIVRDARMAGSFGCFNMSEHTKDDIVDSSNQTSNLAKPGAQENFLFSLKRS					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	GIDK-LIPIAESSNINYQNFFQVGSALIFQYGIDVDNASTATTVVSSCAAISKPGKQIPT					
	: :	: : : :	: : :	: : :	: : : : : : :	: : : : : : :

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```

g247      GMDKQLIPVAESIDIKYPGFIQRLNALVFQYGIDDLASAETVVVSSCSKIAKPGKKIST
           130           140           150           160           170           180

m247.pap  170           180           190           200           210           220
LEDAKKELKIPDQDKEQNGNIARQRHVVNAYAVGRIAD-EESLFRFQLDDKGKWNPNQL
|::||: |:| ::|| ||||:|::| |||||:::| ||||| ||||| ||||| |||||
g247      LQEAKSALQITNDDK-QNGNITRQKHVVNAYAVGRFGNNEESLFRFQLDDKGKWNPNQLL
           190           200           210           220           230

g247      VKKVKRMDVRYIYVSGCPEDEDAGKEEFYRNTKFKDSKNAVTPAGVEVLLDSGLNAKIA
           240           250           260           270           280           290

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 951>:

```

a247.seq
  1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCATGCCT  AGTATGATTG
101 TCCTGATGGC  GGTCCGATCG  AGCTACTTCA  CATCCCAGAA  ATTAATATGAT
151 CGGGCAAACG  AGCGTCTTTC  CGGCAACACG  GATTTCGCGA  ATGCGCGAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGCTTCGGT  GTTTTCAATA
251 TGTCCGAGCA  TACTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAAC
301 CAACATGTCC  CTGTAAAAAC  CGGTGCCAAA  CAGAAAAATC  CCTTTTTTTC
351 TTTAGAGTGG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAAATTGA
401 TTCTTATTCG  TGAATCCACA  GATATTAAT  ATCCGGGTTT  TGCCCAAGCT
451 CGTCCGGCAT  TGATTTTCCA  ATACGGCATC  GATGATCTTG  ATGCGAGTGC
501 TGAGACTGTT  GTAGTCAGCA  GCTGTTCCAA  AATAGCAAAA  CCGGGTAAGA
551 AAATATCTAC  CTTGCAAGAA  GCAAGAGAGT  CATTACAGAT  TACTAATGAT
601 GATAACAAAA  ATGGAATAT  CACCCGTCAA  AGGCATGTGG  TCAATGCCTA
651 TCGCGTCGGC  AGGATTGCCG  GTGAGGAAG  TTTGTTCCGC  TTCCAATTGG
701 ATGATAAGGG  CAAGTGGGGT  AATCCTCAGT  TGCTCGTGAA  AAAGATTAGA
751 CATATGAAAG  TGCGGTATAT  CTATGTTTCC  GACTGTCCTG  AAGATGACGA
801 TGCCGGCAAA  GAGGAAAAAT  TCAATATATC  GGGTACATTG  GACAGCTCCA
851 CAAATGCTGT  TACGCCCCGC  GGGGTGGAGG  TTTTATTGAG  TANCGGTACT
901 GATACCAAGA  TTGCCGCTTC  TTCAGACAAT  CATATTTATG  CTTACCGTAT
951 CGATCGGACA  ATACGCGGGG  GAAATGTATG  CGCAACACGA  ACACTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 952; ORF 247.a>:

```
a247.pep
  1  MRRKMLNVPK  GNYDGMKGFT  IIEFLVAGML  SMIVLMAVGS  SYFTSRKLNQ
51  AANERLSAAQ  DLRNAATLIV  RDARMAGGFG  CFNMSEHTKN  DIIVDPSSKQT
101 QHPVPKPGAK  QENPLFSLEW  ANTNTNNNT  AKLPIAEST  DIKYPGFAQA
151 RPALIFQYGI  DDLDAEATV  VVSSCSKIAK  PGKKISTLQE  AKSALQITND
201 DKQNGNITRV  RHVVNAYAVG  RIAGEEGLFR  FLDLDDKGWG  NPQLLVKKIR
251 HMKVRYIYVS  DCPEDDDAGK  EEKFYTGTF  DSSTNAVPTA  GVEVLLSXGT
301 DTKIAASDND  HIYAYRIDAT  IRGNVNCANR  TL*
```

m247/a247 70.9% identity in 244 aa overlap

```

      10      20      30      40      50      60
m247.pep  XRRKMLNVXKSGSYDGMKGFTIIIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAAANERLAAQQ
          ||||| |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a247      MRRKMLNVPKGNVDGMKGFTIIIEFLVAGMLSMIVLMAVGSSYFTSRKLNDAAANERLSAQQ
          10      20      30      40      50      60

      70      80      90      100
m247.pep  DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQONSPFSLK-
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a247      DLRNAATLIVRDARMAGGFGCFNMSEHTKNDIIVDPSKQTQHVVPVKGPAGAKQENPLFSLEW
          70      80      90      100      110      120

      110      120      130      140      150      160
m247.pep  -----RNGIDKLIPIAESSNINYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISK
          |: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a247      ANTNTNTNNTAKLIPIAESTDIKYPGAQARPALIFQYGIDDLASAETVVVSSCSKIAK
          130      140      150      160      170      180

```

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	170	180	190	200	210	220
m247.pep	PGKQIPTLED AKKELKIPDQDKEQNGNIARQRHVVNAYAVGRIADEESLFRFQLDDKGKW					
a247	PGKKISTLQEA KSALQITNDDK-QNGNITRQRHVVNAYAVGRIAGEEGLFRFQLDDKGKW					
	190	200	210	220	230	
m247.pep	GNPQL					
a247	GNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKYTGTFDSSTNAVTPAGVEVLLSXG					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

g247-1.seq (partial) ..

1	CCCGGTGCCA	AACAAGAAAA	TCCCCTTTT	TCCTTAAAA	GGAGCGGCAT
51	GGATAAACAA	CTGATTCCCG	TGCTGAATC	CATAGATATT	AAATATCCGG
101	GTTTTATCCA	GCGCCTTAAC	GCATTGGTTT	TCCAATACGG	TATCGATGAT
151	CTTGATGCGA	GTGCTGAGAC	TGTTGTAGTC	AGCAGCTGTT	CCAAAATAGC
201	AAAACCGGGT	AAGAAAATAT	CTACCTTGCA	AGAAGCAAAG	AGTGCATTAC
251	AGATTACTAA	TGATGATAAA	CAAAATGGAA	ATATCACCCG	TCAGAAACAT
301	GTGGTCAATG	CCTATGCGGT	CGGCAGGTTT	GGCAATAATG	AGGAAAGTTT
351	GTTCCGCTTC	CAATTGGATG	ATAAGGGCAA	GTGGGGTAAT	CCTCAGTTGC
401	TCGTGAAAA	GGTTAAACGT	ATGGATGTGC	GGTATATTTA	TGTTCCCGGT
451	TGTCCTGAAG	ATGAAGATGC	CGGCAAAGAG	GAAAAATTCA	GATATACGAA
501	TAAATTCGAC	AAATCCAAAA	ATGCTGTTAC	GCCTGCCGGG	GTGGAGGTTT
551	TATTGGATAG	CGGCCTTAAT	GCCAAGATTG	CCGCTTCTTC	AGACAATAGT
601	ATTTATGCTT	ACCGTATCAA	TGCGACAATA	CGCGGGGGAA	ATGTATGCGC
651	AAACAGAAC	CTTTGA			

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

g247-1.pep (partial) ..

1	PGAKQENPLF	SLKRSGMDKQ	LIPVAESIDI	KYPGFIQRLN	ALVFQYIGIDD
51	LDASAEVTVV	SSCKIAKPG	KKISTLQEAK	SALQITNDDK	QNGNITRQKH
101	VVNAYAVGRF	GNNEESLFRF	QLDDKGKWN	PQLLVKKVKR	MDVRYIYVSG
151	CPEDEDAGKE	EKFRTYNKFD	KSKNAVTPAG	VEVLLDSGLN	AKIAASSDNS
201	IYAYRINATI	RGGNVCANRT	L*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

m247-1.seq

1	ATGAGACGTA	AAATGCTAAA	CGTACCAAAA	GGCAGTTATG	ATGGTATGAA
51	AGGTTTTACC	ATTATTGAAT	TTTTGGTTGC	GGGCCGTGTC	AGTATGATTG
101	TCCGTGATGC	GGTCGGATCG	AGTTACTTCA	CATCCCGGAA	ATTAATGAT
151	GCGGCAACAG	AGCGTCTTGC	CGCGCAACAG	GATTTGCGGA	ATGCGGCAAC
201	ATTGATTGTC	CGCGATGCGA	GAATGGCAGG	CGGCTTCGGT	TGTTTCAATA
251	TGTCGAGCA	TCCTGCAACT	GATGTTATTC	CCGATACGAC	GCAACAAAAAT
301	TCTCCTTTT	CCTTAAAAAG	GAACGGTATA	GATAAACTTA	TTCCTATAGC
351	GGAATCTTCA	AATATCAATT	ATCAGAATTT	TTTCCAGGTT	GGTAGCGCAT
401	TGATTTTTCA	ATACGGAATC	GATGATGTTA	ATGCAAGCAC	CGCGACTACC
451	GTCGTCAGCA	GCTGTGCCGC	AATATCGAAA	CCGGGCAAGC	AAATCCCTAC
501	TTTAGAAGAT	GCAAAAAAAG	AATTGAAGAT	TCCGGATCAG	GATAAGGAGC
551	AAAAATGGCA	TATAGCGCGT	CAAAGGCATG	TGGTCAATGC	CTATGCGGTC
601	GGCAGGATTG	CCGATGAGGA	AGGTTGTTC	CGCTTCCAAT	TGGATGATAA
651	GGGCAAGTGG	GGTAATCCTC	AGTTGCTCGT	GAAAAAGGTT	AGACATATGA
701	AAGTGCGGTA	TATCTATGTT	TCCGGCTGTC	CTGAAGATGA	CGATGCCGGC
751	AAAGAGGARA	CATTCAAATA	TACGGATAAA	TTTCGACAGC	CCCAAAATGC
801	TGTTACGCCC	GCCGGGGTGG	AGGTTTATT	GAGTAGCGGT	ACTGATACCA
851	AGATTGCCGC	TTCTTCAGAC	AATCATATTT	ATGCTTACCG	TATCGATGCG
901	ACAATACGCG	GGGGAATGT	ATGCGCAAC	AGAACACTTT	GA

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

m247-1.pep

1	MRRKMLNVFK	GSYDGMKGFT	IIIEFLVAGLL	SMIVLMAVGS	SYFTSRKLND
51	AANERLAAQQ	DLRNAATLIV	RDARMAGGFG	CFNMSEHPAT	DVIPDTTQQN
101	SPFSLKRNGI	DKLIPIAESS	NINYQNFFQV	GSALIFQYGI	DDVNASTATT
151	VVSSCAAIK	PGKQIPTLED	AKKELKIPDQ	DKEQNGNIAR	QRHVVNAYAV
201	GRIADEEGLF	RFQLDDKGKW	GNPQLLVKKV	RHMKVRYIYV	SGCPEDDDAG
251	KEETFKYTDK	FDSAQNAVTP	AGVEVLLSSG	TDTKIAASSD	NHIYAYRIDA
301	TIRGGNVCAN	RTL*			



569

m247-1 / g247-1 72.1% identity in 222 aa overlap

```

              70      80      90      100      110      120
m247-1.pep  NAATLIVRDARMAGGFGCFNMSEHPATDVIPDTTQQNSPFSCLKRNGIDK-LIPIAESSNI
g247-1              PGAKQENPLFSLKRSMDKQLIPVAESIDI
                      10      20      30

              130      140      150      160      170      180
m247-1.pep  NYONFFQVGSALIFQYIGDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDK
g247-1      KYPGFIQRLNALVFQYIGDDLDASAETVVVSSCSKIAKPGKKISTLQEAKSALQITNDDK
                      40      50      60      70      80      90

              190      200      210      220      230      240
m247-1.pep  EQNGNIARQRHVVNAYAVGRIAD-EEGLFRFQLDDKGKGNPQLLVKKVRHMKVRYIYVS
g247-1      -QNGNITRQKHVVNAYAVGRFGNNEESLFRFQLDDKGKGNPQLLVKKVRMDVRYIYVS
                      100      110      120      130      140

              250      260      270      280      290      300
m247-1.pep  GCPEDDDAGKEETFKYTDKFDQAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDAT
g247-1      GCPEDDAGKEEFKFRYTNKFDKSKNAVTPAGVEVLLDGLNAKIAASSDINSIYAYRINAT
                      150      160      170      180      190      200

              310
m247-1.pep  IRGGNVCANRTLX
g247-1      IRGGNVCANRTLX
                      210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

a247-1.seq (partial)

```

1  AATAATACAG CTAATTGAT TCCTATTGCT GAATCCACAG ATATTAAATA
51  TCCGGGTTTT GCCCAGGCTC GTCCGGCATT GATTTTCCAA TACGGCATCG
101 ATGATCTTGA TGCGAGTGCT GAGACTGTTG TAGTCAGCAG CTGTTCCAAA
151 ATAGCAAAAC CGGGTAAGAA AATATCTACC TTGCAAGAAG CAAAGAGTGC
201 ATTACAGATT ACTAATGATG ATAAACAAAA TGGAAATATC ACCCGTCAAA
251 GGCATGTGGT CAATGCCTAT GCGGTCGGCA GGATTGCCGG TGAGGAAGGT
301 TTGTTCCGCT TCCAATTGGA TGATAAGGGC AAGTGGGGTA ATCCTCAGTT
351 GCTCGTGAAA AAGATTAGAC ATATGAAAGT GCGGTATATC TATGTTCCCG
401 ACTGTCCTGA AGATGACGAT GCCGGCAAAG AGGAAAAATT CAAATATACG
451 GGTACATTCG ACAGCTCCAC AAATGCTGTT ACGCCCGCCG GGGTGGAGGT
501 TTTATTGAGT AGCGGTACTG ATACCAAGAT TGCCGCTTCT TCAGACAATC
551 ATATTTATGC TTACCGTATC GATGCGACAA TACGCGGGGG AAATGTATGC
601 GCAAACAGAA CACTTTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 958; ORF 247-1.a&gt;:

a247-1.pep (partial) ..

```

1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLASA ETVVSSCSK
51  IAKPGKKIST LQEAQSALQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQLDDKG KWGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEFKYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIYAYRI DATIRGGNVC
201 ANRTL*

```

m247-1 / a247-1 80.6% identity in 206 aa overlap

```

              10      20      30
a247-1.pep  NNTAKLIPIAESTDIKYPGFAQARPALIFQ
m247-1      GFGCFNMSEHPATDVIPDTTQQNSPFSCLKRNGIDKLIPIAESSNINYNQFFQVGSALIFQ
              80      90      100      110      120      130

              40      50      60      70      80      89
a247-1.pep  YGIDDLASAETVVVSSCSKIAKPGKKISTLQEAQSALQITNDDK-QNGNITRQRHVVN
m247-1      YGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVN
              140      150      160      170      180      190

              90      100      110      120      130      140      149
a247-1.pep  YAVGRIAGEEGLFRFQLDDKGKGNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKY

```

570

```

m247-1      YAVGRIADEEGLFRFQLDDKGKWNPNQLLVKKVRHMKVRYIYVSGCPEDDDAGKEETFKY
            200      210      220      230      240      250

a247-1.pep  150      160      170      180      190      200
            TGTFDSSSTNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            |  |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m247-1      TDKFDSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            260      270      280      290      300      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

```

g248.seq
1   atgcgcaaac agaacacttt gacaggaatc ccgacttctg acggacagag
51  ggggtccgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgccgccagc tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggtcttgcc
201 ggagggcgaa tttcagggtt tggatttggg atatgctgag gacagtaagg
251 ttacgtttag cgaaaactgt gaaaaaggct tgtgtaccgc agtgaatgtg
301 cggacaaata ataattgtag tgaagaggct tttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttcttgccct gcaaagtctg
401 gcaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aaaggcgagg caggcgctcag caaatgcccg cgctatatta tcgaatatct
501 aggcgtgaag aacggacaaa atgtttatcg gggtactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcaataat
601 gatgagcaat aa

```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

```

g248.pep
1   MRKQNTLTGI PTSDGQRGSA LFIVLMVMIV VAFLVVTAAG SYNTEQRISA
51  NESDRKLALS LAEALREGE FQVLDLEYAA DSKVTFSENC EKGLCTAVNV
101 RTNNGSEEA FGNIVVQKPK AVEAVKRSCP AKSGKNSTDL CIDNKGMEYN
151 KGAAGVSKMP RYIIYLGVK NGQNVYRVTA KAWGKNANTV VVLQSYVGN
201 DEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

```

m248.seq (partial)
1   ..GGGTTGAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.TyWT
51  gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTkCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGTCTT TGGCCGAGkC GkCTwTGCGG
151 GAAGGCGAAC TTCAGGTTTT GGATTGGAA TATGATACGG ACAGTAAGGT
201 TACATTTAGC GAAACTGTG GAAAAGGTCT GTsTGCCGCA GTGAATGTGC
251 GGACAAATAA TGATAATGAA GAGGCTTTTG ACAATATCGT GGTGCAAGGC
301 AAGCCCACCG TTGAGGCGGT GAAGCGTTCT TGCCCTGCAA ATTCTACCGA
351 CCTGTGCATT GACAAGAAAG GGwTGGAATA TAAGAAAGGC ACGAGAAGCG
401 TCAC.AAAAT GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGAACGGA
451 GAAATGTTT ATCGGGTTAC TGCCAAGGCT TGGGGtAAGA ATGCCAATAC
501 CGTGGTCGTC CTTCAATCTT ATGTAAGCAA TAATGATGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

```

m248.pep (partial)
1   ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISXNESDRKL AXSLAEXXXR
51  EGELQVLDLE YDTSKVTFS ENCGKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS CPANSTDLCI DKKGKEYKKG TRSVTKMPRY IIEYLGvXNG
151 ENVYRVTAKA WGKNANTVVV LQSYVSNND *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248/g248

```

m248.pep
            10      20      30      40
GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
|  ||:|||| |||| | ||||| ||||| ||||| |||||

```

571

```

g248      MRKQNTLTGIPTSDGQRGSALFIVLMVMIVVAFVLTAAQSYNTEQRISANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGLXAAVNVRTNND-NEEAFDNIVVQGKP
           |||  |||:||||| :||||||| ||| :|||||: :||| |||||
g248      LAEALREGEFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNGSSEAFGNIVVQGKP
           70      80      90      100      110      120

           110      120      130      140      150
m248.pep  TVEAVKRSCPA----NSTDLCIDKKGXKEYKKGTRSVTKMPRYII EYLVGXNGENVYRVTA
           :||||||| |||||:| |||:| :|:||||||| |||:|||||
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYII EYLVGXNGQNVYRVTA
           130      140      150      160      170      180

           160      170      180
m248.pep  KAWGKNANTVVVLQSYVSNINDEX
           |||||:||||
g248      KAWGKNANTVVVLQSYVGNDEQX
           190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAAAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAAATGT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVLTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQKPT VEAVKRSCA KSTGLCIDNK GMEYKKGTS
151 VSKMPRYIIE YLVGXNGENV YRVTAWGWK NANTVVVLQS YVSNND*

```

m248/a248 89.4% identity in 180 aa overlap

```

m248.pep      GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
               |||:||||| |||| | ||||| ||||| ||||| |
a248          MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLTAAQSYNTEQRISANESDRKLALS
               10      20      30      40      50      60

               50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGLXAAVNVRTNNDNEEAFDNIVVQGKPT
           |||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      LAEALREGEFQVLDLEYDTSKVTFSENCGLXAAVNVRTNNDNEEAFDNIVVQGKPT
           70      80      90      100      110      120

               110      120      130      140      150      160
m248.pep  VEAVKRSCPANSTDLCIDKKGXKEYKKGTRSVTKMPRYII EYLVGXNGENVYRVTAWGWK
           ||||| :|| ||||:| ||||:|: ||||| ||||| ||||| ||||| |||||
a248      VEAVKRSCAKSTGLCIDNKGMEYKKGTSVSKMPRYII EYLVGXNGENVYRVTAWGWK
           130      140      150      160      170      180

               170      180
m248.pep  NANTVVVLQSYVSNINDEX

```

a248

|||||  
NANTVVVLQSYVSNINDEX  
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq

```
1 ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51 GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAGGTC TGTGTCCCGC AGTGAATGTG
301 CGGACAATA ATGATAATGA AGAGGCTTT GACAATATCG TGGTCAAGG
351 CAAGCCACC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA
```

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep

```
1 MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVLVTTAAQ SYNTEQRISA
51 NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQKPT VEAVKRSCPA NSTDLCIDKK GMEYKKGTRS
151 VSKMPRYIIE YLGVKNGENV YRVTAKEWK NANTVVVLQS YVSNDE*
```

m248-1/g248 89.1% identity in 202 aa overlap

```
10 20 30 40 50 60
m248-1.pep MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS
g248 MRKQNTLTGIPTSDGQRGSALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS
10 20 30 40 50 60

70 80 90 100 110 119
m248-1.pep LAEALREGELQVLDLEYDTDSKVTFSNCGKGLCAAVNVRTNND-NEEAFDNIVVQKGP
g248 LAEALREGEFQVLDLEYAADS KVTFSNCKGLCTAVNVRTNNGSEAFGNIVVQKGP
70 80 90 100 110 120

120 130 140 150 160 170
m248-1.pep TVEAVKRSCPA----NSTDLCIDKKGMEYKKGTRSVSKMPRYIIEYLGKNGENVYRVTA
g248 AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYIIEYLGKNGQNVYRVTA
130 140 150 160 170 180

180 190
m248-1.pep KAWGKNANTVVVLQSYVSNINDEX
g248 KAWGKNANTVVVLQSYVGNNDQX
190 200
```

m248-1/a248 97.0% identity in 197 aa overlap

```
10 20 30 40 50 60
m248-1.pep MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS
a248 MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS
10 20 30 40 50 60

70 80 90 100 110 120
m248-1.pep LAEALREGELQVLDLEYDTDSKVTFSNCGKGLCAAVNVRTNNDNEEAFDNIVVQKGP
a248 LAEALREGELQVLDLEYDTDSKVTFSNCGKGLCTAVNVRTNNDNEEAFDNIVVQKGP
70 80 90 100 110 120

130 140 150 160 170 180
m248-1.pep VEAVKRSCPANSTDLCIDKKGMEYKKGTRSVSKMPRYIIEYLGKNGENVYRVTAKEWK
a248 VEAVKRSCSTAKSTGLCIDNKGMEYKKGTSVSKMPRYIIEYLGKNGENVYRVTAKEWK
130 140 150 160 170 180
```

```

              190
m248-1.pep  NANTVVVLQSYVSNNDEX
              |||||
a248        NANTVVVLQSYVSNNDEX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

```

g249.seq
1  atgaagaata atgattgctt gcgcctgaaa aatccccagt ccggtatggc
51  gttgatagaa gtcttggtcg ctatgctcgt tctgaccatc ggtattttgg
101 cattgctgtc cgtacagttg cggacagtcg cttccgtcag ggaggcggaa
151 acgcaaacca tcgtcagcca aatcacgcaa aacctgatgg aaggaatggt
201 gatgaatccg accattgatt tggacagcaa caagaaaaac tatagtcttt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgcttgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tgccggatgc ggtagctatt cattacgccg
401 tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcggtgct
451 ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagtgag cggcgacaat atcgtatata cctatcaggc aagggtcggg
601 ggtcgtgaat ga

```

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

```

g249.pep
1  MKNNDCLRLK NPQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDLDSNKK N YSLYMGKQTL SAVDGEFMLD
101 AEKSKAQLAE EQLKRFSHEL KNALPDAVAI HYAVCKDSSG DAPTLSDSGA
151 FSSNCDNKAN GDTLIKVLWV NDSAGDSDIS RTNLEVSGDN IVITYQARVG
201 GRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

```

m249.seq
1  ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CGGACAGTCN NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATT TGCATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTAG
351 TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTTCGCAG GGGATTCGGA TATTTCCTCGT ACGAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTTCGAGGT
601 CGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

```

m249.pep
1  MKNNDCFRLK DSQSGMALIE VLVAMLVLT I GILALLSVQL RTVXXXXXXXX
51  XXXXXXXXXXX XLMEGMLMNP TIDSDSNKK N YNLYMGNHTL SAVDGDFAID
101 AMKTKGQLAE AQLKRFSYEL KNALPDAAAI HYAVCKDSSG NAPTLSGNAF
151 SSNCDNKANG DTLIKVLWVN DSAGDSDISR TNLEVSGDNI VITYQARVGG
201 RE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

m249/g249

```

              10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXX
           |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

574

```

g249      MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     120
m249.pep  XLMEGMLMNPIDSDSNKKNYNLYMGNHTLSAVDGDFAIDAMKTGQLAEALKRFSYEL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      NLMEGMLMNPIDLSDSNKKNYSLYMGKQTL SAVDGEFMLDAEKSQAQLAEELKRFSHEL
           70      80      90      100     110     120

           130     140     150     160     170     179
m249.pep  KNALPDAAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVND SAGSDSDI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      KNALPDAAAIHYAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLWVND SAGSDSDI
           130     140     150     160     170     180

           180     190     200
m249.pep  RTNLEVSGDNIVYTYQARVGGREX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      RTNLEVSGDNIVYTYQARVGGREX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```

a249.seq
1  ATGAAGAATA ATGATTGCTT CCGCCTGAAA AACCCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGGTCG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTTCAGTTG CGGACAGTCG CTTCCGTCAG GGAGGCAGAG
151 ACGCAAACCA TCGTCAGTCA AATCAGCAGAA AACCTGATGG AAGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATCATGCA CTATCAGTTG TGGATGGCGA TTTTCAGGTT
301 GATGCCATAA AAAC TAAGAC GCAGTTGGCA GAGGCACAAT TGAAGAGATT
351 TAGTTATGAG CTGAAAAATG CCTTGCCGGA TGCGGCAGCC ATCCATTACG
401 CCGTCTGCAA GGATTCGTCG GGTGTTGCGC CGACATTGTC CGCCGGCAGT
451 ACTTTTCTT CAAATTGCGA TGGTAGTGCA AATGGGGATA CTTTGATTAA
501 AGTATTGTGG GTAAATGATT CGGCAGGGGA TTCGGATATC GCCCGTACGA
551 ATCTTGAGAC GAACGGCAAC AATATCGTAT ATACCTATCA GGCAAGGGTC
601 GGAGGTCGGG AATGA

```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

```

a249.pep
1  MKNNDCFRLK NPQSGMALIE VLVAMLVLTIGILALLSVQL RTVASVREAE
51  QTIVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHHA LSVVDGDFQV
101 DAIKTKTQLA EAQLKRFSYE LKNALPDAAA IHYAVCKDSS GVAPTLSAGS
151 TFSSNCDGSA NGDTLIKVLW VND SAGSDSI ARTNLETNGN NIVYTYQARV
201 GRE*

```

m249/a249 81.9% identity in 204 aa overlap

```

           10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      MKNNDCFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     119
m249.pep  XLMEGMLMNPIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAEALKRFSYE
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      NLMEGMLMNPIDSDSNKKNYNLYMGNHHALSVVDGDFQVDAIKTKTQLAEALKRFSYE
           70      80      90      100     110     120

           120     130     140     150     160     170
m249.pep  LKNALPDAAAIHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVND SAGSDSI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      LKNALPDAAAIHYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTLIKVLWVND SAGSDSI
           130     140     150     160     170     180

```

575

```

          180      190      200
m249.pep  SRTNLEVSGDNIVYTYQARVGGREX
          :|||||:|:|||||:|||||
a249      ARTNLETNGNNIVYTYQARVGGREX
          190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 973>:

## m249-1.seq

```

1  ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CCGACAGTCG CTCCCGTCAG GGAGGCGGAG
151 ACACAAACCA TCGTCAGCCA AATCACGCAA AACCTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CCGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATT TCGGATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTAG
351 TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTCCGCAG GGGATTCCGA TATTTCCCGT ACGAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTCGGAGGT
601 CGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 974; ORF 249-1>:

## m249-1.pep

```

1  MKNNDGFRLE DSQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHTL SAVDGDFAID
101 AMKTKQLAE AQLKRFSYEL KNALPDAAAI HYAVCKDSSG NAPTLSGNAF
151 SSNCNDKANG DTLIKVLWVN DSAGDSDISR TNLEVSGDNI VYTYQARVGG
201 RE*

```

m249-1/g249 90.1% identity in 203 aa overlap

```

          10      20      30      40      50      60
m249-1.pep MKNNDGFRLEKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
          |||||:|:|: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249       MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
          10      20      30      40      50      60

          70      80      90     100     110     120
m249-1.pep NLMEGMLMNP TIDSDSNKKN YNLYMGNHTL SAVDGDFAIDAMKTKQLAE AQLKRFSYEL
          |||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||
g249       NLMEGMLMNP TIDSDSNKKN YNLYMGKQTL SAVDGEFMDAEKSKAQLAE AQLKRFSHEL
          70      80      90     100     110     120

          130     140     150     160     170     179
m249-1.pep KNALPDAAAIHYAVCKDSSGNAPTLSGN-AFSSNCNDKANGDTLIKVLWVNDSDS
          |||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||
g249       KNALPDVAIHYAVCKDSSGDAPTLSDSGAFSSNCNDKANGDTLIKVLWVNDSDS
          130     140     150     160     170     180

          180     190     200
m249-1.pep RTNLEVSGDNIVYTYQARVGGREX
          |||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||
g249       RTNLEVSGDNIVYTYQARVGGREX
          190     200

```

## a249/ L36117

gi|643582 (L36117) prepilin leader sequence requires cleavage to be active [Pseudomonas aeruginosa]  
 >gi|1161222 (L48934) involved in type 4 fimbrial biogenesis; contains pre-pilin like leader sequence [Pseudomonas aeruginosa]  
 >gi|1246299 (L76605) reference L36117, L48934 [Pseudomonas aeruginosa] Length = 185  
 Score = 50.4 bits (118), Expect = 9e-06  
 Identities = 45/183 (24%), Positives = 84/183 (45%), Gaps = 26/183 (14%)

Query: 13 QSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQNLMEGMLMNP 72  
 QSG ++IEVLVA+L+++IG+L ++++Q +T+ ++ + + + NL+E M +P  
 Sbjct: 12 QSGFSMIEVLVALLISIGVLGMIA MQGKTIQYTADSVERNKAAMLGNNLLESMRASP 71  
 Query: 73 DSDSNKKNYNLYMGNNHLSVVDGDFQVDAIKTKQLAE---QLKRFSYELKNALPDAA 129

576

D + M G A + T L + A + L ++ ++KN LP A  
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAGSAFPTAPSSCTPLPDAIKDRLGCWAEQVKNELPGAG 126  
 Query: 130 AI---HYAVCKDSSGVAPTLASGSTFSSNCDGSANGDTL-IKVLWVNDASGDSIARTNL 185  
 + Y + C + S + CDG G L I ++ W + A ++  
 Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSMLIIRLAWRGKQGACVNAADSSA 172  
 Query: 186 ETN 188  
 + T +  
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ				
a249	MKNND	CFRLKDPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ				
	10	20	30	40	50	60
	70	80	90	100	110	119
m249-1.pep	NLMEGMLMNP	TIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAEALKRFSYE				
a249	NLMEGMLMNP	TIDSDSNKKNYNLYMGNHHSVVDGDFQVDAIKTKTQLAEALKRFSYE				
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKNALPDAAAIHYAVCKDSSGNAP	TLGNAFSSNCDNKANGDTLIKVLWVNDASGDSI				
a249	LKNALPDAAAIHYAVCKDSSGVAP	TLASGSTFSSNCDGSANGDTLIKVLWVNDASGDSI				
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRTNLEVSGDNIVYTYQARVGG	GREX				
a249	ARTNLETNGNNIVYTYQARVGG	GREX				
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1 atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51 aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggta
101 tgcagggcgg gcaaaaaggt atgggcccggc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctcgaattt gccacggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatgccac cataaccttt atgattaatt
251 cgcggcataat cctgatgggg ggcggcgctt gccacgcaca tgaaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1 MHTASPRDE FIRIKESP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51 GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRARAV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1 ATGCACACCT TCCCCGATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51 CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAATACT CGGTATGCAG
101 GGCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTGTGTGA TGACCAGTAT
151 GAACTTCGCC GCGGCTCCG AGTTGCCAC GGTC AACCTG TGGGCGAAGC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTATGAT TAATCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAaaaaAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1 MHTPSPHNEF IRGIKESPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51 MNFAGGSEFA TVNLWAEPL ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*
  
```



Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

m250/g250

```

      10      20      30      40      50      59
m250.pep  MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWLEMLLMTSMNFAGGSEF
           ||::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g250       MHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKGMGRLEMLLMTGMNFAGGSEF
           10      20      30      40      50      60

      60      70      80      90     100     110
m250.pep  ATVNLWAEPLPILLIATVTFMINSRHILMGGGACPAPERNTAEKSRARTVFYVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g250       ATVNLWAEPLPILLIATITFMINSRHILMGGGACHAHERNTAEKSRARAVFYV
           70      80      90     100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 979>:

a250.seq

```

      1  ATGACACACA TAAGCTCGCC CCGTAACGAA TTTATACGCG GCATCAAAGA
     51  AAGTTCGCCC ATGCTGATCG GGCTTTTGCC TTGGGCATTA ATACTCGGTA
    101  TGCAGGTGG  ACAAAAAGGC ATGAGCTGGC TGGAAATGTT GTTGATGACC
    151  GGTATGAACT TCGCCGGCGG CTCCGAGTTT GCCACGGTCA ACCTGTGGGC
    201  GGAACCTCTG CCGATACTGC TTATCGCCAC CGTAACCTTT ATGATTAATT
    251  CTCGGCATAT CCTGATGGGG G.CGGCACTT GCCCCGCACC TGAAGAGAAAT
    301  ACCGCTGAAA AAAGCCGTGC CCGCACTGTT TTTTATGTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 980; ORF 250.a>:

a250.pep

```

      1  MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MSWLEMLLMT
     51  GMNFAGGSEF ATVNLWAEPL PILLIATVTF MINSRHILMG XGTCPAPERNT
    101  TAEKSRARTV FYV*

```

m250/a250 94.6% identity in 111 aa overlap

```

      10      20      30      40      50
59
m250.pep  MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWLEMLLMTSMNFAGGSEF
           |
           ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a250       MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWLEMLLMTGMNFAGGSEF
           10      20      30      40      50
60

      60      70      80      90     100     110
m250.pep  ATVNLWAEPLPILLIATVTFMINSRHILMGGGACPAPERNTAEKSRARTVFYVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a250       ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCPAPERNTAEKSRARTVFYVX
           70      80      90     100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 981>:

g251.seq

```

      1  atgcctgacc caatagggat tcttttcgct gccctcgagg ttgatttttt
     51  tgccgttgtt ttgagggggc gttttcaacg aataggcgcg gttggcatgt
    101  tgataataat aatcctgatg gcggaggtcg gaacccaaac ggtcgttaacc

```

```

151 gaggttgacg ctcaggttgt ggcggatttt ggcggtatcg aaggattttt
201 tgaatgccgc ctgcaagagc ctgtggcttt ccccgtaaat cacgcggctg
251 gatttgtagt aggaagacgg cttgtcggca ctcgggcggc aatattgtc
301 cgaaccgtcg gcggaacagt gcgtctgctg aaaatgattg tccaaaccga
351 tgccctgccg gtcgtaagag aggcgggcat aatccgcca agtgtcttta
401 tcggcattgg tatagacata ttccaaaccg tagcggcttt tgggtgctg
451 ctcgtcgtaa aacacgcccg taccgtattc cgcgccacc tccgcaccgt
501 tttcacggtt ggtaatcagc ccgctgtatt tgcggccgcc cgcgtatttg
551 ccgtagcctc ttatcgatcc gtatttttta tttcatcaa aaaccgcctt
601 ggtcaggaat gccggaaccg tcatatcgcg cgtgtcgaaa gtttgctg
651 tgcgttcgag tatgccgccg atgtagtgcc gttgttttc aaaacgaaaa
701 cccggcgga acagccacga ccggctttcg tatga

```

This corresponds to the amino acid sequence <SEQ ID 982; ORF 251.ng>:

```

g251.pep
1  MPDPILGIFA AVGVDFFAVV LRGRFORIGA VGLIIIIILM AEVGTKTVVT
51  EVDAQVVADF GGIEGFFEER LQEPVAFPNV HAVGFVVGRR LVGTRAAIFV
101 RTVGGTVRLL KMIQTDALP VVREAGIIRP SVFIGIGIDI FQTVAAFGVR
151 LVVKHARTVF RAHLRTVFTV GNQPAVFAAA RVFAVASYRS VFFIFIKNRL
201 GQECRNRHIA RVESLLRAFE YAADVVPFVF KTKTRAEQPR PAFV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

```

m251.seq
1  ATGCGTGCTG CGGTAGTCGT AGCGCAAGCC CGCGCCGACA TCCGCCACC
51  TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTACCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACGACATTTC CCCTGCCTAT GGTGACCCAA TAGGGGCTGG
201 TTTCACTGCC GTTGGGGCTG ATTTTTTTGC CGTTGTTTGT AGGGGGCGTG
251 TTCGACGAAT AGGCGCGGTT GGCATGTTGA TAATAATAAT CCTGATGGCG
301 GAGATTAGAG CCAAAGCGGT CAAACCCGAG ATTCACGCTC AGGTTGTGGC
351 GGATTTTGGC GGTATCGAAG GATTTTTTGA ATGCCGCTG CAAGAGCCTG
401 TGGCTTTCCC CGTAAATCAC GCGATCGGAT TTGTAATAGG AAAACGGCTT
451 GTCGGCACTC GGGCGGCAAT ATTTGTCCGA ACCGTCGGCA GAACAGTGCG
501 TCTGCTGAAA ATGATTATCC AAACCGATGC CCTGCCGCTC GTAAGAGAGG
551 CGGGCATAAT CCGCCCAAGT GTCTTTATCG GCATTGGTAT AGACATATTC
601 CAAACCGTAG CGGCTTTTGG TGTGCGTCTC GTCGTAAAC ACGCCCGTAC
651 CGTATTCGCG GCCCACCAGC GCACCGTTT CGCCGTTGGT AAACAGTCCG
701 CCGTATTTGT GGTGCGCGC GTATTGCGG TTACCGGCA AAGAACCGC
751 CTGTTTTTTA TTTGCATCAA AAACCGCCTT GGTCAGGAAT GCCGGAACCG
801 TCATATCGCG CGTGTGAAA GTTTGTTGCG TGTGTTGAG TATGCCGCG
851 ATGTAGTGCC GCTTATTCTC AAAACGAAAA CCCGGCGGA ACAGCCACGA
901 CCGGCTTTCT TATGA

```

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

```

m251.pep
1  MRAAVVVAQA RADIRPPAQT DIVPNCRVIA FTVDAARRAV RISIVAQAAD
51  LPRNDISPAY GDPAGGFTA VGADFFAVVL RGRVRRIGAV GMLIIIIILMA
101 EIRAKAVKPE IHAQVADFG GIEGFFEERL QEPVAFPNH AIGFVIGKRL
151 VGTRAAIFVR TVGRTVRLK MIIQTDALPV VREAGIIRPS VFIGIGIDIF
201 QTVAAFGVRL VVKHARTVFR AHQRTVFAVG KQSAVFVAR VFAVTGQRT
251 LFFICIKNRL GQECRNRHIA RVESLLRVFE YAADVPLIL KTKTRAEQPR
301 PAFV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

```

          40      50      60      70      80      90
m251.pep  TVDAARRAVRISIVAQAADLPRNDISPAYGDPAGGFTA VGADFFAVVL RGRVRRIGAVG
          ||||  |::||:|||||||  :|||||
g251      MPDPILGIFA AVGVDFFAVV LRGRFORIGA VGLIIIIILM AEVGTKTVVT
          10      20      30

```

579

	100	110	120	130	140	150
m251.pep	MLIIIIILMAEIRAKAVKPEIHAQVVADFGGIEGFFECRLQEPVAFPVNHAIGFVIGKRLV					
g251	MLIIIIILMAEVTGKTTVTEVDAQVVADFGGIEGFFECRLQEPVAFPVNHAVGVVGRRLV					
	40	50	60	70	80	90
	160	170	180	190	200	210
m251.pep	GTRAAIFVRTVGRTVRLLKMIQTDALPVVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV					
g251	GTRAAIFVRTVGGTVRLLKMIQTDALPVVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV					
	100	110	120	130	140	150
	220	230	240	250	260	270
m251.pep	VKHARTVFRAHQRTVFAVGKQSAVFVVARVFAVTGQTRLFFICIKNRLGQECRNRIAR					
g251	VKHARTVFRAHLRTVFTVGNQPAVFAAARVFAVASYRS-VFFIFIKNRLGQECRNRIAR					
	160	170	180	190	200	210
	280	290	300			
m251.pep	VESLLRVFEYAADVPLILKTKTRAEQPRPAFVX					
g251	VESLLRAFEYAADVVPFVKTKTRAEQPRPAFVX					
	220	230	240			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 985>:

a251.seq	1	ATGCGTGCTG	CGGTAGTCGT	AGCGCAACCC	CGCGCCGACA	TCCGCCACAC
	51	TGCCCAAACG	GACATTGTCC	CGAACTGCCG	CGTAATAGCT	TTTGCCGTTG
	101	ATGCTGCGCG	GCGTGCAGTC	CGTATAAGTA	TTGTGCCCCA	AGCGGCAGAT
	151	TTGCCCCGTA	ACCACATTTC	CCCTGCCTAT	GCTGACCCAA	TAGGGTTGGT
	201	CCTTGCCGCC	GTTGGGGTTG	GCGGTTTTAG	GGGGCGTTTT	CGACGAATAG
	251	GCGCGGTTGG	CATGTTGATA	ATAATAATCC	TGATGGCGGA	GATTAGAGTC
	301	AAAGCGGTCA	AAACCGAGAT	TCACGCTCAG	GTTGTGGCGG	ATTTTGGCGG
	351	TATCGAAGGA	TTTTTTGAAT	GCCGCTGCA	AGAGCCTGTG	GCTTTCCCCG
	401	TAAATCACGC	GGTCGGATTT	GTAGTAGGAA	AACGGCTTGT	CGGCACTCGG
	451	GCGGCAATAT	TTGTCCGAAC	CGTCGGCAGA	ACAGTGCGTC	TGCTGAAAT
	501	GATTGTCCAA	ACCGATGCCC	TGCCGCTCGT	AAGAGAGCGC	GGCATAATCC
	551	ACCCAAGTGT	CTTTATCGGC	ATTGGTATAG	ACATATTCCA	AACCGTAGCG
	601	GCTTTTGGTG	TGCGTCTCGT	CGTAAACAC	GCCCGTACCG	TATTCGCGCG
	651	CCACCAGCGC	ACCGTTTTCG	CCGTTGGTAA	ACAGACCGCC	GTATTTGTGG
	701	TCGCCGCGGT	ATTTGCCGTT	GCCTCTTATC	GGTCCGTATT	TTCTATTTTC
	751	ATCAAAAACC	GCCTTGGTCA	GGAATGCCGG	AACCGTCATA	TCGCCGCGTGT
	801	CGAAAGTTTG	TTGCGTGTGT	TCGAGTATGC	CGCCGATGTA	GTGCCGTTTG
	851	TTTTCAAAAC	GAAAACCCGG	GCGGAACAGC	CACGATCGGC	TTTCGTATGA

This corresponds to the amino acid sequence <SEQ ID 986; ORF 251.a>:

a251.pep	1	MRAAVVVAQP	RADIRPPAQT	DIVPNCRVIA	FAVDAARRAV	RISIVAQAAD
	51	LPRNHISPAY	ADPIGLVLAA	VGVGGRFRGF	RRIGAVGMLI	IIILMAEIRV
	101	KAVKTEIHAQ	VVADFGGIEG	FFECRLQEPV	AFPVNHAVGF	VVGKRLVGTR
	151	AAIFVRTVGR	TVRLLKMIVQ	TDALPVVREA	GIIHPSVFIG	IGIDIFQTVA
	201	AFGVRLVVKH	ARTVFRAHQ	TVFAVGKQTA	VFVVARVFAV	ASYRSVFSIF
	251	IKNRLGQECR	NRHIAVESL	LRVFEYAADV	VPFVFKTKTR	AEQPRSAFV*

m251/a251 88.5% identity in 304 aa overlap

	10	20	30	40	50	60
m251.pep	MRAAVVVAQARADIRPPAQTDIVPNCRVIAFTVDAARRAVRISIVAQAADLPRNDISPAY					
a251	MRAAVVVAQPRADIRPPAQTDIVPNCRVIAFAVDAARRAVRISIVAQAADLPRNHISPAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m251.pep	GDFIGAGFTAVGADFFAVVLRGRVRRIGAVGMLIIILMAEIRAKAVKPEIHAQVVADFG					
	:     :   :                   :					

580

```

a251      ADPIGLVLAAVGVGGF----RGRFRRIGAVGMLIIIIILMAEIRVKAVKTEIHAQVVDVFG
              70              80              90              100             110

m251.pep      130      140      150      160      170      180
GIEGFFECLRLQEPVAFPNVHAIGFVIGKRLVGTRAAIFVRTVGRTVRLLKMIQTDLAPV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      GIEGFFECLRLQEPVAFPNVHAGVFVVGKRLVGTRAAIFVRTVGRTVRLLKMIQVTDALPV
              120      130      140      150      160      170

m251.pep      190      200      210      220      230      240
VREAGIIRPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVFAVGKQSAVFVVAR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VREAGIIHPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVFAVGKQTAVFVVAR
              180      190      200      210      220      230

m251.pep      250      260      270      280      290      300
VFAVTGQRTRLFICIKNRLGQECNRNRIARVESLLRVFEYAADVVPILKTKTKTRAEQPR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VFAVASYSR-VFSIFIKNRLGQECNRNRIARVESLLRVFEYAADVVPFVKTKTKTRAEQPR
              240      250      260      270      280      290

m251.pep      PAFVX
              ||||

a251      SAFVX
              300

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 987>:

g253.seq

1	atgatcgaca	gggaccgtat	gttgcgggac	acggtggaac	gtgtgctgtc
51	ggggtcgttc	tggttatggg	tgggtgtggc	atcgatgatg	tttaccgccc
101	gatttttcagg	cacttatctt	ctgatggaca	atcaggggct	gaatttcttt
151	ttagtthttg	cgggagtggt	gggcataaat	acgctgatgc	tggcagtatg
201	gttggaacag	tgttctctgc	cgctgaagat	gggacgggtt	ttcagcagtc
251	cggcgacgtg	tttctggggc	aaagccctcg	taaatcaggc	ggtgtgtccg
301	ctgtatgcgg	accagtgggc	gcaaccttcg	gtacgatgga	aatatggcgc
351	aacggcgcac	agcttctggc	tctgcacgct	gctcggaaatg	ctgggtgtcgg
401	tattgctgct	gcttttggtg	cggcaatata	cgttcaactg	ggaagacacg
451	ctgttgagca	atgccgcctc	ggtagcgcgc	gtggaaatgt	tggcatggct
501	gcgctcgaaa	ctcggthttc	ctgtccccga	tgcgcggggc	gtcatcgaa
551	gtcgtctgaa	cggcaatatt	ccgatctgcg	gggcttggtc	ggggctctgt
601	gtcggcagta	tcgtctgcta	cggcatcctg	ccgcgcctct	tggcttgggt
651	agtgtgtaaa	atccttttga	aaacaagcga	aaacggattg	gatttggaaa
701	aaacctatta	tcaggcggct	atccgcccgt	ggcagaacaa	aatcacccat
751	gcggatcacg	ctcgggaaac	cgtgtccgcc	gtttcccgca	aaatcgtctt
801	gaacgatgcg	cgaaatggg	cgtctatgct	ggagaccgag	tggcaggacg
851	gccaatgggt	cgaaggcagg	ctggcgcagg	aatggcttga	taaggcgctt
901	gccgccaatc	gggaacaggt	tgcgcgcgtg	gagacagagc	tgaagcagaa
951	accggcgcga	ctgcttatcg	gcgtacgcgc	caaactgtg	ccggaccggg
1001	gcgtgctgcg	gcagatttgg	cggctttcgt	aagcggcgca	gggcgcgcgc
1051	gtggtgcagc	ttttgcgga	acaggggctt	tcagacgacc	ttctggaaaa
1101	gttggaaacat	tggcgtaacg	cgtctaccga	atgcggcgcg	gcgtggcttg
1151	agcctgacag	ggtggcgcag	gaaggccggt	tgaagaacca	ataa

This corresponds to the amino acid sequence <SEQ ID 988; ORF 253.ng>:

g253 . pep

1	MIDRDRMLRD	TLERVAGSF	WLWVVASMM	FTAGFSGYL	LMNQGLNFF
51	LVLAVGLGMN	TLMLAVWLAT	LFLRVKVGFR	FSSPATWFRG	KGPVNQAVLR
101	LYADQWRQPS	VRWKIGATAH	SLGWCTLLGM	LVSULLLLLV	QYTFNWEST
151	LLSNAASVRA	VEMLAWLPKS	LGLFPVDPARA	VIEGRNLNGNI	ADARAWSGLL
201	VGSIVCYGIL	PRLLAWVVCK	ILLKTSENGL	DLKETYQAV	IRRWNQKITD
251	ADTRRETVSA	VSPKIVLND	PKWALMLETE	WQDQWFQFV	LAQEWLDKGV

301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRLQIV RLSEAAQGGG  
351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRVAO EGRLKDO\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 989>:

```
m253.seq
1  ATGATTGACA  GGAACCGTAT  GCTGCGGGAG  ACGTTGGAAC  GTGTGCGTGC
51  GGGGTCGTTT  TCGTTTGTGG  TGGTGGCGGC  GACGTTTGCA  TTTTACCCTG
101 GTTTTTCACT  CACTTATCTT  CTAATTGGACA  ATCAGGGTCT  GAATTTCTTT
151 TTGGTTTGGG  CGGGCGGTGT  GGGCATGAAT  ACGCTGATGC  TGGCAGTATG
201 GTTGGAATG  TTGTTCTCTG  GTGTGAAAGT  GGGGCGTTTT  TTCAGCAGTC
251 CGGCGACGTG  GTTTCGGGGC  AAAGACCCTG  TAAATCAGGC  GGTGTTGCGG
301 CTGTATGCGG  ACGAGTGGCG  GCAACCTTCG  GTACGTTGGA  AAATAGCGCG
351 AACCTCGCAC  AGCCTGTGGC  TCTGCACGCT  GCTCGGAATG  CTGGTGTCTG
401 TATTGTTGCT  GCTTTTGGTG  CGGCAATATA  CGTTCAACTG  GGAAGACACG
451 CTGTTGAGCA  ATGCCGCTTC  GGTACGCGCG  GTGGAAATGT  TGGCATGGCT
501 GCCGTCGAAA  CTCGTTTCC  CTGTCCCGA  TGC GCGGGG  GTCATCGAAG
551 GCCGCTGAA  CGGCAATATT  CGCCATGCGC  GGGCTTGGTC  GGGGCTCGTG
601 GTCGGCAGTA  TCGCCTGCTA  GCGCATCTCG  CGCGCCTGCG  TGGCTTGGGT
651 AGTGTGTA  ATCCTTTTGA  AAACAAGCGA  AAACGGATTG  GATTGGA  A
701 AGCCCTATTA  TCAGGCGGTC  ATCCGCGGCT  GGCAGAACAA  AATCACCAGT
751 GCGGATACGC  GTCGGGAAAC  CGTGTCCGCC  GTTTCACCGA  AAATCATCTT
801 GAACGATGCG  CCGAAATGGG  CGGTCTATGCT  GGAGACCGAG  TGGCAGGACG
851 GCGAATGGTT  CGAGGGCAGG  CTGGCGCAGG  AATGGCTGGA  TAAGGCGGTT
901 GCCACCAATC  GGGAACAGGT  TGCCGCGCTG  GAGACAGAGC  TGAAGCAGAA
951 ACCGGCGCAA  CTGCTTATCG  GCGTGC GCGC  CCAAACGTG  CCGGACCGCG
1001 GCGTGTGTCG  GCAGATTGTC  CGACTCTCGG  AAGCGGCGCA  GGGCGGCGCG
1051 GTGTGTCAGC  TTTTGGCGGA  ACAGGGGCTT  TCACAGCGAC  TTTCGGAAAA
1101 GTCGGAACAT  TTGCGTAACG  CGCTGGCCGA  ATGCGGCGCG  CGGTGCGTTG
1151 AGCCTGCAG  GCGCGCGCAG  GAAGGGCGTT  TGAAGACCA  ATAA
```

This corresponds to the amino acid sequence <SEQ ID 990; ORF 253>:

m253.pep

1	MIDRNRMLRE	TLERVAGSF	WLWVVAATFA	FFTGFSVTYL	LMDNOGLNFF
51	<u>LVL</u> AGVLGMN	<u>TLML</u> AVWLAM	LFLRVKVGRF	FSSPATWFRG	KDPVNQAVLR
101	LYADEWRQPS	VRWKIGATSH	<u>SLWLCTLLGM</u>	<u>LVS</u> VLLLLLV	RQYTFNWEST
151	LLSNAASVRA	VEMLAWLPSP	LGFPVPDARA	VIEGRNLNGNI	ADARAWSGLL
201	<u>VGS</u> IACYGIL	PRLLAWVVCK	ILLKTSENGL	DLEKPYQAV	IRRWQNKITD
251	ADTRRETVSA	VSPKIIINDA	PKWAVMLETE	WQDGEWFEGR	LAQEWLDKVG
301	ATNREQVAAL	ETELQKPAQ	LIGLVRAQTV	PDGRVLRQIV	RLSEAAQGGA
351	VVQLAEQGL	SDDLSEKLEH	WRNALAECGA	AWLEPDRAAO	EGRLKDO*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

m253/q253

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLEVRAGSFVLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
	:     :     :     :     :     :     :     :     :     :					
g253	MIDRDRMLRDTLEVRAGSFVLWVVASMMFTAGFSGTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFLRVKVGREFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	:     :     :     :     :     :     :     :     :					
g253	TLMLAVWLATLFLRVKVGREFSSPATWFRGKGPVNQAVLRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGLMVSVLLLLLVLRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
	:     :     :     :     :     :     :     :     :					
g253	SLWLCTLLGLMVSVLLLLLVLRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
	130	140	150	160	170	180

582

	190	200	210	220	230	240
m253 . pep	VIEGRNLNGNIADARAWSGLLVGSIAICYGILPRL LAWVVKILLKTS ENGLDLEKPYQAV					
g253	VIEGRNLNGNIADARAWSGLLVGSIVCYGILPRL LAWVVKILLKTS ENGLDLEKTYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253 . pep	IRRWQNKITDADTRRET VSAVSPK IILNDAPKWAVMLETEWQDGEWFEGR LAQEWLDKGV					
g253	IRRWQNKITDADTRRET VSAVSPK IIVLNDAPKWALMLETEWQDQWFEGR LAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253 . pep	ATNREQVA ALETELKQKPAQLLIGVRAQTV PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	:					
g253	AANREQVA ALETELKQKPAQLLIGVRAQTV PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253 . pep	SDDLSEKLEHWRNALAE CGAAWLEPDRAAQEGRLKDQX					
g253	SDDLSEKLEHWRNALTE CGAAWLEPDRAAQEGRLKDQX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

```

a253 . seq
1  ATGATCGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC
51  GGGGTCGTTC TGGTTGTGGG TGGCGGCGGC GACGTTTGGC TTTTTCACCG
101 GTTTTTCAGT TACTTATCTT CTAATGGACA ATCAGGCTCT GAATTTCTTT
151 TTGGTTTGG CGGGCGTGTG GGGCATGAAT ACGCTGATGC TGGCAGTATG
201 GTTGGCAATG TTGTTCTGCG CCGTGAAAGT GGGGCGTTTT TTCAGCAGTC
251 CGGCGACGTG GTTTCGGGGC AAAGACCTTG TCAATCAGGC GGTGTTGCGG
301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTGGGA AAATAGGCGC
351 AACGTCGCAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGGTGTGCG
401 TATTGTTGCT GCTTTTGGTG CGGCAATATA CGTTCAACTG GGAAAGCACG
451 CTGTTGGGCG ATTCTCTTTC GGTACGGCTG GTGGAATGT TGGCATGGCT
501 GCCTGCGAAA CTGGGTTTTC CCGTGCCTGA TGC GCGGGCGG GTCATCGAAG
551 GTCGTCTGAA CGGCAATATT GCCGATGCGC GGGCTTGGTC GGGGCTGCTG
601 GTCGGCAGTA TCGCCTGCTA CGGCATCCTG CCGCGCCTCT TGGCTTGGGC
651 GGTATGCAAA ATCCTTTTGA AAACAAGCGA AAACGGCTTG GATTTGGA
701 AGCCCTATTA TCAGGCGGTC ATCCGCGCTG GGCAGAACAA AATCACCAGT
751 GCGGATACGC GTCGGGAAAC CGTGTCCGCC GTTTCGCCGA AAATCGTCTT
801 GAACGATGCG CCGAAATGGG CGGTCATGCT GGAGACCGAA TGGCAGGACG
851 CGCAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGCGCTT
901 GCCGCCAATC GGGAACAGGT TGCCGCGCTG GAGACAGAGC TGAAGCAGAA
951 ACCGCGCAAA CTGCTTATCG GCGTGC GCGC CCAAAGTGTG CCCGACCGCG
1001 GCGTGTGCG GCAGATCGTC CGACTTTCGG AAGCGGCGCA GGGCGGCGCG
1051 GTGGTGCAGC TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTCGGAAAA
1101 GCTGGAACAT TGGCGTAACG CGCTGACCGA ATGCGGCGCG GCGTGGCTGG
1151 AACCCGACAG AGCGGCGCAG GAAGGCCGTC TGA AAACCAA CGACCGCACT
1201 TGA

```

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

```

a253 . pep
1  MIDRNRMLRE TLERVRAGSF WLWVAATFA FFTGFSVTYL LMDNQGLNFF
51  LVLAVGLGMN TLMLAVWLAM LFLRVKGRF FSSPATWFRG KDPVNQAVLR
101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSLLLLLV RQYTFNWEST
151 LLGDSSSVRL VEMLAWLPAK LGFFVPDARA VIEGRNLNGNI ADARAWSGLL
201 VGSIAICYGIL PRL LAWAVCK ILLKTS ENGL DLEKPYQAV IRRWQNKITD
251 ADTRRET VSA VSPKIVLND A PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
301 AANREQVAAL ETELKQKPAQ L LIGVRAQTV PDRGVLRQIV RLSEAAQGGA
351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRAAQ EGRLKTNDR
401 *

```

m253/a253 97.2% identity in 395 aa overlap

m253.pep	10	20	30	40	50	60
	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
a253	MIDRNRMLRETLERVAGSFWLWVAAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
m253.pep	70	80	90	100	110	120
	TLMLAVWLAMLFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMLFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
m253.pep	130	140	150	160	170	180
	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLGDSSSVRLVEMLAWLPSKLGFPVPDARA					
	130	140	150	160	170	180
m253.pep	190	200	210	220	230	240
	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLAWVVKILLKTSENGLDLEKPYQAV					
a253	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLAWAVCKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
m253.pep	250	260	270	280	290	300
	IRRWQNKITDADTRRETSAVSPKIIINDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253	IRRWQNKITDADTRRETSAVSPKIVLNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
m253.pep	310	320	330	340	350	360
	ATNREQVAALETELKQKPAQLLIGVRAQTVPRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
a253	AANREQVAALETELKQKPAQLLIGVRAQTVPRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
m253.pep	370	380	390			
	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRLKDQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRLKTNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcgcg gcaggtttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg ttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccggtt gcaactggtt ctttgagaaa cgggcccggc
301 tggacggtat ttctactgtc ctggctgctg gcggctgcag gaatcgacac
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggtcttgg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacacgctc ggcatctact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aacccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```

51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMY VLIAGSYTPF ALVSLRNGPG  
 101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIAIYVMGW MVLAVMKSIL  
 151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF  
 201 VSVYGYVI\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

m254.seq (partial)  
 1 ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTTGA GTTCCTGGCT  
 51 GTACCACGGA ATTGCAGCCG GAAAACTGAA AAGCATTTTG AAAAAACCG  
 101 ACCACTGCAT GATTATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA  
 151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG  
 201 GCTGCTGGCG GCTGCAGGAA TCGACAAGA ACTCACCATC GGACGGAAAA  
 251 GCGAAAAACG TCTGCTGTCT ATTGTGATTT ATGTCGTCAT GGGTTGGATG  
 301 GTCTTGGCGG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT  
 351 GGCTTGGCTG GCGGCAGGCG GTATGCTGTA CAGTGTCCGC ATTTACTGGT  
 401 TTGTAAACGA TGAATAATC CGACACGGC ACGGAATCTG GCATCTGTTT  
 451 GTATTGGGCG GCAGCATCAC CCAATTTGTC AGCGGTGACG GTTACGTAAT  
 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

m254.pep (partial)  
 1 ..VSVYGISLLL LYLSSWLYHG IAAGKLKSI LKKTDHCMYV LIAGSYTPFA  
 51 LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLLS IVIYVVMGW  
 101 VLAVMKSILTA SLPSAGLAWL AAGGMLYSV GIYWFVNDEK IRHGHGIWHLF  
 151 VLGGSITQFV SVYGYVI\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

m254/g254

m254.pep				10	20	30
				VSVYGISLLL	LYLSSWLYHG	IAAGKLKSI
g254	HL	SL	L	L	L	L
	20	30	40	50	60	70
m254.pep		40	50	60	70	80
		KKTDH	CMYV	VLIAG	SYTPF	ALVSLR
g254		KKTDH	CMYV	VLIAG	SYTPF	ALVSLR
	80	90	100	110	120	130
m254.pep		100	110	120	130	140
		IVIYV	VMGW	MVLAV	MKSIL	TASLP
g254		IAIYI	VMGW	MVLAV	MKSIL	TASLP
	140	150	160	170	180	190
m254.pep		160				
		VLGGS	ITQF	VSVY	GYVI	X
g254		VLGGS	ITQF	VSVY	GYVI	X
		200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

a254.seq  
 1 ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTGGA GCGGTTTGAT  
 51 TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG  
 101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT  
 151 CTGCTCTATT TGAGTTCTC GCTGTACCAC GGAATTGCAG CCGGAAAAC  
 201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTAT GTGCTGATTG  
 251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CCGGCCGGGG



a254 . pep

```

1  MYTGERFNTY SHLSGLILAA AGLALMLLKT IGHGDGYRIF SVSVYGISLL
51  LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIATYIVMGW MVLAVMKSLL
151 ASLPYPAGLA LAAGGMLYSV GIYWFVNDEK IRHGHIWHL FVLGGSITQF
201 VSLVPGYVI*

```

```

30                                         10                                20
m254.pep
VSVYGISLLLLLYLSSWLYHGIAAGKLSIL
                                     |||
|||||||
a254
HLSGLILAAAGLALMLLKTIHGHDGYRIFSVSVYGISLLLLLYLSSSLYHGIAAGKLSIL
              20               30               40               50                60
70
              40               50               60               70                80
90
m254.pep
KKTDHCMIIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
|||||
a254
KKTDHCMIIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
              80               90               100              110                120
130
              100              110              120              130                140
150
m254.pep
IVIIYVMGWMVLAVMKSLTASLPSAGLAWLAAGGMYSVGIIYWFVNDEKIRRHGGIWHLF
      |:||:|||||
|||||
a254
IAIIYIVMGWMVLAVMKSLTASLPAGLAWLAAGGMYSVGIIYWFVNDEKIRRHGGIWHLF
              140              150              160              170                180
190
              160
m254.pep          VLGGSI TQFVS VYG YVIX
                  |||
a254             VLGGSI TQFVS VYG YVIX
                   200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

q255.seq

1	atggttggac	aggaagcctt	gcggggtcag	ttcgtcgcg	tgttcgctgc
51	cgcgttgcgt	tacgctgtca	aaacctgcgc	cgatttccac	gcctttgacg
101	gcgttgatgc	ccatcatcgc	gtaggcgatt	tcggcatcga	ggcggtcgaa
151	aacgggttcg	cccaaaccca	cggggacgtt	ggcggttcg	atatgcagtt
201	tcgcgccgac	ggaatccaag	gatttgcgca	caccgtccat	atatgtttcc
251	agttgcgcga	tttggctttg	gtttggcgca	aaaaaaggat	tttggaatat
301	gtgttcgctg	ccttcaaacc	ggattttttt	ttcgccgact	tgggttaacgt
351	aggcggtgat	ttcgtgccc	aatttttctt	tcagccattt	tttggcaacg
401	gctccggcgg	caacgcgggc	tcgggtttcg	cgggcggaac	tcttgcgcc
451	gccccggtag	tcgcgcgtac	cgtatttgtg	ccaataggta	tagtcgcgct
501	gcggcgggcg	gaaggcggtg	gcgatgtcgc	cgtagtcttc	gctgcgctgg
551	tcqgttttgc	qqattaac			

This corresponds to the amino acid sequence <SEQ ID 1000; ORF 255.ng>:

g255 . pep

1 MVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAAHR VGDFGIEAVE  
51 NGFAQTGDGV GGFDMQFRAD GIQGFHAHTVH IVQFGDLAL VGGKKRILGN  
101 VFAAFKPDDF FADLGNVGGD FRAEFFFQPF FGNSSGNAG CGFAGGTPAA  
151 APVVARTVFV PIGIVGVSGA EGGGDVAVVE AALVGVAD\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1001>:

m255.seq

1	GTGGTTGGAC	AGGAAGCCTT	GCGGGGTCAG	TTCGTCGCCG	TGTTTCGCTGC
51	CGCGTTGCGT	TACGCTGTCA	AAACCTGCGC	CGATTTCAC	GCCTTTGACG
101	GCGTTGATGC	CCATCATCGC	GTAGGCGATT	TCGGCATCGA	GCGCGTCAAA
151	AACAGGTTTCG	CCCAAGCCGA	CAGGGACATT	GGCTGCTTCG	ATATGCTTCT
201	TGCTCGGCAC	GGAAATCCAAG	GATTTCGCAC	CGCTGTCATT	ATAGTATTTCC
251	ACGCGCGCAA	TTTGGCTATG	GTTGGCGCGA	AAAAAAGAT	TTTGGGAAT
301	GTGTTTCGAC	CCTTCAAACC	GGATTCTTT	TTGCGCGACT	TGGGTAACGT
351	AGGCGGTGAT	TTCCGTGCCG	AATTTTTCTT	TCAACCAATT	TTTGGCAACG
401	GCTCCGCGAC	CAACGCGGGC	GGCGGTTTCA	CGGGCGGAGC	TCCTGCCGCC
451	GCCGCGGTAG	GCGCGCGTGC	CGTATTTGTG	CCAATAGGTA	TAGTCGCGGT
501	GCGCGGGGCG	TAAGCTGGTG	GCGATGTTGC	CGTAGTCTTT	GCTGCGCTGG
551	TCGGTATTGC	GGATTAA			

This corresponds to the amino acid sequence <SEQ ID 1002; ORF 255>:

m255 . pep

1 VVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAAHR VGDFGIEAVK  
51 NRFAQADRDI GCFDMQLRAD GIQGFHAVH IVFQLGNLAM VGGKKRILGN  
101 VFAAFKPDFF FADLGNVGGD FRAEFFFQPF FGNNGSGNAG GGFTGGAPAA  
151 AAVVARAVFV PIGIVGAGA EAGGDVAVF AALVGIAD\*

**Computer analysis of this amino acid sequence gave the following results:**

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

m255/q255

[illegible]

	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
	:					
g255	AALVGVADX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```

a255.seq
1  GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG TGTTGCTGC
51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCAC GCCTTTGACG
101 GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GCGGTCGAA
151 TACGGGTTCG CCAAGCCGA CGGGACGTT GCGGCTTCA ATATGCAGCT
201 TCGCGCCGAC GGAATCCAAG GATTGCGCA CGCTGTCCAT ATAGTTTTC
251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
301 GTGTTTCGAG CCTTCAAACC GGATTTCCTT TTCGCCGACT TGGGTAACGT
351 AGGCGGTGAT TTCCGTGCCG AATTTTCTT TCAACCATT TTTGGCAACG
401 GCTCCGGCGG CAACGCGGGC GCGGTTTCG CGGGCGGAAC TCCTGCCGCC
451 GCCCCGGTAG TCGCGCGTGC CGTATTGTG CCAATAGGTA TAGTCGGCGT
501 GGCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTT GCTGCGCTGC
551 TCGGTATTGC GGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

```

a255.pep
1  VVGQEALRGE FVAVFAAALR YAVKTCADFH AFDGVDAAHG VGDGIEAVE
51  YGFAQADGDV GGFNMQLRAD GIQGFHAVH IVFQLGNLAM VGGKKRILGN
101 VFAAFKPDFF FADLGNVGGD FRAEFFQPF FGNGSGNAG GGFAGTTPAA
151 APVVARAVFV PIGIVGVAGA EAGGDVAVVF AALVGIAD*

```

m255/a255 93.1% identity in 188 aa overlap

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDGIEAVKNRFAQADRD					
	:					
a255	VVGQEALRGEFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDGIEAVEYGFAGADGDV					
	10	20	30	40	50	60
m255.pep	GCFDMLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	:					
a255	GGFNMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	70	80	90	100	110	120
m255.pep	GCFDMLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	:					
a255	GGFNMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	70	80	90	100	110	120
m255.pep	FRAEFFQPFNGSGSNAGGGFTGGAPAAAVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	:					
a255	FRAEFFQPFNGSGSNAGGGFAGGTAAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
m255.pep	FRAEFFQPFNGSGSNAGGGFTGGAPAAAVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	:					
a255	FRAEFFQPFNGSGSNAGGGFAGGTAAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
a255	AALVGIADX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```

g256.seq
1  atgctcgcgg tacgcaatcg gggttggcac ggcgcagtcg tccatttccg
51  cagctcgggc ggcgtagcga acaccgcccc ggtgttctac cacttgggtg
101 ataccgccga aatcgctttt gctttggaca cgctaccgcg gcgttaccgt
151 gaaatatacg ccgtcgcgt atcgctgggc ggcaacgcgc cggcaaaata
201 ttggggcgaa cagggcaaaa aggcattgcc gcacgcctcg gccgccgtat
251 ccgccccgt tgatgcagag gcggcaggca gccgcttcga cagcggcatc
301 acgcggctgc tctacacgcg ctacttctc cgcacactga taccctaaagc

```

```

351  acgttcgctc  caaggttttc  agacggcatt  tgccgcaggg  tgcaaaacac
401  tgggcgagtt  tgacgaccgt  ttcaccgcac  cgctgcacgg  ctttgccgac
451  cggcacgact  actaccgcca  aacttctctg  aaaccgctgc  tcaaacacgt
501  tgccaaaccg  ctgctcctgc  tcaatgccgc  caacgacccc  ttcttgccgc
551  ccgaagccct  gccccgtgca  gacgaagcgt  ccgaagccgt  taccctgttc
601  caactctgac  acggcgggca  cgccggcttt  gtcagcagca  ccggcggcag
651  gctgcacctg  caatggctgc  cgcagaccgt  cctgtcttat  tttgacagct
701  tccgcacaaa  caggcgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1006; ORF 256.ng>:

g256 . pep

1	MLAVNRNRGW	GAVVHFRSCG	GVANTAPVVFY	HLGDTAEIAF	ALDTLTARYR
51	EIYAVGVSLG	GNAPAKYLGE	QGKKALPHAS	AAVSAPVDAE	AAGSRFDSGI
101	TRLLYTRYFL	RTLIPKARSL	QGFQTAFAAG	CKTLGFEDDR	FTAPLHGFPD
151	RDDYYRQTSC	KPLLKHVAKP	LLLLNAANDP	FLPPEALPRA	DEASEAVTLF
201	QPAHGGHAGF	VSSSTGRLHL	QWLQPTVLSY	FDSFRTNRR*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1007>:

m256.seq

1	ATGCTTGCGG	TACGCGATCG	GGGTTGGCAC	GGCGTAGTCG	TCCATTTCGG
51	CAGCTGCGGC	GGCATTGCCA	ACACCGCTCC	GGTGTTCCTAC	CA. CTtGGCG
101	ATACCGGACCA	AATCGCCTTT	ACTTTGGACA	CGTTACGCCG	CGGTTACCGT
151	GAATATACG	CCGTGGCGT	ATCGCTGGGC	GGCAACGGCG	TGGCAAAATA
201	TTTGGGCGAA	CAGGGCAAAA	AGGCATTGCC	CGAAGCGCT	CGCGTCATCT
251	CCGCCCCCGT	CGATGCAGAG	GCGGCAGGCA	GACGCTTCGA	CAGCGGCATC
301	ACGCGCGTGC	TCTACACGCG	CTACTTCCTC	CGCACCTGTA	TACCCAAAGC
351	AAAATCGCTC	CAAGGTTTTT	AGACGGCATT	TGCCGCAAGG	TGCAAAACAC
401	TGGGCGAGTT	TGACGACCGC	TTACCCGACC	CGCTGCACGG	CTTTGCCGAC
451	CGGCACGACT	ACTACGCCCA	AACCTTCCTG	AAACCGCTGC	TCAAAACAGT
501	TGCCAAACCG	CTGCTCCTGC	TCAATGCCGT	CAACGACCCC	TTCCTGCCGC
551	CCGAAGCCCT	GCCCCGCGCA	GACGAAGTAT	CCGAAGCCGT	TACCCTGTTC
601	CAGCCGGCAT	ATGGTGGTCA	TGTCGGCTTT	GTCAGCAGCA	CCGGCGGCAG
651	GCTGCACCTG	CAATGGCTGC	CGCAGACCGT	CCTGTCCTAT	TTCGACAGCT
701	TCCGCACAAA	CAGGCGTTAA			

This corresponds to the amino acid sequence <SEQ ID 1008; ORF 256>:

m256 . pep

```

1  MLAVRDRGW  GVVVHFRSCG  GIANTAPVFY  XLGDTAEIAF  TLDTFAARYR
51  EIYAVGVSLG  GNALAKYLGE  QGKKALPQAA  AVISAPVDAE  AAGRFRDSGI
101  TRLLYTRYFL  RTLIPKAKSL  QGFQTAFAAG  CKTLGEFDDR  FTAPLHGFPAD
151  RHLLYQKQST  KPLLKHVAKP  LLLNNAVDNF  FLPEALPRA  DEVSEAVTLF
201  QPAYGGHVGF  VSSSTGRLHL  QLLPQTVLSY  FDSFRTNRR*

```

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

m256/g256

589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	:     :     :     :     :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

a256.seq

```

1  ATGCTCGCGG TACGCGATCG GGGTTGGAAC GCGTAGTCG TCCATTTCGG
51  CAGCTGCGGC GCGTAGCGA ACACGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACGCGCGA AATTGCCTTT ACTTTGGACA CGCTCGCCG GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGG GCAACGCGC TGGCAAATA
201 TTTGGGCGAA CAGGGCGAAA ACGCGCTGCC GCAAGCCGC GCCGTCATCT
251 CCGCACCCGT CGATGCAGAG GCGGCAGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCGCGCA GACGAAGTGT CCGAAGCCGT TACCTGTTC
601 CAGCCGACAC ACGTGGTCA TGTGCGCTT GTCGCGAGCA CCGCGGCAG
651 GCTGCACCTG CAATGGTTG CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

a256.pep

```

1  MLAVRDRGWN GVVVHFRSCG GVANTAPVFY HLGDTAEIAF TLDTLAARYR
51  EIYAVGVSLG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSCI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVG FVSTGGRLHL QWLPQTVLSY FDSFRTNRR*

```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVHFRSCGGIANTAPVFYXLDGTAEIAFTLDTFAARYREIYAVGVSLG					
	:     :     :     :     :					
a256	MLAVRDRGWNGVVHFRSCGGVANTAPVFYHLGDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQKKALPQAAVISAPVDAEAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	:     :     :     :     :					
a256	GNALAKYLGEQGENALPQAAVISAPVDAEAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCPKLLKHVAKPLLLLNAVNDP					
	:     :     :     :     :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCPKLLKHVAKPLLLLNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	:     :     :     :     :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

g256-1.seq

```

1  ATGATTTTGA CACCGCCGGA CAGCCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAT TCCTGCAACA CCGCACCC GCATACCGCC

```

```

101 GCGAGATGCT TCCCACAGC ACGGGTAAAA CAAAACCGC CTACGACTTT
151 TCAGCAGGCG GCATTTCGCC CGATGCGCCG CTGGTCGTGC TGTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTGCAACTG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GGCAGTCG TCCATTTCGG CAGCTGCGGC
301 GCGTAGCGA ACACCGCCCC GGTGTCTAC CACTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACC GCCTTACCGT GAAATATACG
401 CCGTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTGGGCGAA
451 CAGGCAAAA AGGCATTGCC GCACGCTCG GCCGCCGTAT CCGCCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG TACTTCCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAAACAGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCCTGCCGC CCGAAGCCCT
801 QGFCGTAAG CACGAAGCGT CCGAAGCCGT TACCTGTTC CAACCTGCAC
851 ACGGCGGGCA CGCCGGCTTT GTCAGCAGCA CCGGCGGCAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCTAT TTTGACAGT TCCGCACAAA
951 CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVNRGWH GAVVHFRSCG
101 GVANTAPVYF HLGDTAEIAF ALDTLTARYR EIYAVGVS LG NAPAKYLGE
151 QGKKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFCGTAAG CKTLGEFDDR FTAPLHGFA DHDYRQTSCK PLLKHVAKP
251 LLLNAANDP FLPEALPRA DEASEAVTLF QPAHGGHAGF VSSTGGRHL
301 QWLPTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCC GCGCCC GCATACCGCC
101 GAGAGCTGCT TCCCACAGC ACGGGTAAAA CCAAGTCGCT CTACGACTTT
151 TCAGACGGCA TTTCGCCGGA TGCGCCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGACGCC ATTACGCGGT CGAACTGATG CTTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTTCGCGAG CTGCGGCGGC
301 ATTGCCAACA CCGCTCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCGC
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAAATATTT GGGCGAACAG
451 GGCAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCCCCTCGA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAG CGGCTGCTCT
551 ACACGCGCTA CTCCTCCGC ACCCTGATAC CCAAAGCAA ATCGCTCCAA
601 GGTTTTCAGA CGGCATTGCG CGCAGGCTGC AAAACACTGG GCGAGTTTGA
651 CGACCGCTTC ACCGCACCGC TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCTGTCTCA ATGCCGTCAA CGACCCCTTC CTGCGGCGCG AAGCCCTGCC
801 CCGGCGAGAC GAAGTATCCG AAGCCGTTAC CCTGTTCCAG CCGGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGCTGCCGC AGACCGTCCT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPDTPF FLRNGNADTI AAKFLQHPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVRDRGWHG VVVHFRSCGG
101 IANTAPVYFH LGDTAEIAFT LDTFAARYRE IYAVGVS LGG NALAKYLGEQ
151 GKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPKAKSLQ
201 GFQTAFAGC KTLGEFDDRF TAPLHGFA DR HDYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGGHGVFV SSTGGRHLQ
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

```

10 20 30 40 50 59
m256-1.pep MILTPDTPFFLRNGNADTIAAKFLQHPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
|||||:|||||:|||||:|||||:|||||:|||||
g256-1 MILTPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
10 20 30 40 50 60
60 70 80 90 100 110 119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVRDRGWHGVVVHFRSCGGIANTAPVYFHLGDTAEIAF

```

591

```

|||||
g256-1  LVVLFHGLEGSSRSHYAVELMLAVRNRGWGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
              70      80      90      100     110     120

120      130      140      150      160      170      179
m256-1.p  TLDTFAARYREIYAVGVSLGGNALAKYLGEQGKKALPQAAAVISAPVDAEAAGRFRDSDGI
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1    ALDTLTARYREIYAVGVSLGGNAPAKYLGEQGKKALPHASAAVSAPVDAEAAGSRFRDSDGI
              130      140      150      160      170      180

180      190      200      210      220      230      239
m256-1.p  TRLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRFAPLHGFADRHDIYRQTSC
          |||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1    TRLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFAPLHGFADRHDIYRQTSC
              190      200      210      220      230      240

240      250      260      270      280      290      299
m256-1.p  KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHGVFVSSTGGRLHL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1    KPLLKHVAKPLLLNNAANDPFLPPEALPRADESEAVTLFQPAHGGHAGFVSSTGGRLHL
              250      260      270      280      290      300

300      310      319
m256-1.p  QWLPQTVLSYFDSFRTNRRX
          |||||:|||||:|||||
g256-1    QWLPQTVLSYFDSFRTNRRX
              310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```

a256-1.seq
1  ATGATTTTGA  CACCGCCGGA  CACACCCTTT  TTCTCCGCA  ACGGCAATGC
51  CGACACGATT  GCCGCCAAAT  TCCTGCAACG  CTCGCACCT  GCATACCGCC
101 GCGAGCTGCT  TCCCGACAGC  ACGGGTAAAA  CCAAAACCGC  CTACGACTTT
151 TCAGACGGCA  TTTCGCCCGA  TCGCGCGCTG  GTCGTGCTGT  TTCACGGTTT
201 GGAGGCGGCG  AGTGGCAGCC  ATTACGCGGT  CGAACTGATG  CTCGCGGTAC
251 GCGATCGGGG  TTGGAACGGC  GTAGTCGTCC  ATTTCCGCAG  CTGCGGCGGC
301 GTAGCGAACA  CCGCCCCGGT  GTTCTACCAC  TTGGGCGATA  CCGCCGAAAT
351 TGCCTTTACT  TTGGACACGC  TCGCCGCGCG  TTACCGTGAA  ATATACGCCG
401 TCGGCGTATC  GCTGGGCGGC  AACGCGCTGG  CAAAATATTT  GGGCGAACAG
451 GCGGAAAACG  CGCTGCCGCA  AGCCGCCGCC  GTCATCTCCG  CACCCGTCGA
501 TGCAGAGGCG  GCAGGCAACC  GCTTCGACAG  CGGCATCACA  CGGCTGCTCT
551 ACACGCGCTA  CTTCTCCGCG  AACTGATAC  CCAAAGCAGC  GTCGCTCCAA
601 GGTTCCTCAG  CGGCATTGCG  CGCAGGGTGC  AAAACACTGG  GCGAGTTTGA
651 CGACCGTTTC  ACCGCACCGC  TGCACGGCTT  TGCCGATCGG  CACGACTACT
701 ACCGCCAAAC  TTCCTGCAAA  CCGCTGCTCA  AAGACGTTGC  CAAACCGCTG
751 CTCCTGCTCA  ATGCCGTCAA  CGACCCCTTC  CTGCCGCCCG  AAGCGCTGCC
801 CCGCGCAGAC  GAAGTGTCGG  AAGCCGTTAC  CCTGTTCCAG  CCGACACACG
851 GTGGTCATGT  CGGCTTTGTC  GGCAGACCG  GCGGCAGGCT  GCACCTGCAA
901 TGGTTGCCGC  AGACCGTCCT  GTCCTATTC  GACAGCTTCC  GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```

a256-1.p  1  MILTPDTPF  FLRNGNADTI  AAKFLQRSAP  AYRRELLPDS  TGKTKTAYDF
51  SDGISPDAPL  VVLFHGLEGG  SGSHYAVELM  LAVRDRGWNG  VVHFRSCGG
101 VANTAPVFYH  LGDTAEIAFT  LDTLAARYRE  IYAVGVSLGG  NALAKYLGEQ
151 GENALPQAAA  VISAPVDAEA  AGNRFDSDGI  RLLYTRYFLR  TLIPKARSLQ
201 GFQTAFAAGC  KTLGEFDDRF  TAPLHGFADR  HDYYRQTSC  PLLKHVAKPL
251 LLLNAVNDPF  LPPEALPRAD  EVSEAVTLFQ  PTHGGHGVFV  GSTGGRHLHQ
301 WLPQTVLSYF  DSFRTNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

10      20      30      40      50      60
a256-1.p  MILTPDTPFFLRNGNADTIAAKFLQRSAPAYRRELLPDSTGKTKTAYDFSDGISPDAPL
          |||||:|||||:|||||:|||||:|||||:|||||
m256-1    MILTPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFSDGISPDAPL
          10      20      30      40      50      60

70      80      90      100     110     120
a256-1.p  VVLFHGLEGGSGSHYAVELMLAVRDRGWNGVVHFRSCGGVANTAPVFYHLGDTAEIAFT
          |||||:|||||:|||||:|||||:|||||:|||||
m256-1    VVLFHGLEGSSRSHYAVELMLAVRDRGWNGVVHFRSCGGIANTAPVFYHLGDTAEIAFT

```

592

	70	80	90	100	110	120
	130	140	150	160	170	180
a256-1.pep	LDTLAARYREIYAVGVS LGGNALAKYLGEQGENALPQAAAVISAPVDAEAAAGNRFD SGIT					
m256-1	LDTFAARYREIYAVGVS LGGNALAKYLGEQGGKALPQAAAVISAPVDAEAAAGRRFDSGIT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a256-1.pep	RLLYTRYFLRTLIPKARSLQGFTAFAGCKTLGEFDDRFTAPLHGFA DRHDYYRQT SCK					
m256-1	RLLYTRYFLRTLIPKARSLQGFTAFAGCKTLGEFDDRFTAPLHGFA DRHDYYRQT SCK					
	190	200	210	220	230	240
	250	260	270	280	290	300
a256-1.pep	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPTHGGHVG FVSTGGRLHLQ					
m256-1	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVG FVSS TGGRLHLQ					
	250	260	270	280	290	300
	310	319				
a256-1.pep	WLPQTVLSYFDSFR TNRRX					
m256-1	WLPQTVLSYFDSFR TNRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

g257.seq

```

1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcggcggttt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgcg atgaaaatgt gtttttctgg
151 aaaggtgtcg cgctgggttc cggcgcgag ctgcgctgt tcggcggtga
201 cgacagacag gcggcggtt tggtaataa ggttttggcg gaagtggcgc
251 gtttggaata aatgttcagc ctttaccgtg aagacagcct gatcagcgt
301 ctgaacgcgc acggttatct gacttcgcct ccggcggtt ttttggaaat
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

g257.pep

```

1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMF S LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIFTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

m257.seq

```

1  ATGGGCAGGC ATTTCGGGCG .CAGCGTTT CTGACGGTTG CCGCCGTTGC
51  GGCGGGGAC GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGGAT GAAAAACGCA ATGAAATGT GTTTTCTGG
151 AAAGGTGTCT CACTGGGTTC CGGTGCGG. CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA ATTGTTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTATCT GACTTCGCGG TCGGCGGATT TTTTGGAACT
351 GkTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

m257.pep

```

1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNMD EKRNNVFFW
51  KGVALGSGAX LRLFGVDDR AADLVNKLVA EVARLEKLF S LYREDSLISR
101 LNRDGYLTSP SADFLXLXSL AAIFTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

10 20 30 40 50 60



593

```

m257.pep  MGRHFGRQRFLTVAAVAAGTAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVALGSGAD
          |||||:||||:||||: ||||| ||||| |||||:||||:|||||:|||||:
g257      MGRHFGRRRRFLTAAAVAVAGAASFLPNPFAAGGEKRNMDKKRDENVFFWKGVALGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRRAADLVNKKVLAEEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:||||:||||: ||||| ||||| |||||:||||:|||||:|||||:
g257      LRLFGVDDRQAADLVNKKVLAEEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC ATTTCGGGCG CAGGCGTTTT TTGACAGTTG CCGCCGTTGC
51  GCGGCGCGGC GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAATAAAGAT GAAAAACGCA ATGAAAATGT GTTTTCTGG
151 AAAGGTGTCTG CACTGGGTTC CGGTGCGGAG CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251 GTTTGAAAAA AATGTTTCTG CTTTACCGTG AAGACAGCCT GATCAGCCGT
301 CTGAACCGTG ACGGTTATTT GACTTCGCCG CCGGCGGATT TTTTGGAACT
351 GTTGAGCCTG GCCGTGATAT TCACGCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF LTVAAVAAG AAVSFLPNPF AADDEKRNKD EKRNNVFFW
51  KGVALGSGAE LRLFGVDDRR AADLVNKKVLA EVARLEKMFS LYREDSLIS
101 LNRDGYLTSP PADFLELLSL AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGRQRFLTVAAVAAGXAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVALGSGAX
          ||||| :|||||: ||||| ||||| |||||
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a257      MGRHFGRRRRFLTVAAVAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAE
          10      20      30      40      50
60

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRRAADLVNKKVLAEEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          ||
a257      LRLFGVDDRRRAADLVNKKVLAEEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110
120

m257.pep  AAIFTX
          |||||
a257      AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

g258.seq

```

1 atgcgcccgt tcctaccgat cgcagccata tgcgcccgtc tcctgctgta
51 cggattgacg gcggcgaccg gcagcaccag ttcgctggcg gattatttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctggtggt gtccgcccgtt
151 ttggcacggt atgtcatatt gctgttgaaa gacaggcgca acggcgtggt
201 cggttcgcag attgccaaac gcctttccgg gatgttcacg ctggtcgccc
251 tactgcccgg cttgttcctg ttccggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtgggtcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggccggcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgccca
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccgcga aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgaa agcataggcg gcgtattgta
651 cgcgcaggga tggttgtcgg caggtagcga caacggcgcg gattacgcgc
701 tgttcttccg ccagccgatt cccgaaaatg tggcacagga tgccgttctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgagttaca gaaaaaagg
801 tttgcagacc ttttttctgg taacctgctg gattgcctcg ctgctgtcga
851 tttttcttgc gctggtaatg gcaactgtatt ttgcccgcg tttcgtcgaa
901 cccattctgt cgcttgccga gggcgcaaag gcggtggcg aggggtgattt
951 cagccagacg cgccccgtat tgcgcaacga cgagttcggg cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcg ggaagccgcc cgtcactacc tcgagtgcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctentacccc ctctcttgtt
1151 gccgtaccgc ggtgttttcc acttgctcatt cctccccctt ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

g258.pep

```

1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVLSAV
51 LARYVILLK DRRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFNG
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVFPVQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKRGLQT FFLVTLIAS LLSIFLALVM ALYFARFVE
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLDG LTTGVVVSYP LSCCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

m258.seq

```

1 ATGCGCCGTT TTCTACCGAT CGCAGCCATA TCGCCCGTCG TCCTGTGTGA
51 CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTCTT
101 GGTGGATTGT TCGTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCCG CGTGTTCCTG TTCGGCGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTTG AGCAAGTCCG CATTGAATTT GGCGGCAGAC AACGCCCTCG
401 GCAACGCCGT CCCCCTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCTT
701 TGTTTTTCCG TCAGCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAAGG
801 TTTGCAGACC TTTTCTCTGG CAACCCTGCT GATTGCCTCG CTGCTGTCGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCCGCCG TTTCTGCGAA
901 CCCGTCCTAT CGCTTGCCGA GGGGGCGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TGCGCAACGA CGAGTTCGGA CGCTTGACCA

```

```
1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGGCATTATC TTGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACsTT CAACAAAGCG GCGGAACAGA TTYTGGGGAT GCCGCTTACC
1201 CCCcTGtGGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGGCAACg GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAA GAAGCCGCGT
1451 GGGGCGAAgt GGCGaAgCGG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCCAGC TTTCCGCCGA ACgGsTGGCG TkGAAATTGG GCGGGAAGCT
1551 GGATGAGCAG GATGCGCAAA TCCTGACGCG TTCGACCGAC ACCATCGTCA
1601 AACAGGTGGC GGCATTGAAG GAAATGGTCG AAGCATTCCG CAATTATGCG
1651 CGTTCCCCTT CGCTCAAATT GGAATATCAG GATTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATTGTATG AAGCCGGTCC GTGCCGTTT GCGGCGGACT
1751 TGCCGGCGAA CCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

m258.pep

```
1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51 LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSQAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAVPOQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QRAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDfsQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAAQSSL AEFVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERXA XKLGKLEDEQ DAQILTRSTD TIVKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AADLPANR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

m258/g258

```
10 20 30 40 50 60
m258.pep MRRFLPIAAICAVVLLYGLTAATGSTSSLADYFWWIVAFSAML VLSAVLARYVILLK
|||||
g258 MRRFLPIAAICAVVLLYGLTAATGSTSSLADYFWWIVSFSAM L VLSAVLARYVILLK
10 20 30 40 50 60

70 80 90 100 110 120
m258.pep DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
|||:|||||
g258 DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLFGISAQFINGTINSWFGNDTHEALERSLNL
70 80 90 100 110 120

130 140 150 160 170 180
m258.pep SKSALNLAADNALGNAVPOQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
|||:|||||:|||||:|||||:|||||
g258 SKSALDLAADNAVSNAPVQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK
130 140 150 160 170 180

190 200 210 220 230 240
m258.pep SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
|||:|||||:|||||:|||||:|||||
g258 SINPHQFDQPLPDKEHWEIQQTGSVRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI
190 200 210 220 230 240
```

	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAELSSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE					
g258	PENVAQDAVLIEKARAKYAELSSYSKKGLQTFFLVTLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDFSQTRPVLNRNDEFGRLTKLFNHMTEQLSIAKEADERNRRREEAA					
g258	PILSLAEGAKAVAQGDFSQTRPVLNRNDEFGRLTKLFNHMTEQLSIAKEADERNRRREEAA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVFDEQGCLKTFPNKAAEQILGMPLTPLWGSSRRHGWHGVSAAQSSL					
g258	RHYLECVLDGLTTGVVVSYPPLSCCRTAVFSTCHSSPLSYFX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1027>:

```

a258.seq
1 ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCG TCCTGTTGTA
51 CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTTC
101 GGTGGATTGT TGCCTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCGGTT
151 TTGGCAGCTT ATGTCAATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGAG ATTGCCAAAC GCCTTTCCGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTTTCTG TTCGCGGTTT CCGCACAGTT TATCAACGGC
301 ACGATTAAAT CGTGGTTCGG CAACGATACC CACGAGCGCG TTGAACGCGA
351 CCTCAATTGG AGCAAGTCCG CATTGAATCT GCGCGCAGAC AACGCCCTTG
401 GCAACGCCAT CCCCGTGCAG ATAGACCTCA TCGCGCGCGC TTCCTGCCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAGCT CGATCAGCCG TTTCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACAGCGCG GTTTCGGTCAG GGATTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGCG TGGCTGTCGG CAGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGCGCAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTCTCTGG AACCTGCTG GATTGCTCG CTGCTGTGCA
851 TTTTCTTGCT ACTGGTCATG GCACTGTATT TCGCCGCGCG TTTCTGCGAA
901 CCCGTCTAT CGCTTGCCGA GGGGCGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TGCGCAACGA CGATTCGGA CGCTTGACCA
1001 AGTTGTTCAA CCACATGACT GAGCAGCTTT CCATCGCCA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCGCGC AGACATTATC TCGAATCGGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACCTT CAACAAAGCG GCGGAACAGA TTTTGGGGAT GCCGCTTACC
1201 CCCCCTGGG CGACGAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTTCTTGCTT GCCGAGGTGT TTCCGCCAT CCGCGCGCGC GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGC AACGGCAAGG GCGTGGTAA
1401 GGTGATTGAC GACATCACC TTGGATACA CGCGCAAAA GAAGCCCGGT
1451 GGGGCGAAGT GGCAAAACGG CTCGACACG AAATCCGCA TCCGCTACG
1501 CCCATCCAGC TTTCTGCCGA ACGGCTGGCG TGGAATTTGG CGCGGAAGCT
1551 GGACGAGCAG GACGCGCAAA TCCTGACACG TTCGACCGAC ACCATCATCA
1601 AACAAGTTGC GGCATTAATA GAAATGGTCG AGGCATTCCG CAATTACGCG
1651 CGTTCCTCTT CGTCAAATT GAAAAATCAG GATTGAACG CCTTAATCGC
1701 CGATGTGTTG GCATTGTACG AAGCTGGTCC GTCCGGTTT CCGCGCGAAG
1751 TTGCCGCGA ACCGCTGATG ATGGCGGCGG ATACGACCGC CATGCGGCAG
1801 GTGCTGCACA ATATTTTCAA AAATGCCGCC GAAGCGGCGG AAGAAGCCGA
1851 TGTGCCCGAA GTCAGGGTAA AATCGGAAG GGGGCAAGG GGCAGGATTG
1901 TCCTGACAGT TTGCGACAA GGCAGAAGGT TCGCGAGGAA ATAGTCTGAC
1951 AATGCCTTCG AGCCGTATGT AACGGACAAA CCGGCTGGAA CGGGATTGGG
2001 ACTGCCCGTG GTGAAAAAAA TCATTGAAGA ACACGGCGCG CGCATCAGCC
2051 TGAGCAATCA GGATGCGGGC GCGCGGTGTG TCAGAATCAT CTTGCCAAAA
2101 ACGGTAGAAA CTTATCGGTA G

```

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```
a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQQ WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLNRNDEF RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLDEQ DAQILTRSTD TIIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIFKNAA EAAEEADVPE VVRKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIIEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*
```

m258/a258 99.0% identity in 584 aa overlap

```

      10      20      30      40      50      60
m258.pep  MRRFLPIAAICAVVLLYGLTAATGSTSSSLADYFWWIVAFSAML VLSAVLARYVILLK
          |||
a258      MRRFLPIAAICAVVLLYGLTAATGSTSSSLADYFWWIVAFSAML VLSAVLARYVILLK
          |||
      70      80      90     100     110     120
m258.pep  DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
          |||
a258      DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
          |||
     130     140     150     160     170     180
m258.pep  SKSALNLAADNALGNAVFPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||
a258      SKSALNLAADNALGNAIPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||
     190     200     210     220     230     240
m258.pep  SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQQWLSAGTHNGR DYALFFRQPV
          |||
a258      SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQQWLSAGTHNGR DYALFFRQPV
          |||
     250     260     270     280     290     300
m258.pep  PKGVAEDAVLIEKARAKYAELSYSKKGLQTF FLATLLIASLLSIFLALVMALYFARRFVE
          |||
a258      PKGVAEDAVLIEKARAKYAELSYSKKGLQTF FLATLLIASLLSIFLALVMALYFARRFVE
          |||
     310     320     330     340     350     360
m258.pep  PVLSLAEGAKAVAQGDFSQTRPVLNRNDEFGR LTKLFNHMT EQLSIAKEADERNRRREEAA
          |||
a258      PVLSLAEGAKAVAQGDFSQTRPVLNRNDEFGR LTKLFNHMT EQLSIAKEADERNRRREEAA
          |||
     370     380     390     400     410     420
m258.pep  RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLT PLWGSSRHGW HGVSAQQSLL
          |||
a258      RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLT PLWGSSRHGW HGVSAQQSLL
          |||
     430     440     450     460     470     480
m258.pep  AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
          |||
a258      AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
          |||
```

598

	430	440	450	460	470	480
	490	500	510	520	530	540
m258 . pep	EAAWGEVAKRLAHEIRNPLTPQLSAERXAXKLGGKLEQDAQILTRSTDITVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPQLSAERLAWKLGGKLEQDAQILTRSTDITIKQVAALK					
	490	500	510	520	530	540
	550	560	570	580	589	
m258 . pep	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNIKFNAEEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

```

g259 . seq
1  atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaatctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgcgcgatt gtccgcgctc
151 gcgctggtgt ggctggcggtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaatgctc
301 gccctgctgg tcaaaaacca cggcaaaagg atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccg acgacgaaga cgcgcgcacg attgccgccc
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgcctcg
451 ggcgaaacct atgggcgcggt gtccgccgat attttcgagt tgcggcgccg
501 tttggaaagg cgcgcgttca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcgttga gggaaatctc gaaaacgccc gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

```

g259 . pep
1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKKHLRRC LPFGNGVGFG
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

```

m259 . seq (partial)
1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAATACTTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACKGACGC GGTCCGCTCG
451 GCGGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGmGGC
501 TTTGGAAGGG CGCGCGTCA AAGGAATGTT GAACTGACG GCGGAATATA
551 AA . AACATCT TCGmGATGC CTGCCGTTCG GAAACGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCC GG .

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

```

m259 . pep (partial)
1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS

```

599

151 GETYGRVPAD IFELSXALEG RAFKGLMLKT AEYKXHLRRC LPFGNGVGVG  
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVPADIFELSXALEGRAFKGLMLKT					
g259	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVPADIFELSAALERRAFKGLILKT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRCCLPFGNGVGVGRQTQSGVAGDFKNIR					
g259	AEYKXHLRRCCLPFGNGVGFGRQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

```

1  ATGATGATGC  ACGCTTCTGT  CCAAAGCCGT  TTCGCACCGA  TACTTTATGT
51  TTTGATTTTC  TTTGCCGGTT  TTTTGACCGC  GCAAACTCTG  TCAATCAGA
101 AAGCCTATAC  TGAAGAGCTG  CCTCCGCTTC  TGTCCGCATT  GTCCGCCGTC
151 GCGCTGGTGT  GGCTGGCGTG  GGCCTTCGTG  TCGGCGCGTT  CAAAGGCTAA
201 GCGCGAAAAG  TTCTACCGCG  AAAAAATGAT  ACAGAACGAA  AGCATAACAC
251 CCGTCTCTGA  CGCTTCTTTG  CAACACTTGG  AACACAAGCC  GCAAATGCTC
301 GCCCTGCTGG  TCAAAAACCA  CGGCAAAGGG  ATGGCGGAAC  AGGTCAGGTT
351 CAAGGCGGAA  GTGCTGCCCC  ACGACGAAGA  CGCGCGCAGC  ATTGCCGCCG
401 AGTTGGCAAA  AATGGATATG  TTTGCATTGG  GGACGGACGC  GGTGCGCTCG
451 GCGGAAACCT  ATGGACGCGT  GTTCGCCGAT  ATTTTCGAGT  TGTGCGCGGC
501 TTTGGAAGGG  CGCGCGTTCA  AAGGAATGTT  GAAACTGACG  GCGGAATATA
551 AAAA.CATCT  TCGGCGATGC  CTGCCGTTTC  GAAACGGCGT  TGGAGTTGGG
601 CGCGCTCAAT  CAGGCGTTGC  AGGAGATTTC  AAAACATCG  GAAAAGTCCA
651  A

```

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

```

1  MMMHASVQSR  FAPILYVLIF  FAGFLTAQIW  FNQKAYTEEL  PPLLSALSAV
51  ALVWLAWAFV  SARSKAKAEK  FYREKMIQNE  SIHPVLHASL  QHLEHKPQML
101 ALLVKNHGKG  MAEQVRFKAE  VLPDDEDART  IAAELAKMDM  FALGTDVAS
151 GETYGRVPAD  IFELSAALEG  RAFKGLMLKT  AEYKXHLRRC  LPFGNGVGVG
201 RAQSGVAGDF  KNIGKVQ

```

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					

600

	10	20	30	40	50	60
m259.pep	70	80	90	100	110	120
a259	70	80	90	100	110	120
m259.pep	130	140	150	160	170	180
a259	130	140	150	160	170	180
m259.pep	190	200	210			
a259	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGTGCGTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GCGGAAACCT ATGGCGCGGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GCGGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG CGCGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCCG AAACGGCGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTTC AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGLMLLT AEYKNIFGDA CRSETALELG
201 ALNQLQEIIS KTSEKSKRIF Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap



601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALS AVLVWLAWAFV					
m259-1	MMMHASVQSRFAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALS AVLVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGMAEQVRFKAE					
m259-1	SARSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALE					
m259-1	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALEGRAFGMLKLT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1  ATGATGATGC  ACGCTTCTGT  CCAAAGCCGT  TTCGCACCGA  TACTTTATGT
51  TTTGATTTTC  TTTGCCGGTT  TTTTGACCGC  GCAATCTGG  TTCAATCAGA
101 AAGCCTATAC  TGAAGAGCTG  CCTCGCTTC  TGTCCGCATT  GTCCGCCGTC
151 GCGCTGGTGT  GGCTGGCGTG  GCGTTCGTG  TCGGCGCGTT  CAAAGGCTAA
201 GCGGAAAAG  TTCTACCGCG  AAAAAATGAT  ACAGAACGAA  AGCATACACC
251 CCGTCCTGCA  CGCTTCTTTG  CAACACTTGG  AACACAAGCC  GCAATGCTC
301 GCCCTGCTGG  TCAAAAACCA  CGGCAAAGGG  ATGGCGGAAC  AGGTCAGGTT
351 CAAGGCGGAA  GTGCTGCCCG  ACGACGAAGA  CGCGGCACG  ATTGCCGCGG
401 AGTTGGCAAA  AATGGATATG  TTTGCATTGG  GGACGGACGC  GGTGCGCTCG
451 GCGGAAACCT  ATGGACGCGT  GTTCGCCGAT  ATTTTCGAGT  TGTGCGCGGC
501 TTTGGAAGGG  CGCGCGTTCA  AAGGAATGTT  GAACTGACG  CGCGAATATA
551 AAAACATCTT  CGCGGATGCC  TGCCGTTGCG  AAACGGCGTT  GGAGTTGGGC
601 GCGCTCAATC  AGGCGTTGCA  GGAGATTTC  AAAACATCGG  AAAAGTCCAA
651 ACGGATATTT  TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1  MMMHASVQSR  FAPILYVLIF  FAGFLTAQIW  FNQKAYTEEL  PPLLSALSAV
51  ALVWLAWAFV  SARSKAKAEK  FYREKMIQNE  SIHPVLHASL  QHLEHKPQML
101 ALLVKNHKGK  MAEQVRFKAE  VLPDDEDART  IAAELAKMDM  FALGTD AVAS
151 GETYGRVFAD  IFELSAALEG  RAFKGLMLLT  AEYKNIFGDA  CRSETALELG
201 ALNQLQEIIS  KTSEKSKRIF  Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALS AVLVWLAWAFV					
m259-1	MMMHASVQSRFAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALS AVLVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGMAEQVRFKAE					
m259-1	SARSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALEGRAFGMLKLT					
m259-1	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALEGRAFGMLKLT					
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALELGALNQLQEIISK TSEKSKRIFYX					
m259-1	AEYKNIFGDACRSETALELGALNQLQEIISK TSEKSKRIFYX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

```

1  atgggtgcgg gtgtagtatt cgttgtcttt cagccgttct tcagcctgtt
51  tcgagcggtg ttcgagggcg gagtcggtat agtcgagggg gcgcacgatg
101 ccgctgaatg cgacttcttg tccgaggaat ttaccctgat ccggatcggg
151 gatgttttta ttgattcggg aggtcagata acggcccggt tctttcaggc
201 ctttggtgta aaccctggcg cctttggtgt acagcagcct gccttcggg
251 cccgagagca ggcgcggcgc ggcagcgggt tctttgcggg aaacgatttg
301 cgggtgctgc ataaagacgc ggtagaagtt gacatcgatg gcgggaatac
351 cgtatccgga cacttcctta tccggactga ttttgacgac ggggatgccc
401 tctgtctgtt ccaagccgag gcgcgggttc ccgccaacgt agcgcaacac
451 caatacctgg cccggataaa tcaggtcggg attgtggatt tgatcccggt
501 tcgcgcccc caggggggga ccattgccac gggctgtaca ggtatttgcc
551 cgaaataccc cacagggtgt cgccctgttt ga

```

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

g260.pep

```

1  MGAGVVFVVF QPFSSLFRL FEGGVGIVEG AHDAAECDL PEEFTRIRIG
51  DVFIDSVGQI TARFFQAFGV NPGAFGVQP AFRAREQARR GSGFFAGNDL
101 RVLHKDAVEV DIDGNTVSG HFLIRTFDD GDAVCLFAE ARFAANVAQH
151 QYLARINQVG IVDLIPVRAP QGGTIATGCT GICPKYPTGC RPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1043>:

m260.seq

```

1  ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTSTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCCTGGTG CTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGwCA sGCGCGyGC GGCAGCGGTT TCTTTCGGG AAACGATTG
301 CGGATGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTG CCGTCAACGT GCGCAACAC
451 CAATACCTGG TCCGGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTyCCA CAG

```

This corresponds to the amino acid sequence <SEQ ID 1044; ORF 260>:

m260.pep

```

1  MGAGMVVFVF RPFSSLFRL FEDRVGIVEG AHDAAECDL PEEFTRIRIG
51  DVFIDSVGQV AARLFQAFGV NPGAFGVQP AFRARXXARX GSGFFAGNDL
101 RMPHKDAVEV DIDGNTVSG HFLIRTFDD GDAVCLFAE ARFAVNVAQH
151 QYLVRINQVG IVDLIPVRVP Q

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

```

          10      20      30      40      50      60
m260.pep  MGAGMVVFVFRPFSSLFRLFEDRVGIVEGAHDAAECDLP EEFTRIRIGDVFIDSVGQV
          |||:||||:| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g260      MGAGVVFVVFQPFSSLFRLFEGGVGIVEGAHDAAECDLP EEFTRIRIGDVFIDSVGQI
          10      20      30      40      50      60

          70      80      90      100     110     120
m260.pep  AARLFQAFGVNPGAFGVQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGNTVSG
          |:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g260      TARFFQAFGVNPGAFGVQPAFRAREQARRGSGFFAGNDLRVLHKDAVEVDIDGNTVSG
          70      80      90      100     110     120

          130     140     150     160     170
m260.pep  HFLIRTFDDGDAVCLFAEARFAVNVAQH QYLVRINQVGIVDLIPVRVPQ
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g260      HFLIRTFDDGDAVCLFAEARFAANVAQH QYLARINQVGIVDLIPVRAPQGGTIATGCT
          130     140     150     160     170     180

```

g260 GICPKYPTGCRPV  
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

a260.seq  
1 ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTCT CCAGCCTGTT  
51 TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACCATG  
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT  
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC  
201 CTTTGGTGTA AACCTGGTG CTTTGGTGT ACAGCAGCCT GCCTTCCGGG  
251 CCCGAGAGCA GGCGCGGCGC GGCAGCGGTT TCTTTCGCGG AACGATTTG  
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC  
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG  
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTTC CCGTCAACGT GGCGCAACAC  
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT  
501 TCGCGTCCCA CAGGCGGCC. CCATTGCCAC GGGCTGTACA GGTATTGACC  
551 CGAAATGCCC CACAGGTGT CGCCTGTTT GA

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

a260.pep  
1 MGAGMVVFVF RPFSSLFRL FEDRVGIVEG AHDAECDL PEEFTRIRIG  
51 DVFIDSVGV AARLFQAFGV NPGAQVQPA AFRAREQARR GSGFFAGNDL  
101 RVPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH  
151 QYLVQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV\*

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFSSLFRLFEDRVGIVEGAHDAECDLPEEFTRIRIGDVFIDSVGVQV					
a260	MGAGMVVFVFRPFSSLFRLFEDRVGIVEGAHDAECDLPEEFTRIRIGDVFIDSVGVQV					
	10	20	30	40	50	60
m260.pep	AARLFQAFGVNPGAQVQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
a260	AARLFQAFGVNPGAQVQPAFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVPQ					
a260	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVQAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
						190

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

g261.seq  
1 atggagcttg ggcatatcgt attccttgtg ctttgcgcgc gttcagacgg  
51 cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag  
101 ctccggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt  
151 ctgttcgcgg atgtagtcga acacgcccatt ttcgtccgcg aacgcccacg  
201 tttgcgcctt ggtcaggtac atcagcggcg tgtggatttg aaaatcgtag  
251 tccatcgcca gattaagggt aacgttcgat gatttgacga acacgccgcg  
301 gcagtcggga tagcccgaaa aatcggtttc gcacacgccc gcgatgatgt  
351 gccggatacc ctgccctttg gcaaaaatgg cggcgtaaaag caggaaaagc  
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgttg cggcggtttc  
451 gatggcggcg gtttcgatgg cggcggtttc gtccatcagg gcgttgtgcg  
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa  
551 tcctgcgcga tccactctgc gcgttcacgc tcgacggcat ggcgttgccc  
601 gtatcggaag gtgatggctt ggacgttttc gcgcccgtag gtttgattg



651 cctgaatcag gcaggtggtc gaatcctgac cgcccgagaa gatgaccaag  
701 gcttttttqqt ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep

1	MELGHIVFLV	LCARSDGLFT	FQTFRQPAFA	QDARAFAAA	ADDTLVAGVG
51	LFADVQHAH	FVRQRPRLRL	GQVHQRRVDL	KIVVHRQIKG	NVHGDFEHA
101	AVGIARKIGF	AHARDDVPDT	LPFGKNGGVK	QEKRVTPVHK	GIGNAVVGGF
151	DGGGFDGGG	VHQGVVRNLP	HQAQIEYGLT	DTQILRDLPL	AFQLDGMALP
201	VSEGDGLDVF	APVGLDCLNQ	AGGRILTARE	DDOGLFV*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq

1	ATGGAGCTTG	GGCATATCGT	ATTCTTATG	GTTTGCGCGT	GTTCAGACGG
51	CCTTTTACT	TTCCAGATAT	TCCGCCAGCC	cGcGTTcGCG	CAAGATACAG
101	CTCGGGCAT	CCGCGcGACC	GCCGACGAT	CCGTTATAG	AGGTGTGGGT
151	TTTGCGCGG	ATATAGTCCA	GcAGCCCAT	TTcGTcCGCC	AACGCCACG
201	TTTGCGCCT	GGTCAGATAC	ATCAGCGGCG	TGTGGATTTG	AAAATCATAG
251	TCCATCGCCA	AATTAGGGT	AACGTTcATC	GATTTGACAA	ACACGTcGCG
301	GCAGTcGGGA	TAGcCGGAGA	AGTcGGTTTC	GCACACGCC	GGcATGATGT
351	GCCGTATCCC	CTGCCCTTTG	GGCTAAATCG	CGGCATAGAG	CAGGAAAGcG
401	gcGTTCGCGC	CGTCTACAAA	GGTATTCGGA	AcGCCGTTTT	CGCGAAGTTTC
451	GATGGCGGCG	GTGTCGTCCA	TCAGGGcATT	GTGCGTAATC	TGCCGCATCA
501	GgCTcAAGTC	GAGTACGGTT	TGTTTGACGC	CCAAATcCTG	CGCAATCCAG
551	CGGGcACGCT	CCAGcCTCGAC	GGcATGGcCT	TGCCCgTATT	GGAAAGTAAAT
601	GGCTTGcAGT	TTTTCGCGCC	CGTAGGTTTG	GATTGCCTGA	ATCAGGcAGG
651	TGGTCGAATC	CTGACCGCCC	GAAAGATGA	CcAGGCTTTG	TTGgTTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep

1	MELGHIVFLM	VCACSDGLFT	FOIFRQPAFA	QDTARAFAAA	ADDAVIAGVG
51	LLADTVQHAH	FVRQRPRRL	GQIHQRRVDL	KIIVHRQIKG	NVHRFDKHVA
101	AVGIAGEVGF	AHARDLVPYV	LPFGVNRGIE	QEKRVAAVYK	GIRNAVFGSF
151	DGGGVVHQGI	VRNLPHQAQV	EYGLFDAQIL	RNPAGTFQLD	GMALPVLSEN
201	GLDVFAPVGL	DCLNQAGGRI	LTARKDDOGL	LV*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/q261

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQD	TARAF	AAAADD	AVIAGV	GLLADI	VQHAH
	: :                                 : : :         :   :					
g261	MELGHIVFLVLCA	RSDGLFTFQTFRQPAFAQD	TARAF	AAAADD	TLVAGV	GLFADV
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQI	HQRRVDLKIIVHRQIKGNV	HFRDKHVA	AVGIAGEV	GF	AHARD
	:             :                             :   :					
g261	FVRQRPRLRLGQV	HQRRVDLKIIVHRQIKGNV	HGFDEHAA	AVGIARKIG	F	AHARD
	70	80	90	100	110	120
	130	140	150	160	170	
m261.pep	LPFGVNRGIEQE	KRVA	AVYKGIRNA	VFGSFDGGGV	-----VHQGI	VRNLPHQ
	: :         :   :                                   :					
g261	LPFGKNGGVKQ	EKRVT	TPVHKGIGNA	VVGFFDGGG	FDGGGFVHQGV	VRNLPHQ
	130	140	150	160	170	180
	180	190	200	210	220	230
m261.pep	DAQILRN	PAGTFQ	LDGMALP	VLES	NGLDV	FAPVGLDCLNQ
	:       :   :                 : :                                 :   :					
g261	DTQILRD	PLCAFQ	LDGMALP	VSEGD	GLDV	FAPVGLDCLNQ
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCAAG
201 TTTGCGCCTT GGTCAGATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTGT GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCCGA ACGCCGTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTTTGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGCC CGTAGGTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPSLRL GQIHQRRVDL KIIVHRQIKG NVHGFDKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAPVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQRAH					
	10	20	30	40	50	60
m261.pep	70	80	90	100	110	120
	FVRQRPRRLRGQIHQRRVDLKIIVHRQIKGNVHRFDKHVAAVGIAGEVGFHARDDVPYP					
a261	FVRQRPSLRLRGQIHQRRVDLKIIVHRQIKGNVHGFDKHVTAVGIAGEVGFHARDDVPYP					
	70	80	90	100	110	120
m261.pep	130	140	150	160	170	180
	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV EYGLFDAQIL					
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV EYGLFDAQIL					
	130	140	150	160	170	180
m261.pep	190	200	210	220	230	
	RNPAGTFQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGFVLX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgccaa
51  accgcgcgta gaggccgtac ccaaaaacaa cggctttatc cccaacctca
101 tcggcggtatt ggcaaacgcc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgcccgaac cagcctgacc gccggcggaag tcgaagtgat
201 ccggatcatc gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acaccaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgccccgc ctttggcggc aggtaaatct gacgatgcc aactcggcgc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

451 gtcgaagtcg taatgggcgt agccttggca actttgtgca actacgccaa  
501 caacctcgcc caaacccgaaa tcaaccccaa attgcaggca tacgcctaa

This corresponds to the amino acid sequence <SEQ ID 1054; ORF 263.ng>:

g263 . pep

1 MARLTVHTLE TAPEAAKPRV EAVPKNNGFI PNLIGVLANA PEALAFYQEV  
51 GKLNAANSLT AGEVEVIRII AVR TNQCSFC VAGHTKLATL KKL LSEQSLN  
101 AARALAAGKS DDAKLGALAA FTQAVMAKKG AVSDDELNAF LEAGYNRQQA  
151 VEVVMGVALA TLCNYANNLA QTEINPKLQA YA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1055>:

m263.seq (partial)

```

1      ..GCAGCAGGCG AATTTGACGA TGCCAAACTC GGC GCGCTCG CCGCCTTCAC
51     CCAAGCCGTA ATGCGCAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101    CATTTTTCGA TGCGGGGTCA AACCCAGCAGC AGGCAAGTCGA AGTCGTGATG
151    GGCGT.AsyC TgGCAACTCT GTCAACTAC GTCAACAACC TCGGACAAAC
201    CGAATCAAC CCCGAATTGC AGGCTTACGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1056; ORF 263>:

m263.pep (partial)

```

1      ..GCAGCAGGCG AATTTGACGA TGCCAAACTC GGCGCGCTCG COGCTTCAC
51     CCAAGCCGTA ATGCGCAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101    CATTTTTCGA TGCGGGGTCA AACCAGACAG AGGCAGTCGA AGTCGTGATG
151    GGCGT.AsyC TgGCAACCTC GTGCAACTAC GTCAACAACC TCGGACAAAC
201    CGAAATCAAC CCGGAATTGC AGGCTTACGC

```

Computer analysis of this amino acid sequence gave the following results:

**Homology with a predicted ORF from *N. gonorrhoeae***

ORF 263 shows 85.7% identity over a 77 aa overlap with a predicted ORF (ORF 263.ng) from *N. gonorrhoeae*:

m263/q263

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1057>:

a263.seq

1	ATGGCACGTT	TAACCGTACA	CACCTCGAA	ACCGCCCCG	AAGCGCCAA
51	AGCGCGCGTC	GAGGCGGTAC	TTCAAACAA	CGGCTTTATC	CCCAACCTTA
101	TCGGCGTATT	ATCAAACGCC	CCCGAAGCCT	TGGCGTTTTA	CCAAGAAGTC
151	GGCAAGCTCA	ACCGCGCCAA	CAGCCTGACC	GCCGGCGAAG	TCGAAGTAAT
201	CCAGATTATT	GCCGCCCGCA	CCAACCAATG	CGGCTTCTGC	GTGGCAGGGC
251	ACACCAAAC	CGCAACCTG	AAAAAACTCC	TTCCGAACA	ATCCGTCAAA
301	GCCGCGCGCG	CTTTGGCGGC	AGGCGAATTT	GACGATGCTA	AACTCGGCGC
351	GCTCGCCGCT	TTTACCCAAG	CCGTAATGGC	AAAAAAAGGC	GCGGTATCCG
401	ACGGAAGACT	CAAGCATATT	TTTGATCGCG	GCTACAACCA	GCACGAGGCA
451	GTCTGAAGTCG	TGATGGGCGT	AGCATTGGCA	ACTTTGTGCA	ACTACGTCAA
501	CAACCTCGGA	CAAACCGAAA	TCAACCCGGA	ATTGCAAGCT	TACGCCTGA

This corresponds to the amino acid sequence <SEQ ID 1058: ORF 263.a>:

a263.pep

1 MARLTVHTLE TAPEAAKARV EAVLQNNGFI PNLIGVLSNA PEALAFYQEV  
51 GKLNAANSLT AGEVEVIQII AARTNQCGFC VAGHTKLATL KLLSEQSVK  
101 AARALAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQQA  
151 VEVVMGVALA TLCNYVNNLG QTEINPELOA YA\*

**m263/a263 97.4% identity in 77 aa overlap**

```

                                10      20      30
m263.pep                      AAGEFDDAKLGALAAFTQAVMAKKGAVSDE
                                |||||
a263      QCGFCVAGHTKLATLKKLLSEQSVKAARALAAGEFDDAKLGALAAFTQAVMAKKGAVSDE
           80      90      100      110      120      130

           40      50      60      70
m263.pep  ELKAFFDAGYNQQQAVEVVMGXSLATLCNYVNNLGQTEINPELQAYAX
           |||||
a263      ELKAFFDAGYNQQQAVEVVMGVALATLCNYVNNLGQTEINPELQAYAX
           140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

```
g264.seq
1   ttgactttaa cccgaaaaac ccttttcctc ctcaccgcgc cggttcggcac
51  acactccctt cagacggcat ccgcgcgacgc agtggtcaag ccggaaaaaac
101 tgcacgcctc gcccaaccgc agctacaaag tcgcggaatt caccgaaacc
151 ggcaacgcct cgtgggtacgc cggcagggtt caccggcgca aaacttcogg
201 cggagaccgc tacgatatga acgcctttac cgccgcccac aaaaccctgc
251 ccatccccag ccatgtgcgc gtaaccaaca ccaaaaacgc caaaagcgtc
301 atcgtcgcgc tcaacgcacc cggcccccctt caccgcgaac gcatcatcga
351 cgtatccaaa gccgcgcgcg aaaaattggg ctttgtcagc caagggcagg
401 ccacgctcaa aatcgaacaa atcgtccgcg gccaatccgc accggttgcc
451 gaaaacaaag acatctttat cgacttgaaa tctttcggta cggaacacga
501 agcacaagcc tatctgaacc aagccgccca aaatttcgcc gcttcgtcat
551 caagcccga cctctcggtt gaaaaacgcc gttacgaata cgttgtcaaa
601 atgggccgtt ttgctcgcta ggaacgcgcc cgcgaagccg aagcgcaggc
651 acgcggtatg gttcgggcgc tactgacctc cgggtga
```

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

g264.pep

1	<u>LT</u> LT <u>TR</u> KT <u>LT</u> FL <u>LT</u> AAFG <u>TH</u> SL QTASADAVVK PEKLHASANR SYKVAEFTQT
51	GNASWYGGRF HGRRTSGGDR YDMNAFTA AH KTLPTPSHVR VTNTKNGKSV
101	IVRVNDRGPF HGNRIIDVSK AAAQKLGFVS QGTAHVKIEQ IVPQGQSAPVA
151	ENKDIFIDLK SFGTEHAQA YLNQAAQNFA ASSSSPNLSV EKRRYEVVVK
201	MGPFASQERA AEAEAQARGM VRVLTSG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

m264.seq

```
1   TTGACTTTAA CCCGAAAAAC CCTTTTCCTT CTCACGCCG CATTCCGGCAC
51  ACACTCCCTT CAGACGGCAT CCGCCGACGC AGTGGTCAAG GCAGAAAAAC
101 TGCACGCCTC CGCCAACCGC AGTACAAAG TCGCCGGAAA ACGCTACACG
151 CCGAAAAAAC AAGTCGCCGA ATTCACGCAA ACCGGCAACG CCTCGTACGTA
201 CGGCGGCAGG TTTCACGGGC CAAAAAATTC CGCGGAGAA CGATACAGTA
251 TGAACGCCTT TACCGCGGCC CAAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGTA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAAAAT GGGCTTTGTC AACCAAGGGA CGGCACAACG CAAAATCGAA
451 CCAATCGTCC GCGGCCAATC CGCACCGGTT GCGGAAAACA AAGACATCTT
501 TATCGACTTG AAATCTTTCG GTACGGAAAC GAAGCACAA GCCTATCTGA
551 ACCAAGCCGC CAAAACCTTC GCCGTTTCGT CATCGGGTAC GAACCTCTCG
601 GTTGA AAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTTACCTC
651 CGGAGGAACG GCCGCCGAAG CCGAAGCTCA GCGCGCGGAT ATGGTTCGGG
701 CGGTATTGAC CGCCGGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264 . pep

1	<u>LT</u> LT <u>TR</u> KT <u>LF</u> LT <u>FL</u>	<u>LT</u> AA <u>FG</u> TH <u>SL</u>	<u>QT</u> ASADAVVK	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGG	R	FHGRKTS	SGGE
101	RV	TNTKNGKS	V	VIVRNDRGP	F
151	Q	IVPGQSAPN	A	ENKDFIDP	L
201	VE	KRRYEVV	K	MGPP	TSQER

AAEEAQAARG MRAVLTA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKAELHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKAELHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHHGRKTSGGERYDMNAFTAHHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHHGRKTSGGDRYDMNAFTAHHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLGFSVQGTAAHVKEIQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ					
g264	FHGNRIIDVSKAAQKLGFSVQGTAAHVKEIQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPFQSQERAAEAQARGMVRVLTAGX					
g264	AYLNQAAQNFAASSSPNLSVEKRRYEYVVKMGPFASQERAAEAQARGMVRVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

1	TTGACTTTAA	CCCGAAAAAC	CCTTTTCCTC	CTCACCGCCG	CATTCCGGCAT
51	ACATTCCTTT	CAGACGGCAT	CCGCCGACGC	AGTGGTCAGG	GCAGAAAAAC
101	TGCACGCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGAAA	ACGCTACACG
151	CCGAAAAACC	AAGTCGCCGA	ATTACGCAG	ACCGGCCAAG	CCTCGTGGTA
201	CGGCGGCAGG	TTTACGGGCG	GCAAACTTC	CGGCGGAGAA	CGATACGATA
251	TGAACGCCTT	TACCGCGGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTCATCGTCC	GCGTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCGG
401	CGCAAAAATT	GGGCTTTGTC	AACCAAGGGA	CGGCGCACGT	CAAAATCGAA
451	CAAATCGTCC	CGGGCCAATC	CGCACCGGTT	GCCGAAAACA	AAGACATCTT
501	CATCGACTTG	AAATCTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCCG	CCAAAACCTG	GCTTCATCGG	CATCAAACCC	GAACCTCTCG
601	GTTGAAAAAC	GCCGTTACGA	ATACGTCGTC	AAAATGGGAC	CGTTTGCCTC
651	GCAGGAACGC	GCCGCCGAGG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTAAC	CGCCGGTTGA			

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

1	LTLTRKTLFL	LTAAFGIHSF	QTASADAVVR	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTSGGE	RYDMNAFTAA	HKTLPIPSYV
101	RVTNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAQKLGFSV	NQGTAAHVKE
151	QIVPGQSAPV	AENKDIFIDL	KSFGTEHEAQ	AYLNQAAQNL	ASSASNPMLS
201	VEKRRYEYVV	KMGPFASQER	AAEAQAQARG	MVRVLTAG*	

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKAELHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	60



	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGTEHEAQ					
a264	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGTEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEVVVKMGPF TSQERAAEAEQA RGMVRAVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEVVVKMGPF TSQERAAEAEQA RGMVRAVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```
m265 . seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCCGGCTTG
51  GCGCGGCTG ATGATTTTGT CTTGTTTGTG GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGCGCGAA
151 ATGCTCAGCA GTGCGGTTGC GCGGAGGTC AAGAGAAGGT GTTTGATGTT
201 CATAT.TTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGCGGTCA ATACCGCCCG AACCATACCG
301 CGCGCCTGAG CTTCCGCTTC GCGGCGCGCT TCCTGCGAGG TAAACGGTCC
351 CATTTTGACG ACGTATTCGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```
m265 . pep
1  MSVILPPTRA NAAFAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFI XFVNRLGLENV DINKVSNNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265 . pep	MSVILPPTRANA AFAWARLMILSCLLCWCAACPWSSSPCPSWWASAGA EMLSSAVAAEV					
g265	MSVILPPTRAQA AFAWARLMILSCLPCWCAACPWSSSPCPSWWASAGA EMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFAFVNRLGLENVDINKVSNNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNGDINKVSNNRQPEVSTARTIPRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

```

a265.seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GGC GCGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCATCA GTGCGGTTGC GCGGCGGTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... . . . .GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCTCGGCG GCGCGTTCC TGCGAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCTGTA

```

a265.pep

1	MSVILPPTRA	NAAFSAWARL	MILSCLLCWC	AACPWSSSPC	PSWWASAGAE
51	MPISAVAAAV	KRRRLKFIFA	PAKYLX..XC	LKDVKAGHQP	AVNTARTIPR
101	A*ASASAARS	CEANGPILTT	YS*		

```

      10      20      30      40      50      60
m265.pep  MSVILPPTRNAAFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSSAVAAEV
          |||||
a265      MSVILPPTRNAAFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMPISAVAAV
          |||||
      10      20      30      40      50      60

      70      80      90     100     110     120
m265.pep  KRRCLMFIXFAFVNRGLENDINKVSNNRQPAVNTARTIPRAXASASAARSCEVNGPILT
          ||| | || : : : : |||||
a265      KRRRLKFI---FAPAKYLXXCLKDVKAGHPAVNTARTIPRAXASASAARSCEANGPILT
          70      80      90     100     110

m265.pep  TYSX
          ||||
a265      TYSX
          120

```

```
g266.seq
1 agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccatcatg
51 accgcaccca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcctc acgaccagac tgttcggcgt ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgatc gagctggcgg cagggttcgc gctgaccgcc
201 tctcttgctc acatcctcga atcccgtgcg ggagcggtag acaatcaggg
251 ttgggaagtt tacgccaccg tcgtctgcct gtacctatt ttgcgccttc
301 cgtgttctgt gcggcgggtat ttttggcaca cgcgcaacaq qqaataa
```

g266.pap  
1 MQFRRHRRRQ CPNRKPIMTA SMYILLVLAL IFANAPFLTT RLFGVAALKR  
51 KHFGHHLIEL AAGFALTASL AYILES RAGA VHNQGWEFYA TVVCLYLIFA  
101 EPCEVRRYFW HTRNRE\*

```
m266.beq      1  ATGCCGTTCC  GCAACGCGtT  cAGACGGCAT  CGCGCCGAC  AACGCCTAAA
               51  CAAAGAGCCC  ACCATGACCC  CATCCATGTA  CATCCTTTTG  GTCTTGGCAC
            101  TCATCTTTG  CACAGGCCCC  TTCCTCACGA  CAGAGCTGTT  CGGCGTGGCC
            151  rCACTCAAGC  GCAAACATTT  CGGACACCAC  ATGATCGAGC  TGGCGGCAGG
            201  TTTCGCGCTG  ACCGCCGTT  TTGCCTACAT  CCTsGAATCC  CGTGCAGGAT
            251  CGGTACACGA  TCAGGGTTGG  GAGT'TTTATG  CCACAGTCGT  CTGCCTGTAC
            301  CTGATTTTTG  CGT'TTCCATG  TTTTGTGTGG  CGGTATTTTT  GGCACACCGG
            351  CAACAGGGAA  TAG
```

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101 LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

```
m266/g266

      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g266      MQFRRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
          10      20      30      40      50

      70      80      90     100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g266      LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLY LIFAFPCFVR RYFWHTRNREX
          60      70      80      90     100     110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTTG CTGCTTGCTT
101 TGATTTTTCG CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151 CCGCTCAAGC GCAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201 TTTCCGCTG ACCGCCGTTT TTGCCTACAT CCTCGAATCC CGTGCGGGAG
251 CGGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301 CTGATTTTTC GGTTCCTCTG TTTCGTGTGG CGGTATTTT GGCACACGCG
351 CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101 LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

```
      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a266      MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTKLFGIVPLKRKHFGHH
          10      20      30      40      50      60

      70      80      90     100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a266      LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          70      80      90     100     110     120

m266.pep  X
          |
a266      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:  
g267.seq

```

1   atgcaagtcg ccttttttct cgccgtggtg ttcaaaaata tgggtttcca
51  caatcgcatc ggtcgggcag gcctcttcgc agaaaccgca gaagatgcac
101 ttggtcaggt cgatgtcgta acgcttggtg cggcgggtgc cgtcttcgcy
151 ttcttccgat tcgatgttga tcgccattgc cggacacacc gcctcgcac
201 atttacacgc gatgcagcgt tcctctccgt tcggaaaacg gcgttgcgcy
251 tgcagaccgc ggaaacgcac ggattgcggc gttttctctt cgggaaaata
301 aattgtgtct ttgcgggcaa aaaagttttt gagcgtttac cccatgcctt
351 tqaccagttc qccaaqcaqa aaqgttttta ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1076; ORF 267.ng>:

q267.pep

1 MQVAFFLAVV FKNMGFHNRI GRAGLFAETA EDALGQVDVV TLGAAGAVFA  
51 FFRFDVDRHC RTHRLAQFTR DAAFLSVRKT ALRVQTAETH GLRRFLFGKI  
101 NCVFAGKKVF ERYAHAFDOF AKOKGEY\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1077>:

m267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	AGTCGGGCAT	GCCTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTAC	CGTCTTCACG
151	TTCTTCCGAT	TCGATGTTAA	TCGCCATTGC	CGGACACACT	GCCTCACACA
201	ACTTACACGC	GATACACCGC	TCTTCGCCGT	TCGGATACCG	CGGCTGCGCG
251	TGCAGACCGC	GGAAACGCAC	GGATTGCGCG	GTTTCTCTTT	CGGGGAAAAA
301	AATAGTGTC	TTGCGGGCGA	AAAAGTTTTC	GAGCGTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAAGCAG	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEO ID 1078; ORF 267>:

m267.pep

1 VQVAFFLAVV FKNMGFHNRI SRACLFAETA EDALGQVDVV TLGAARTVFT  
51 FFRFDVNRHC RTHCLTQLTR DTPFLAVRIP PLRVQTAETH GLRRFLGEBI  
101 NCVFAGEKVF ERYAHTFYQF AKOKGEY\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 267 shows 82.7% identity over a 127 aa overlap with a predicted ORF (ORF 267.ng) from *N. gonorrhoeae*:

m267/g267

		10	20	30	40	50	60
m267.pep		VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDV	VTLGAARTVFTFFRFDVNRHC			
		:	:	:	:	:	:
g267		MQVAFFLAVVFKNMGFHNRI	GRAGLFAETAEDALGQVDV	TLGAAGAVFAFFRFDVDRHC			
		10	20	30	40	50	60
		70	80	90	100	110	120
m267.pep		RTHCLTQLTRDTPLEFAVRI	PPLRVQTAETHGLRRFL	FGAECVCFAGEKVFERYAHTFYQF			
			: :	:	:	:	:
g267		RTHRLAQFTRDAAPLSVRKTALRVQTAETHGLRRFL	FGKINCVFAGKKVFERYAHAFDQF				
		70	80	90	100	110	120
m267.pep		AKQKGFIYX					
g267		AKQKGFIYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1079>:

a267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCGGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	GGTCGGGCAG	GC1TCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTGC	CGTCTTCGCG
151	TTCTTCCGAT	TCGATGTTGA	TGCCAATTGC	GGGGCAAAACG	GCTTCCACACA
201	ATTTACACGC	GATGCAGCGT	TCCTCGCCGT	TTGGATAACG	GC GTTGC GCG
251	TGCAGAGCCG	GGAAACGCAC	GGATTGCGCG	GTTTCTCTT	CGGGAAAATA
301	AATCGTGTCT	TTGCGGGCAA	AAAAGTTTTT	GAGCGTTACG	CCCATACTTT
351	TTACCAATTC	GCCAAGCAGA	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDVV	TLGAARTVFTFFRFDVNRHC			
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFAFFRFDVDRHC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPLFAVRIP	PLRVQTAETHGLRRFLFGE	INCVFAGEKVFERYAHTFYQF			
a267	GANGFTQFTRDAAFLAVWIT	ALRVQTAETHGLRRFLFGK	INRVFAGKKVFERYAHTFYQF			
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaattt
101 cctgcggaag cgaagagact aaagagattt tggcctaaact ggtccgcgac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201 ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251 gtttgggcat aaccgtcgat gaagtcgcaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccgcaga
351 tggtgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgat
451 tatgtcaaaa ctattttctta cagcgctccag ccgacagacg acaaaagcaa
501 aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctgggtgc tatggcactg attaaagagc cggtggacaa agcgaaacaa
601 aggaacgaaa aacttgaagc ggcagaagcc accgcgcagc aagcgaggga
651 ggcagaagaa gcggcggcgc aggaggcatt gggtcgggag caggaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801 ctcgcagaaa acatggaaaa gcggtatgga caagatctgt gccacaatg
851 cgaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901 tgtaaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggtc ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLGINPFSG KEISCGSEET KEILVKLVDR
51  NVEGETVKTF DDAFKDQAF ADIGISHIRR MVERLGITVD EVRTEKTD
101 SSKLKCEAAL KLDVPDDVD YAVANQSIG NSHKKTPDFF EPYYRKEGAY
151 YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSLVSMAL IKEPLDKAKQ
201 RNEKLEAAEA TAQEAAREEE AAAQEALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKLOASQK TWKSGMDKIC ANNAKAEGE PNGIKVSELA
301 CKTAETEARL EELHNRKKAL IDENVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAAGAGCC GTTGACAAA GTGAAACAAA GGAACGAAGA
```

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```

51   ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101  AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCTGCGC
151  AG.CAGTTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201  GCTGCAACCG TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251  CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCAGC
301  GAACTGGCAT GCAAAACGGC GAAACCGAA GCACGCTTGG AAGAGCTGCA
351  CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401  AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1   ..MALIKEPLDK VKQRNEELEA AEEAAAQEAL GREQEAAARVS EWEERYKLSR
51  XQFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

                                10      20
m268.pep                      MALIKEPLDKVKQRNEELEAAE-----
                                |||:|||:|||:|||:|||:|||:|||:|||
g268                          SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQEARE
                                160      170      180      190      200      210

                                30      40      50      60      70      80
m268.pep  --EAAAQEALGREQEAAARVSEWEERYKLSRSQFEQFWKGLPQTQVQNKLP SQKTWKSMD
                                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      AEEAAAQEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTQVQNKLP SQKTWKSMD
                                220      230      240      250      260      270

                                90      100     110     120     130     140
m268.pep  KICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
                                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      KICANNAKAEGKTPNGIKVSELACKTAKTEARLEELHNRKKALIDEMVREEDKKELPKRLX
                                280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

```

a268.seq
1   ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCTGCGC
151 AGCGAGTTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GGAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

```

a268.pep
1   MALIKEPLDK AKQRNEELEA AEEAAAQEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

                                10      20      30      40      50      60
m268.pep  MALIKEPLDKVKQRNEELEAAEEAAAQEALGREQEAAARVSEWEERYKLSRXQFEQFWKGL
                                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a268      MALIKEPLDKAKQRNEELEAAEEAAAQEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

615

	10	20	30	40	50	60
	70	80	90	100	110	120
m268.pep	PQTVQNKLPQSQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
a268	PQTVQNKLPQSQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
	70	80	90	100	110	120
	130	140				
m268.pep	KALIDEMXREADKKELSKRLX					
a268	KALLDEMAREADKKELPKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAGGCC CTTATCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.pep

```

1  VQSRDGLHK FKHCSAAMA LIKEPLDKVK QNEELEAAE EAAAEALGR
51  EQEAAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLPQSQ KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

		10	20	30	
m268-1.pep		VQSRDGLHKFKHCSAAMALIKEPLDKVKQRNE			
g268	KEGAYYVKTISYSVQPTDDKSKIFAELSQAHDIIHPLSELVS--MALIKEPLDKAKQRNE				
	150	160	170	180	190
	200				
	40	50	60	70	80
m268-1.pep	ELEAAE-----EAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
g268	KLEAAEATAQEAREEAEAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
	210	220	230	240	250
	260				
	90	100	110	120	130
m268-1.pep	KLQASQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDE				
g268	KLQASQKTWKSMDKICANNAKAEGKTPNGIKVSELACKTAKTEARLEELHNRKKALIDE				
	270	280	290	300	310
	320				
	150	159			
m268-1.pep	MAREADKKELSKRLX				
g268	MVREEDKKELPKRLX				
	330				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG TCGACCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGGAAAC CGAAGCACGC TTGGAAGAGC

```

401 TGCACAACCG TAAAAAGCC CTTCTCGACG AAATGGCCAG GGAAGCGGAC  
 451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep

1 VQSRDGLHK FKHCSAAMA LIKEPLDKAK QNNEELEAAE EAAAEALGR  
 51 EQEVDVSEW EERYKLSRSE FEQFWKGLPQ TVQNKQASQ KTWKSGMDKI  
 101 CANNKAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LLEDEMAREAD  
 151 KKELPKRL\*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHCSAAMALIKEPLDKAKQ	NRNEELEAAE	EAAAEALGR	EQEVDVSEW	EERYKLSRSE	FEQFWKGLPQ
m268-1	VQSRDGLHKFKHCSAAMALIKEPLDKVQ	NRNEELEAAE	EAAAEALGR	EQEVDVSEW	EERYKLSRSE	FEQFWKGLPQ
	10	20	30	40	50	60
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKQASQ	KTWKSGMDKICANNKA	AEGETP	NGIKFSEL		
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKQASQ	KTWKSGMDKICANNKA	AEGETP	NGIKFSEL		
	70	80	90	100	110	120
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKA	LLEDEMAREAD	KKELPKRLX			
m268-1	ACKTAETEARLEELHNRKKA	LLEDEMAREAD	KKELSKRLX			
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq

1 atggtttggc gtgtgaattg cgcggcaacg gcggcgctga ttttttcgtc  
 51 cagcccttgg atttgggagg tgggtggtgt gtggtcgagg tcggcttttt  
 101 cctgcaaacc ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttggcg  
 151 gtttcgccgt gggactttat ccggaacacg gcttcgcccc aggtgtcggc  
 201 ggctttgatg cacagtttta aaaccaggcg tttggggcgg ttttctgcgc  
 251 cgcccggtgc cattttgctg tccaatcgcg gggttaaaaa accgttgctg  
 301 ttttaagtcg cgctccgtcca agtcgatacg agcgcgcttc tttgccttcc  
 351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep

1 MVWRVNCAAT AALIFSSSPW IWAUVVWWSR SAFSCKPCAS LDASSAPALA  
 51 VSPWDFIRNT ASPKVSAAALM HSFKTRALGR FSAPPVAILL SNRGVKKPLS  
 101 FKSPSVQVDT SALLCLSLRS S\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq

1 ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC  
 51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGTCTCGG TCGGCTTGT  
 101 CTTGCAAACC TTGCGCCaCG TGCCCGCGTC CAGCGCTGTC GTTGATGGTT  
 151 TCGCGGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTGCGCGGC  
 201 TTTGATGCAC AGTTTAAAAA CCAGGGCTTT GGGGCGGTTT TCGTCCGCGC  
 251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TAAAAAGCC GTTGTCGTTT  
 301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGTCTCTCT GCCTTTCGTT  
 351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep

1 MVWRVNCAAT AVLIFSSSPW IWAUVVWWSR SALSCKPCAT CPRPAPALMV  
 51 SPWDFIONTA SPKVSAAALM HSFKTRALGR FSAPPVAILL SNRGVKKPLS  
 101 KFSSVQVDT SALLCLSLRS \*

Computer analysis of this amino acid sequence gave the following results:



Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng) from *N. gonorrhoeae*:

m269.pep	MVWRVNCAATAVLIFSSSPWIWA	59
g269	MVWRVNCAATAALIFSSSPWIWA	60
m269.pep	ASPKVSAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT	119
g269	ASPKVSAALMHSFKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDT	120
m269.pep	SX	121
g269	SX	122

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

a269.seq

1	ATGGTTTGGC	GTGTGAATTG	CGCGGCAACG	GCGGTGCTGA	TTTTTTCGTC
51	CAGCCCTTGG	ATTTGGGCGG	CGGTGTGGGT	GTGGGCGCGG	TCTGCTTTGT
101	CTTGGAGGTT	TTGCCCGAGC	GTGCCCGCGT	CCAGCGCGCC	GGCGTTGACG
151	GTTTCGCCGT	GGGACTTTAT	CCAGAACACG	GCTTCGCCCC	AGGTGTCGGC
201	GGCTTTGATG	CACAGTTTAA	AAACCAGGGC	TTTGGGGCGG	TTTTCGTCGC
251	CGCCTGTCGC	CATTTTGCTG	TCCGGGCGCG	GGGTTAAAAA	GCCGTTGTCG
301	TTTAAATTTT	CGTCCGTCCA	AGTCGATACG	AGCGCGCTTC	TCTGCCTTTC
351	GTTGTGGTCT	TCGTAA			

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

a269.pep

1	MVWRVNCAAT	AVLIFSSSPW	IWA	AVVWWAR	SALSWRFCAS	VPASSAPALT
51	VSPWDFIQT	ASPKVSAALM	HSFKTRALGR	FSSPPVAILL	SGRGVKKPLS	
101	FKFSSVQVD	SALLCLSLWS	S*			

m269/a269 90.1% identity in 121 aa overlap

m269.pep	10	20	30	40	50	59
a269	10	20	30	40	50	60
m269.pep	60	70	80	90	100	110
a269	70	80	90	100	110	120
m269.pep	120					
a269						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

g270.seq

1	atgaataaaa	accgcaaatt	actgcttgcc	gcactgctgc	tgactgcctt
51	tgccgccttc	aagctcggtt	tgttgcaatg	gtggcaggcg	cagcagccgc
101	aagccgtggc	ggcgcaatgc	gatttgaccg	agggttgac	gctgccggac
151	ggaagccgtg	tccgcgccgc	cgccgtttca	accaaaaaac	cgtttgatat
201	ttatatcgaa	cacgcgcccg	ccggcacgga	acaggtcagc	atcagcttca
251	gtatgaaaaa	tatggatatg	ggtttcaacc	gctatatgtt	cgagcggcaa
301	ccgtcgggga	cttggcaggc	agcacgcatt	cgccctgccg	tctgtgtcga
351	aggcaggcgc	gattttacgg	cggacattac	aatcggcagc	cggacatttc
401	agacggcatt	taccgccgaa	taa		

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

g270.pep

```

1  MNKNRLLLLL ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG Ca. CAGCCGC
101 AAGCTGTGGC GCGCAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTTCAACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTT
401 AGACGGCATT TACCGCCGAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep

```

1  MNKNRLLLLL ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng) from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRLLLLLAALLLIAFAAVKLVLLQWWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
g270	MNKNRLLLLLAALLLTAFAAF KLVLLQWWQA QQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
	10	20	30	40	50	60
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRI RLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARI RLPVCVEGRR					
	70	80	90	100	110	120
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRI RLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARI RLPVCVEGRR					
	70	80	90	100	110	120
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG CAGCAGCCGC
101 AAGCTGTGGC GCGCAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCCGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTTCAACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTT
401 AGACGGCATT TACCGCCGAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep

```

1  MNKNRLLLLL ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ

```

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE \*

**m270/a270** 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALLIAFAAVKL	VLLQWQAXQPQAVAAQCDL	TEGCTLPDGS	SRVRAAAVS	
a270	MNKNRKL	LLAALLIAFAAVKL	VLLQWQAXQPQAVAAQCDL	TEGCTLPDGS	SRVRAAAVS	
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDIYIEHAPAGTEQV	SISFSMKNMDMGFNRYMFERQ	PSGTWQAVRI	RLPICVEGRR		
a270	TKKPFDIYIEHAPAGTEQV	SISFSMKNMDMGFNRYMFERQ	PSGTWQAVRI	RLPICVEGRR		
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADITIGS	RTFQTAFTAE				
a270	DFTADITIGS	RTFQTAFTAE				
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

1	atgttcagtt	cgcggtatg	gaggatttg	gcgacgggg	taacggtgtg
51	tatggtcagt	ccgtgtccg	cggtgacgac	caagcccaa	tcgccggcga
101	aatgcgcgc	gttttgatg	cgctcgaa	gcctgattg	ttcggcggtg
151	ctttgtgct	cgccatagc	gcccgtgtg	agctcgaca	cggcgccg
201	gacatcacg	gcggcttga	ttgcctgtc	gtcggcatc	ataaacaagg
251	acacgcgtat	gcccgcgtc	gtcaggatt	tggcgaatt	ggcgattttt
301	tcctgttgc	ccaatacgt	caaaccgct	tcggtcgtg	tttcctgcc
351	tttttcagg	acgatgcac	cgtcttccg	catcacttt	agcggtttt
401	cgagcattt	ttccgtca	gccatttca	ggttcaggc	cgtgcggatg
451	gcgtttttg	cggcaatac	atccgcgtc	ttgatgtgg	ggcggtcttc
501	gcgcaggtg	atggaatca	ggtctgcac	gtgcgtttc	gcaaccagt
551	ccgcctccac	ggggctggg	taa		

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

1	MFSSRMARIW	ATGVTL	CMVS	PCPAL	TTKPK	SPAKCAP	FWM	RSNCLIC	SAW
51	LCASAYAPVC	SSTTGAPT	SR	AAWICL	SSAS	INKDTR	MPAS	VRILANS	PAIF
101	SCCANTSKPP	SVVISCR	FSG	TMHTSS	GITL	SAFSSIS	SVN	AISRFR	RVRM
151	AFLTANTSAS	LMWRRSS	RRC	MVIRSA	PCVS	ATSAAST	GLG	*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

1	AwGTTcagtt	CGCGGatgg	GAGGATTg	GCGATgggg	TAACGTTgtg
51	TATGTCAGT	CCGTGTCCG	CGTTGACG	CAAGCCCAA	TCGCCGGCGA
101	AATGCGCGC	GTTTTGATG	CGCTCGAA	GCCTGATTG	TTCGGCGTGG
151	CTGCGCGCG	CGGCATACG	GCCTGTGTG	AGCTCGACA	CGGGCGCGCC
201	GACATCACG	GCGGCTTGA	TTTGCCTGT	GTCGGCATC	ATAAACAAAG
251	ACACGCGTAT	GCCTGCGTC	GTCAGGATT	TGGTGAACCC	GGCGATTTTT
301	TCCTGTTGCG	CCAATACGT	CAAACCGCT	TCGGTCGTG	TTTCCTGACG
351	TTTTTCAGG	ACGATGCAC	CGTCTTCCG	CATCACTTT	AAAGCGTTTT
401	CCAACATTT	TTCCGTCA	GCCATTCAA	GTTTCAGGC	CGTGCGGATG
451	GCGTTTTTG	CGGCAACAC	GTCCGCTCT	TTGATGTGG	GGCGGTCTTC
501	GCGCAGGTG	ATGGTAATC	AATCCGCAC	GTGCGTTTC	GCAACCAGTG
551	CCGCCTCCAC	GGGGCTGGG	TAA		

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

1	XFSSRMARIW	AMGVTL	CMVS	PCPAL	TTKPK	SPAKCAP	FWM	RSNCLIC	SAW
51	LRASAYAPVC	SSTTGAPT	SR	AAWICL	SSAS	INKDTR	MPAS	VRILVN	PAIF
101	SCCANTSKPP	SVVISXRF	SFG	TMHTSS	GITF	KAFSNI	SVN	AISRFR	RVRM
151	AFLTANTSAS	LMWRRSS	RRC	MVIKSA	PCVS	ATSAAST	GLG	*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLCASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTSKPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANSALFSCCANTSKPPSVVISCRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVISAPCVS					
g271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRISAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271.seq

```

1  ATGTTTCAGTT CGCGGATGGC GAGGATTTGG GCGATGGGGG TAACGTTGTG
51  TATGGTCAGT  CCGTGTCGGG CGTTGACGAC CAAGCCCAA TCGCTGGCAA
101 AATGCGCGCC  GTTTTGGATG GCCTCGAACT GCCTGATTTG TTCGCGGTGG
151 CTGCGCGCGT  CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201 GACATCACGG  GCGGCTTGGA TTGCCTGTC GTCGGCATCG ATAAACAAGG
251 ACACGCGTAT  GCGCGCTCG  GTCAGGATTT TGGTGAATTC GGCAATTTTG
301 TCTTGTTCG  CCAATACGTC CAAGCCGCCT TCGGTCGTGA TTCCTGACG
351 TTTTCCGGC  ACGATGCACA CGTCTCCGG  CATCACTTTA AGCGCGTTTT
401 CGAGCATTT  TTCCGTCAAC GCCATTTCAA GGTTCAGGCG CGTGC GGATG
451 GCGTTTTTGA  CAGCAAACAC GTCCGCGTCT TTGATGTGGC GCGGCTCTT
501 GCGCAGGTGC  ATGGTAATCA GGTCGGCACC GTGCGTTTCG GCAACCAGTG
551 CCGCCTCCAC  GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271.pep

```

1  MFSSRMARIW AMGVTLCMVS PCPALTTKPK SLAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNSAIL
101 SCCANTSKPP SVVIS*RFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRISAPCVS ATSAASTGLG *

```

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTSKPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTSKPPSVVISXRFSG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVKSAPCVS					
a271	:: :     :     :     :     :     :     :					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271						
	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1   atgactgcaa aggaagaact gttcgcattg ctgcgccata tgaacaaaaa
51  caaaggttcc gacctgtttg tgacgaccca tttcccgccc gctatgaagc
101 tggacggcaa aatcaccgcg atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcctcgacc aacgagtgcg atttcgcat cagcctgccc gacaccagcc
251 gcttccgcgt caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggccttgaag gatgttgcgc tgaaaaaacg cgggctggtt atttttgtcg
401 gcggcaccgg ctccggcaca tcgacttcgc tcgcctcgct tatcgactac
451 cgcaatgaaa attcgcttcg acacatcatc accatcgaa gacccgatcg
501 gtttgtccac gaacacaaaa actgcatcat taccagcgc gaggtcggcg
551 tggacacgga aaactggatg gcggcggtga aaaatacgtc gcgtcaggcg
601 ccggtatgta tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc tttgccgaaa cggggcattt gtgtatggcg acgtgcacg
701 ccaacagcac caatcaggcg ctcgaccgca tcatcaactt cttccccgag
751 gagcggcgcg aacaattgct gacggatttg tcgtcaacc ttcaggcggt
801 tatttcgcaa cgctcgttc cgcgagacgg cggcaaggcg aggggtggcg
851 cagtcgaggt gctgctcaat tcgcccctga ttctggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgcgt
1051 ttggcggtac agttgcgcag ccgcagggca caaagttccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1   MTAKEELFAW LRHMNKNKGS DLFVTHFPF AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RAITSKIPKF ESINLPPALK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSGFHII TIEDPIEFVH EHKNCIITQ EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGQMT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDLELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1   ATGACCGCAA AGGAAGAAGT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCC GACCTGTTTC TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCTG ATCAGGACG AACCCTGAC GCGGGAaaaa
151 TGTATGGAAA TCGCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTGCGGC

```

```

551 TGGATACGGA AAACCTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGGAG
751 GAGCGGCGCG AACCAATTGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCtGA TTTCGGAGTT GATTCAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAAATGCC ATTCCGCACA CGATTTCGCT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CaaAGTTyCA GCCCGGATT
1101 GGnACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272 . pep

```

1  MTAKEELFAW LRHMxQNKGs DLFVtTHFPp AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAM IORGATALVF
101 RTITSKIPKF ESLNLPVLK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLcMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLyQLYE KGDISLQeAL KNADSAHDLR
351 LAVQLRSRRA QsXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

m272 . pep	10	20	30	40	50	60
	MTAKEELFAWLRHMxQNKGsDLFVtTHFPpAMKLDGKITRITDEPLTAEKCMElAFSIMS					
g272	MTAKEELFAWLRHMKNKGsDLFVtTHFPpAMKLDGKITRITDEPLTAEKCMElAFSIMS					
	10	20	30	40	50	60
m272 . pep	70	80	90	100	110	120
	AKQAEFSSTNECNFAISLPDTSRFRVNAMIORGATALVFRTITSKIPKFESLNLPVLK					
g272	AKQAEFSSTNECNFAISLPDTSRFRVNAMIORGATALVFRAITSKIPKFESLNLPALK					
	70	80	90	100	110	120
m272 . pep	130	140	150	160	170	180
	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIIITQR					
g272	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIIITQR					
	130	140	150	160	170	180
m272 . pep	190	200	210	220	230	240
	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAIAFAETGHLcMATLHANSTNQA					
g272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAIAFAETGHLcMATLHANSTNQA					
	190	200	210	220	230	240
m272 . pep	250	260	270	280	290	300
	LDRIINFFPEERREQLLTDLsLNlQAFISQRLVPRDGGKGRVAAVEVLN SPLISELIHN					
g272	LDRIINFFPEERREQLLTDLsLNlQAFISQRLVPRDGGKGRVAAVEVLN SPLISELIHN					
	250	260	270	280	290	300
m272 . pep	310	320	330	340	350	360
	GNIHEIKEVMKKSTTLGMQTFDQHLYQLYEKGDISLQeALKNADSAHDLRLAVQLRSRRA					
g272	GNIHEIKEVMKKSTTLGMQTFDQHLYQLYEKGEISLQDALKNADSAHDLRLAVQLRSRRA					
	310	320	330	340	350	360

```

          370
m272.pep  QXSXSPDLXLLX
          || :||| |||
g272      QSSDPDLELLX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272.seq
1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTTCG TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GGCGGAAAAA
151 TGTATGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGTCG
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTTCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AACTGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCATT
801 TATTTGCAA CGCTCGTTC GCGAGACGG CGGCAAGGCG AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCGGAGTT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCCTTGCA GGATGCCTTG AAAAATGCCG ATCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTTCCG GTCCCGATTT
1101 GGAAGTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272.pep
1  MTAKEELFAW LRHMNKNKGS DLFVTTTFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RAITSKIPKF ESLNLPPVLK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI AETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMMT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

          10      20      30      40      50      60
m272.pep  MTAKEELFAWLRHMKNKGS DLFVTTTFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
          ||||| :|||||
a272      MTAKEELFAWLRHMKNKGS DLFVTTTFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
          10      20      30      40      50      60

          70      80      90      100     110     120
m272.pep  AKQAEFFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRTITSKIPKFESLNLPPVLK
          ||||| :|||||
a272      AKQAEFFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRITSKIPKFESLNLPPVLK
          70      80      90      100     110     120

          130     140     150     160     170     180
m272.pep  DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
          ||||| :|||||
a272      DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
          130     140     150     160     170     180

```

	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
	190	200	210	220	230	240
	250	260	270	280	290	300
m272.pep	LDRI INFFPEERREQLLDLSLNQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRI INFFPEERREQLLDLSLNQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272.pep	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G D I S L Q E A L K N A D S A H D L R L A V Q L R S R R A					
a272	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G E I S L Q D A L K N A D S A H D L R L A V Q L R S R Q A					
	310	320	330	340	350	360
	370					
m272.pep	Q S X S P D L X L L X					
a272	Q S S G P D L E L L X					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

g273.seq

```

1  atgagtccttc aggcgggtatt tatataccccc ccaagccgta ccgcacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattccaccg ttttcttgcc gtttcttgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcgga cccgcgccc acattggcat tgtgttcatt
251 gttgttcctt aacggttaaa aaccgcccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcgggccc gtgccgctga aatcaaggcg
351 gtttgagaag tgttccnac gcgcccgc tatgtgccga aatattattt
401 gtcgctcacc tgcaaatcg ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgctg cttttgtgtt ttcaagcagt
501 tttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

g273.pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHTDRR QDIGVFEAGT
51  PFTVFLPFLV AFEIKDDAGK QRGSRARHWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRFEK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFFVQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

m273.seq

```

1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCTCCG TTTCTCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGCA GCGCGCCCG ACATTAGCAT TGTGTTTATT
251 GTTGTTCCTT AATGCTTAAA AACCCGCTG TCCGTGCAAC CGTTTAAAG
301 CGGCAAATTG CAAAATTGT TTGCGGGCGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTTCCTGAC GCGCCGCTT GTGTGCCGGA GTTATTTGTC
401 GCTCACCTGC AAAATCGCCA AGAACGCGT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTACCTGCT TTTGKTWTC AAGCAGTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

m273.pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHADRC QDIGVFKAGT
51  PFPVFLPLL AFEIKDDAGK QRGSRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRRALCAG VICRSPAKSP RTRFAEFPH
151 PLVSYGVYLP FVXQAVFSY *

```

Computer analysis of this amino acid sequence gave the following results:



Homology with a predicted ORF from *N. gonorrhoeae*

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/g273

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGQSGKHADRCQDIGVFKAGTFFPVFLPLL					
g273	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGQSGKHADRCQDIGVFEAGTFFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m273.pep	AFEIKDDAGKQGRSRRHXHCVHCCSLMLKNPPVRATVLRQIAKFVCGRVPLKSGRFEG					
g273	AFEIKDDAGKQGRSRRHXHCVHCCSLTVKNPPGRATVLRREIAKFVCGRVPLKSGRRFEK					
	70	80	90	100	110	120
	130	140	150	160	170	
m273.pep	CSSRA-ALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVLPFVXQAVFSYAX					
g273	CFXRARPMCRNIIICRSPAKSPRTRFAEFPRCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

```

1  ATGAGTCTTC AGGCGGTATT TGTATACCCC CCAAGCCGTA CCGCACAAATA
51  CAACGAAAT  CAGGAAAACG GCGGTAAAGC TCATAACAG  GGACAAAGCG
101 GCAAAACACG  CGACCGCCGT CAGGATATAG GCGTATTCCA GACCGGAAC
151 CCATTCACCG  TTTTCCTGCC GCTTTTGTGC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG  CAGCGCGGCA GCCGCGCCCG ACATTAGCAT AATGTTTATT
251 GTTGTTCCTT  AACGTTTAAA AACCGCCCGG TCCGTGCAAC CGTTTTTAAG
301 AGGCGGTAAA  TCACAAAGTT TGTGGCGGGA CGTGCTCTCT TACAATCAGG
351 GCGGTTTAA  GGGCATGATG CACTGCCCGG TGTGCCGGAT ATTATTTGTC
401 GCTCACCTGC  AAAATTGCCA AGAACGCGCT TTGCGGGATT TCCACATTGC
451 CCACTTGTTT  CATACGGCGT TTGCCTGCTT TTTGTTTTTC AAGCAGTTTT
501 TTCTTACGCG  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

```

1  MSLQAVFVYP PSRTAQYNEN QENGGAHKQ  GQSGKHADRR QDIGVFQGTG
51  PFTVFLPLFV AFEIKDDAGK QRGSRARH*H NVHCCSLTVK NPPVRATVFK
101 RR*ITKFVGG  RALLQSGRFK GHDALPRVPD IICRSPAKLP RTRFAGFPHC
151 PLVSYGVCLL  FVFQAVFSYA *

```

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGQSGKHADRCQDIGVFKAGTFFPVFLPLL					
a273	MSLQAVFVYPPSRTAQYNENQENGGAHKQGGQSGKHADRRQDIGVFQGTGTPFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRRHXHCVHCCSLMLKNPPVRATVLRQIAKFVCGRVPLKSGRFE					
a273	AFEIKDDAGKQGRSRRHXHCVHCCSLTVKNPPVRATVFKRRXITKFVGGRALLQSGRFK					
	70	80	90	100	110	120
	120	130	140	150	160	170
m273.pep	GCSRRALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVLPFVXQAVFSYAX					
a273	GHDALPRV-PDIIICRSPAKLPRTTRFAGFPHCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

```
g274.seq
1  ATGGCGGGGCG  CGATTTTGT  CGTCatCGCC  AgcgTCGCTA  TGTTTTTTGT
51  CGCGCAGCAG  CACGCGACAG  ATTTGGTTAC  GGACGATTAT  TATAAGGATG
101 GCAAGCATAT  CGACATCCAG  CTTTCATCGG  ATGAAGAAGC  CGTCAGACGG
151 CATATCGGGG  TGCAGGTCCT  CATTTCTCCC  GATATGAATG  CGGCAAAAGT
201 GTTTGTCTGG  ggCgagtTTG  ACGGCAACA  GCCTTTGAAC  CTGCTGCTGA
251 TGCACCCGAC  CCGCAAGGCG  GACGATCAAA  CCGTCGCCCT  CAAGCCCGTC
301 GGCAGCGCGC  AGAACGGCAG  GCGGAATAT  GAGGCGGTgt  tcaaAACCT
351 TCCGCCGGCC  AACCACTGGT  ATGTGCGCGT  GGAaggacgCG  GCAGGCGTGT
401 GGCAGCGTCG  GAACAAATGG  ATTACCAGCC  AGGGCAATGC  GGTCGATTGT
451 ACCCCGATGG  ACAAACTTTT  CAATAATGCA  GGAAGCAAAT  AA
```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

```
g274.pep
1  MAGPIFVVIA  SVAMFFVAQQ  HATDLVTDDY  YKDGKHIDIQ  LHRDEEAVRR
51  HIGVQVLISP  DMNAAKVFG  GEFDGKQPLN  LLLMHPTRKA  DDQTVALKPV
101 GSAQNGRAEY  EAVFKTLPPA  NHWYVRVEDA  AGVWRVENKW  ITSQNAVDL
151 TPMDKLFNNA  GSK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

```
m274.seq
1  ATGGCGGGGCG  CGATTTTGT  CGTCATCGCC  AGCGTCGCTA  TGTTTTTTGT
51  CGCGCAGCAG  CACGCGACAG  ATTTGGTTAC  GGACGATTAT  TATAAAGACG
101 GCAAACATAT  CGACATCCAG  CTTTCATCGG  ATGAAGAAGC  CGTCAGACGG
151 CATATCGGGG  TGCAGGTTCT  CATTTCCCCC  GATATGAATG  CGGCAAAAGT
201 GTTTGTCTGG  GGCAGGTTTG  ACGGCAACA  GCCTTTGAAC  CTGCTGCTGA
251 TGCACCCGAC  CCGCAAGGCG  GACGATCAAA  CCGTCGCCCT  CAAGCCCGTC
301 GGCAGCGCGC  AGAACGGCAG  GCGGAATAT  GAGGCGGTGT  TCAAACCT
351 TTCGCCGACC  AACCACTGGT  ATGTGCGCGT  GGAGGACGCG  GCAGGCGTGT
401 GGCAGCGTCG  GAACAAATGG  ATTACCAGCC  AAGGCAATGC  GGTCGATTGT
451 ACCCCGATGG  ACAAGCTTTT  CAATAATACT  GAAAGCAAAT  AA
```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

```
m274.pep
1  MAGPIFVVIA  SVAMFFVAQQ  HATDLVTDDY  YKDGKHIDIQ  LHRDEEAVRR
51  HIGVQVLISP  DMNAAKVFG  GEFDGKQPLN  LLLMHPTRKA  DDQTVALKPV
101 GSAQNGRAEY  EAVFKTLSPT  NHWYVRVEDA  AGVWRVENKW  ITSQNAVDL
151 TPMDKLFNNT  ESK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
m274	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g274.pep	DMNAAKVFG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLPPA					
m274	DMNAAKVFG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
g274.pep	NHWYVRVEDA AGVWRVENKW ITSQNAVDLT PMDKLFNNAGSKX					
m274	NHWYVRVEDA AGVWRVENKW ITSQNAVDLT PMDKLFNNATESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1  ATGGCGGGGC  CGATTTTGT  CGTCATCGCC  AGCGTCGCTA  TGTTTTTTGT
51  CGCGCAGCAG  CACGCGACAG  ATTTGGTTAC  GGACGATTAT  TATAAAGACG
101 GCAAGCATAT  CGACATCCAG  CTTTCATCGG  ATGAAGAAGC  CGTCAGACGG
151 CATATCGGGG  TGCAGGTTCT  CATTCCCCC  GATATGAATG  CGGCAAAAGT
201 GTTTGTCGGC  GGCAGGTTTG  ACGGCAAACA  GCCTTTGAAC  CTGCTGCTGA
251 TGCACCCGAC  CCGCAAGGCG  GACGATCAAA  CCGTCGCCCT  CAAGCCCGTC
301 GGCAGCGCGC  AGAACGGCAG  GCGGAATAT  GAGGCGGTGT  TCAAACCCCT
351 TTCGCCGACC  AACCCTGGT  ATGTGCGCGT  GGAGGACGCG  GCAGGCGTGT
401 GGC GCGTCGA  GAACAAATGG  ATTACCAGCC  AAGGCAATGC  GGTGATTTG
451 ACCCCGATGG  ACAAACCTTT  CAATAATACT  GAAAGCAAT  AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1  MAGPIFVVIA  SVAMFFVAQQ  HATDLVTDY  YKDGKHIDIQ  LHRDEEAVRR
51  HIGVQVLISP  DMNAAKVFVG  GFDGKQPLN  LLLMHPTRKA  DDQTVALKPV
101 GSAQNGRAEY  EAVFKTLSPT  NHWYVRVEDA  AGVWRVENKW  ITSQNAVDL
151 TPMDKLFNNT  ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIVASVAMFFVAQQHATDLVTDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
a274	MAGPIFVVIVASVAMFFVAQQHATDLVTDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
m274.pep	DMNAAKVFVGGFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
a274	DMNAAKVFVGGFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
m274.pep	DMNAAKVFVGGFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
a274	DMNAAKVFVGGFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
m274.pep	NHWYVRVEDAAGVWRVENKWTISQNAVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWTISQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		
m274.pep	NHWYVRVEDAAGVWRVENKWTISQNAVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWTISQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1  atgattttgc  cgccatccat  gacgatgatg  cggtcggcgg  attcgacggt
51  ggtcaggcgg  tgggcgacga  tgatgccggt  gcggttttcc  atcaggcggt
101 cgagcgcttg  ttggacgagg  cggttcggtt  cggtgtccaa  tgcgctggtg
151 gcttcgtcca  ataataatat  cgccgcgtct  tcaaaatgg  cgcgggcgat
201 ggcgacgcgt  tgccgctgtc  cgccggataa  gttgctgccg  ttcgatccga
251 tgggctggtg  cagtcggagc  ggggatgcgt  cgatcaggct  ttgcagggtg
301 gcggcttgga  gggcgacag  gacttcggct  tcgcccgcgt  cgggacggct
351 gtatcggacg  ttttcaaaca  ggggtgtcgt  aaacagggaat  acgtcttggt
401 agacgagggc  gaattgggag  cgcaggcagt  cgagtttgat  gtcggcgatg
451 tcgataccgt  ctatgcagat  gttgccggca  gacggttcga  caaagcgggg
501 cagaagggtg  acgacgggtg  atttgccgct  gccggaacgt  ccgaccaggg
551 cgacgcgttc  gccttgtctg  atgtcgaggt  tgaagtgtgc  gagggctttg
601 atgccgtctg  aacggtattc  gacatcgacg  ttgcggaagc  tgatgcgccc
651 ttcgacacgc  tgcggcgaga  gcgtgccttt  gtctgttctg  ggcggggtgt
701 cgagaaatgc  acatacgccg  tcggcggcga  ggaacatcgt  ctgcataggg
751 atgctgatgt  tggcaaggct  tttgatgggg  gcgtacattt  gcagcatcgc
801 gacgatgaat  gccataaatt  cgccgatggt  ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

```

1  MILPPSMTMM RSADSTVRR WATMMPVRF SIRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLSMSAM
151 SIPSMQMLPA DGSTKRGRRL TTVDLPLPER PTRATRSPCL MSRLKLSRAL
201 MPSEYSTST LRKLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1129>:

m276.seq

```

1  ATGATTTTGC CGTCGTCCAT CACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTGAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGATT CGTTGTCTAA TGCCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCTCT TTCAAATGG CGCGGGCAAT
201 GCGGACGCGT TGCCGCTGTC CGCCGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGGGAGCTGT CAATCAGGCT TTGCAGGTTG
301 GCGGTTTGA GGGCGAACAG GACTTCGGCT TCGCCCGCGT CGGGACGCGT
351 GTATCGGACG TTTTCAAACA GGGTGTCTG AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC GAATTGGGCG CGCAGGCAGT CGAGTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGTTGTC GAGGGCTTTG
601 ATGCCGCTCT AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TGCGGTGCGA GCGTGCCCTT GTCCTGTTG GCGGGGGTGT
701 CGAGAAATGC ACATACACCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTGATGT TGGCAAGGCT TTTGATGGG GCGTACATT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1130; ORF 276>:

m276.pep

```

1  MILPSSITMM RSAPSMVRR WATMMPVRF SIRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GELSIRLCRL
101 AVWRANRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLSMSAM
151 SIPSMQMLPA DGSTKRGRRL TTVDLPLPER PTRATRSPCL MSRLKLSRAL
201 MPSEYSTST LRKLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 276 shows 96.8% identity over a 278 aa overlap with a predicted ORF (ORF 276.ng) from *N. gonorrhoeae*:

m276/g276

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVRRWATMMPVRF SIRRSSACWTRRSDSLSNALVASSNNNIGAS					
g276	MILPSSITMMRSADSTVRRWATMMPVRF SIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
g276	FKMARAMATRCRCPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLSMSAMSI PSMQMLPADGSTKRGRRLTTVDLPLPER					
g276	FSNRVSSNRNTSWETRANWARRQSSLSMSAMSI PSMQMLPADGSTKRGRRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSEYSTSTLRKLMRPSTRCGASVPLSCSGGVSRNAHTP					
g276	PTRATRSPCLMSRLKLSRALMPSEYSTSTLRKLMRPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240

	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

```
a276.seq
1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTGCATGGT
51  GGTCAAGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGGTGTCGTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC AAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTGTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCCT AACCGTATTC GACATCGACG TTGCCGAAGC TGATGCCGCC
651 TTCGACACGC TGCGGTGCAG GCGTGCCTTT GTCCTGTTCG GCGGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATTT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

```
a276.pep
1  MILPSSITMM RSAPSMVVRW WATMPVRF S IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGSR LTTVDLPLPER PTRATRSPLC MSRLKPSRAL
201 MPSEYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*
```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMPVRF S IRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVVRWATMPVRF S IRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKRGSR LTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKRGSR LTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPLMSRLKLSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
a276	PTRATRSPLMSRLKPSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
1  ..atggtacacg tcgcccgtagc ttacggtatt gccgtccggc gtttttgccc
51  aaacgaggtc atagacgttt tccacgcctt gcagggtacat cgccaagcgt
101  tcgatgccgt aggtaatatt gccgagtacg ggcgtgcaat cgataccgcc
151  gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201  cttcccagcc caaaccaccac gcaccgaggg tgggggttttc ccagtctgtc
251  tcgacaaagc ggatgtcgtg gactttggga tcgatgcca attcgcgcag
301  ggagtcgaga tagaggtctt ggatattggc gggggcgggt ttgagggcga
351  cttggaattg gtaatatgtg tgcaggcggc tgggggttgc gccgtagcgg
401  ccgtcttttg ggcggcggct gggttggacg taggcggcaa accaaggctc
451  ggggccgagc gcgcgcaggc aggtggcggg atgggatgtg ccggcaccga
501  cttccatgtc gaagggttg atgacggtgc agcctttgtc tgcccagaag
551  gtttcagtt tgaagatgat ttgttgaag gtaagcatgg cttattgttc
601  gataaaataa aggttttatt ttactgttcc catagccgct tgaatagatt
651  tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
1  ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
51  DLLEIGKLG YFHAVEPDFPA QTPRTGGVF PVVFDKADV DFGIDAQFAQ
101  GVEIEVL D I G G G F E G D L E L V I V L Q A V G V V A V A A V F G A A A G L D V G G K P R L
151  GAERAQAGG MGCAGTDFHV EGLDDGA FV CPEGLQFEDD LLEGKHGLLF
201  DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
1  ATGCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGGC CTTCGTAGTC GTTGAAGTGG
101  CGCAGCAGCC AGTCGCATC GCTGTATTCG AAGTTGTAGG TGGATTGCTC
151  GACTTCGTTT TGGTGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTCGA
201  GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
251  ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301  GTCGATGCCG CCGACTTGTT GGAAATAGGT AAATGGGTT ACTTCCATGC
351  CGTTGAGCCA GACTTCCCAG CCCAAACCC ACGCCCGAG GGTGGGGTTT
401  TCCAGTCGT CTTGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451  CAATTCGCGC AGAGAGTCGA GATAGAGGTC TTGGATATTG CCGGGAGCGG
501  GCTTGAGGGC GACTTGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551  TCGCCGTAGC GGCCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
601  AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651  TGCCGCGACC GACTTCCATG TCGAAGGGT GGATGACGGT GCAGCCTTTG
701  TCTGCCCAGA ATGTTGTCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751  GCCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQQPVG I AVFEVVGGLL
51  DFLVHVH VAV GDGVAVERFC PNEVVDV FYT LQVHRQAFDA VGDFAEYGRA
101  VDAADLLEIG KLG YFHAVEP DFPAQTPRAE GGVFPVFDK ADVVDFGIDA
151  QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAAVF GAAAGLDVGG
201  KPRLGAECAQ AGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251  GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

g277.pep

10 20 30  
MVHVAVAYGIAVRRFCPNEVIDVFHALQVH

631

```

m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVHVAVGDGVAVERFCPNEVVDVFYTLQVH
           30      40      50      60      70      80
           40      50      60      70      80      90
g277.pep  RQAFDAVGNEFAEYGRAIDTADLLEIGKLGYPHVEPDFPAQTPRTEGGVFPVVFDDKADV
           |||||:|:|:|||||:|:|:|||||
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHVEPDFPAQTPRAEGGVFPVVFDDKADV
           90      100     110     120     130     140
           100     110     120     130     140     150
g277.pep  DFGIDAQFAQGVIEVLDIGGGGFEGLDELIVLVQAVGVVAVAAVFGAAAGLDVGGKPR
           |||||:|:|:|||||:|:|:|||||
m277      DFGIDAQFAQGVIEVLDIGGGGFEGLDELIVLVQAVGVVAVAAVFGAAAGLDVGGKPR
           150     160     170     180     190     200
           160     170     180     190     200
g277.pep  GAERAQAGGGMGCAGTDFHVEGLDDGAAAFVCPPEGLQFEDDLLEGKHGL
           |||||:|:|:|||||:|:|:|||||
m277      GAECAQAGGGMGCAGTDFHVEGLDDGAAAFVCPPEGLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTCGTAGTC GTTGAAGTGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGTTT
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTAACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT GAACTGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTGACAAA GCGGATGTCG TGCACTTTGG GGTGATGCC
451 CAATTCGCGC AGGGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGTT GGATGACGGT GCAGCCTTTG
701 TCTGCCCAGA ATGTTTGCA TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DFVLVHVAV SYCITVQRF PNEVIDVFHA LQVHRQAFDA VGDFAEYGG
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GGVPVVFDDK ADVVHFGVDA
151 QFAQGVIEV LDIGGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPRLGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCPPECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

m277.pep  10      20      30      40      50      60
MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLFDFVLVHVAV
|||||:|:|:|||||:|:|:|||||
a277      10      20      30      40      50      60
MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLFDFVLVHVAV
|||||:|:|:|||||:|:|:|||||

m277.pep  70      80      90      100     110     120
GDGVAVERFC PNEVVDVFYTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHVEP
: :|||:|:|:|||||:|:|:|||||
a277      70      80      90      100     110     120
SYCITVQRF PNEVIDVFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGYFHTVEP
|||||:|:|:|||||:|:|:|||||

130     140     150     160     170     180

```

632

```

m277.pep  DFPAQT PRAEGGVFPVVDKADVVDFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQA
a277      DFPAQT PRAEGGVFPVVDKADVVHFGVDAQFAQGVIEVLDIGGSGLEGDLELVIVLQA
           130      140      150      160      170      180

           190      200      210      220      230      240
m277.pep  VGVVAVAAVFGAAAGLDVGGKPRLGAECAQAGGGMGCAGTDFHVEGLDDGAAFVCPCLQ
a277      VGVVAVATVFGAAAGLDVGGKPRLGAECAQTGGGMGCAGTDFHVEGLDDGAAFVCPCLQ
           190      200      210      220      230      240

           250
m277.pep  FEDDLLEGKHGLX
a277      FEDDLLEGKHGLX
           250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

g278.seq (partial)

```

1  ttgcgtgcaa tcacgccccg tgcgattttt tgcacagggg cggtcacaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcatcgacga
101 cgcgtccgac caattcgcg tccgaccggca cttctaaaat acggccggta
151 caggtaaccg tgcgccttc tttaatatgt tcgtactcgc ccaacactac
201 ggcaccgacg gactcgcgct ccagggttcac cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcatcg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcatttaca gacagatttt cgtcttggc tttaatcaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgtca tagtcgtgta
451 caaagcactc agtttgcctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

g278.pep (partial)

```

1  LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

m278.seq..

```

1  TTGCGCGCAA TCACGCCCGG TGCgATTtTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CCGGTCCGAC CAGTTCCGCT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTCAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGcATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTtTACA GACAGATTtTT CGATCTTGGC TTTAATCAAA TCGCTAATTt
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTtGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTcAGC ATTtGCACCA ACTCGCCGAC
601 CTGTTTGTcG GTCAACGGAT AGGCACTGTA AATGACGGCA GATTtGATAT
651 GGTtGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

m278.pep

```

1  LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPQVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLHLAD
201 LFVGQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:



Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278.pep	LRAITPGAIFSTGAVKVV	LIGPLPSIGRPNASTTR	PTNSRPTGTSKIRPVQ	TVTVSPSLIC		
m278	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNASTTR	PTSSRPTGTSKIRPVQ	TVTVSPSLMC		
	10	20	30	40	50	60
	70	80	90	100	110	120
g278.pep	SYSNNTTAPTESRSR	FIAPKPKVLPGNSSIS	PCIASDKPWMRTIPS	VTETVPRVLTSAFT		
m278	SYSNNTTAPTESRSR	FIAPKPKVLPGNSSIS	PCIASDKPWMRTIPS	VTETVQVRTSAFT		
	70	80	90	100	110	120
	130	140	150	160	170	
g278.pep	DRFSILALIRSLIS	AGLSCMKTLIRHSRV	QSTQFALYRQIQNL	LITHFNF		
m278	DRFSILALIKSLIS	AGLSCMKTLIRHSRV	QGTQFALYRQIQNL	LITHFNFYANQLRF	DF	
	130	140	150	160	170	180
m278	DRDFQLAVETLIQHL	HLQLADLFVGQRIG	TVNDGRFDMVE*			
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278.seq

```

1  TTGCGCGCAA TCACGCCCGG TCGGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GCGCGCGACG GAGTCGCGCT CCAGGTCAT  CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGATTG  CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTGGC  TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTGTGCG GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

```

1  LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QTVTVSPSLIC SCSNNTTAPT ESRSRFIAPK KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLRLQLAD
201 LFVGQRIGTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNASTTR	PTSSRPTGTSKIRPVQ	TVTVSPSLMC		
a278	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNASTTR	PTSSRPTGTSKIRPVQ	TVTVSPSLIC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m278.pep	SYSNNTTAPTESRSR	FIAPKPKVLPGNSSIS	PCIASDKPWMRTIPS	VTETVQVRTSAFT		
a278	SCSNNTTAPTESRSR	FIAPKPKVLPGNSSIS	PCIASDKPWMRTIPS	VTETVPRVRTSAFT		
	70	80	90	100	110	120

	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
a278	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
	130	140	150	160	170	180
	DRDFQLAVETLIQHLQLADLFVQGRIQTVNDGRFDMVEX					
m278.pep	DRDFQLAVETLIQHLQLADLFVQGRIQTVNDGRFDMVEX					
a278	DRDFQLAVETLIQHLQLADLFVQGRIQTVNDGRFDMVEX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279.seq

```

1   atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgcg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 cggcagcggg caggcgcggt ttggtccggg cttctttggc ggcagccatg
151 gtgcgtccga cggcggcggc gttgcctgca atcacgactt gtccggcgca
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcattc tccaaaccca aaatggccgc cattgcgcct
301 acgccttgag gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcgcggaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279.pep

```

1   MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCGELKL TASTTSPCAD SAQICLTCS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

```

1   ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGGTTTTCA GGGCTTCGGC
51  AAGTTTGTCT GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGGCGCGGG CAGGCGCGGT TTGGCACC GGCTTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGGCGGGC GTTGCCTGCA ATCAGGATTT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACCTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGCGGTGT
401 ATTCGCCGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTTT GCCGCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1   ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPAP
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120

635

```

m279.pep  ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g279       ITTCPGELKLTASTTSPCADSAQICLTCSSSKPKMAAIAPTPCGTADCISSARRRTSLTA
           70      80      90      100     110     120

           130     140     150
m279.pep  SAKFNAPAATSAVYSPRLCPATAAGVLPASKX
           ||| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g279       SAKSNASAATSAVYSPRLCPATAAGVLPPTSKX
           130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1149>:

```

a279.seq
1  ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNN GGGCTTCGGC
51  GAGTTTGTCT GCGGCGGGTT TCATGAGGCT GCAATGGGA GGTACNGACA
101 CNGGCAGCGG CAGGCGCGCT TTGGCGCCG CTTCTTTGGC GGCAAGCATA
151 GCGCGCTCGA CGGCGGCGGC ATTGCCTGCA ATCAGCACT GTCCGGGCGA
201 GTTGAAGTTG ACGGCTTCAA CCACTTCATC CTGTGCGGAT TCGGCGCAAA
251 TTTGTTTTAC CTGTTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA NGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GCGGCAACN AGTGCGGTGT
401 ATTCGCCGAN GCTGTGTCCG GCAACGGCGG CAGGCGTTTT GCCGCCGCT
451 TCCGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1150; ORF 279.a>:

```

a279.pep
1  MTXICGCLIS TVXRASASLS AAGFMRLQWE GTDTGSGRAR LAPASLAASI
51  ARSTAAALPA ITTCPGELKL TASTTSSCAD SAQICFTCSS SKPRIAAIAP
101 TPCGTADCIS SARXRTSLTA SAKSNAPAAT SAVYSPXLCP ATAAGVLPAP
151 SE*

```

m279/a279 88.2% identity in 152 aa overlap

```

           10      20      30      40      50      60
m279.pep  ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRRARLAPASLAAMARPTAAALPA
           :| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a279       MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRRARLAPASLAASIARSTAAALPA
           10      20      30      40      50      60

           70      80      90      100     110     120
m279.pep  ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA
           || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a279       ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRTSLTA
           70      80      90      100     110     120

           130     140     150
m279.pep  SAKFNAPAATSAVYSPRLCPATAAGVLPASKX
           ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a279       SAKSNAPAATSAVYSPXLCPATAAGVLPASEX
           130     140     150

```

#### Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1   atgaaacacc tcaaaacttac ccttattgcc gcattgctgg ccaccgcccgc
51  aactgccgca ccccttcgcg ttgtaaccag tttcagcatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgtcggg
151 gccaaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttgagg cttgaagccg
251 ccgacatcca acgcgccgctc aaacagagca aagatcccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagcaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgaata tgacccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccata acgtcgctga aaccctgata aaggccgcat ccgaaggcaa
501 agtttattat caacaacgct tgggcaacta ccaaatgcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcatttaatg ccgtccctgc cgccaacgc
601 aaagtccctga ccgggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtagg cagcgaagcc gagccgtccg
701 ccaacaagat cgccgccatc atccggcaaa tcaaacgcga aggcacataa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtg accgcatcgc
801 caaagaaacc ggcgtcaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcgcca tgtaccgcca caacgtcgaa
901 gccttgacca acgcatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1   MKHLKLTLIA ALLATAATAA PLPVVTSFSI LGDVAQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADIQRAV KQSKVSYAEA
101 TKGIQPLKAE EGGHHHDHHD HDHDHDHDEGH HDHDEYDPH VWNDFVLMDS
151 YAQNVATLTI KADPEGKVYY QORLGNYYMQ LKKLHSDAQA AFNAVPAKR
201 KVLTHGDAFS YMGNRYNISF IAPQVSSEA EPSAKQVAI IRQIKREGIK
251 AVFTENIKDT RMDVRIAKET GVNVSGLKLYS DALGNAPADT YIGMYRHNV
301 ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1   ATGAAACACC TCAAACTCAC CCTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTACGATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAACTCG TCCTGCTCAA CGGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG AAGGACACCA CCATGACCAC GGCGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCCTA TGCCCAAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CCTTTTCCTA TATGGGCAA CGTTACCATA TCGAATTCAT
651 CGCCCCGCAA GCGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AACGCGAAG GCATCAAAGC CGTCTTTACC
751 GAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACCGCCCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1   MKHLKLTLIA ALLTASATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEADVQRAV KQSKVSYTEA
101 TKGIQPLKAE EGGHHHDHHD HDHEGHHHDH GEYDPHVWND PVLMSAYAQN
151 VAKALIKADP EGKVVYQQL GNYQMQLKKL HSDAQAAFNA VPAKRKVL

```

201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KQVAIIIRQI KREGIKAVFT  
251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNKALTN  
301 AMKQ\*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N.gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng) from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLT	LIAALLTASATAAPLPVVT	SFSILGDVAKQIGGERVSIQSLV	GANQDTHAYHM		
		:		:		
g280	MKHLKLT	LIAALLATAATAAPLPVVT	SFSILGDVAKQIGGERVAVQSLV	GANQDTHAYHM		
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKL	VLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE	EEGGHHHDH-			
		:	:			
g280	TSGDIKKIRSAKL	VLLNGLGLEAADIQRAVKQSKVSYAEATKGIQPLKAE	EEGGHHHDH			
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---	DHDHEGHHHDHGEYDPHVWNDPVLMSAYAQNVAKALIKADPEGK	VVYQORLGNYQMQ			
			:			
g280	HDHDHDH	EGHHHDHGEYDPHVWNDPVLMSDYAQNV	AEATLIKADPEGKVVYQORLGNYQMQ			
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAA	FNAPPAKRKVL	TGHDAFSYMGKRYHIEFIAPQGVSSAEPSAKQVAAI			
			:			
g280	LKKLHSDAQAA	FNAPPAKRKVL	TGHDAFSYMGKNRYNISFIAPQGVSSAEPSAKQVAAI			
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAV	FTENIKDTRMV	DRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNIK			
				:		
g280	IRQIKREGIKAV	FTENIKDTRMV	DRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNVE			
	250	260	270	280	290	300
	300					
m280.pep	ALT	NAMQOX				
g280	ALT	NAMQOX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

1	ATGAAACACC	CCAAACTCAC	CCTTATCGCC	GCATTGCTGA	CCACTGCCGC
51	AAC TGCCGCC	CCCCTGCCG	TTGTAAACC	CTTACGATT	TTAGGCGACG
101	TAGCCAAACA	AATCGGCGGA	GAGCGCATAT	CCATACAAAG	TTTGGTCGGA
151	GGCAACCAAG	ATACGCACGC	CTATCATATG	ACCAGCGCGC	ACATTAAAAA
201	AATCCGCAGT	GCAAAACTCG	TCCTGATTAA	CGCCTTAGGA	CTTGAAGCTG
251	CCGACATCCA	ACGTGCGCTT	AAACAGAGCA	AAGTATCCTA	TGCCGAAGCG
301	ACCAAAGGCA	TCCAACCCCT	CAAAGCCGAA	GAGAAGCGCG	GACACCATCA
351	CGACCACGAT	CATGACCACG	ACCTATGACCA	CGAAGGACAC	CACCCACGAC
401	ACGGCGAATA	TGACCCCCAC	GTCTGGAACG	ACCCCGTCTT	TATGTCGGCC
451	TATGCCCAAA	ACGTCGCCGA	AGCCCTGATA	AAGGCGCGAC	CCGAAGGCCAA
501	AGTTTATTAT	CAACAACGCT	TGGGCAACTA	CCAATGCGAC	CTCAAAAAAC
551	TGCACAGTGA	CGCAACAAGC	GCATTTAATG	CCGTCCCTGC	CGCCAAACGC
601	AAAGTCCTGA	CCGGGCACGA	TGCCTTTTCC	TATATGGGCA	AACGTTACCA
651	TATCGAATTC	ATCGCCCCAC	AAGGTGTGAG	CAGCGAAGCC	GAGCCTTCAG
701	CAAAACAAGT	CGCCGCCATC	ATCCGACAAA	TCAACACGCA	AGGCATCAAA
751	GCCGTATTTA	CCGAAAATAT	CAAGACACC	CGCATGGTTG	ACCGCATCGC

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG  
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA  
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep  
 1 MKHPKLTLIA ALLTTAATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG  
 51 ANQDTHAYHM TSGDIKKIRS AKLVLINGLG LEAADIQRAV KQSKVSYAEA  
 101 TKGIQPLKAE EGGHHHDHD HDHDHDEGH HDHGEYDPH VWNDPVLMSA  
 151 YAQNVAEALI KADPEGKVYY QQRLGNYQMQ LKKLHSDAQA AFNAVPAKR  
 201 KVLTHGDAFS YMGKRYHIEF IAPQGSSEA EPSAKQVAI IRQIKREGIK  
 251 AVFTENIKDT RMVDRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNK  
 301 ALTNAMKQ\*

m280/a280 96.4% identity in 308 aa overlap

m280.pep	10	20	30	40	50	60
	MKHLKLTLIAALLTASATAAPLPVVTFSILGDAVQIGGERVSIQSLVGANQDTHAYHM					
a280	MKHPKLTLIAALLTTAATAAPLPVVTFSILGDAVQIGGERVSIQSLVGANQDTHAYHM					
	10	20	30	40	50	60
m280.pep	70	80	90	100	110	120
	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EGGHHHDHD					
a280	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAE EGGHHHDHD					
	70	80	90	100	110	120
m280.pep	130	140	150	160	170	
	HDH---EGHHHDHGEYDPHVWNPVLMSAYAQNVAKALIKADPEGKVYYQQRLGNYQMQ					
a280	HDHDHDEGHHDHGEYDPHVWNPVLMSAYAQNVAEALIKADPEGKVYYQQRLGNYQMQ					
	130	140	150	160	170	180
m280.pep	180	190	200	210	220	230
	LKKLHSDAQA AFNAVPAKRKVLTHGDAFSYMGKRYHIEF IAPQGSSEA EPSAKQVAI					
a280	LKKLHSDAQA AFNAVPAKRKVLTHGDAFSYMGKRYHIEF IAPQGSSEA EPSAKQVAI					
	180	190	200	210	220	230
m280.pep	240	250	260	270	280	290
	IRQIKREGIK AVFTENIKDTRMVDRIAKET GNVVSGKLYS DALGNAPADTYIGMYRHNK					
a280	IRQIKREGIK AVFTENIKDTRMVDRIAKET GNVVSGKLYS DALGNAPADTYIGMYRHNK					
	240	250	260	270	280	290
m280.pep	300					
	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:  
 g281.seq

1 atgcactacg ccctcgcatc cgtcttctgc ctgtccctca gcgcgcacc  
 51 cgctggcgta ttctcgtca tgcgcgctat gagcctgata ggcgacgcat  
 101 tgagccacgc cgtcctgccc ggtgcccgcg tcggctacat gtttgccggc  
 151 ttgagcctgc ccgctatggg tgtggcgagg tttgccgcg gtatgctgat  
 201 ggcgctgctt gccggactcg tcagccgctt taccacctg aaagaagatg  
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc  
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc  
 351 tgtgcttgcc gtcgatattc ccgcactgca actcatcgcc gccgtctccg  
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa  
 451 agcatagacc cccttttctc caagtcgctc aacggcaaa gcgggctttg

501 gcacgtcatt ttcctcatcc tcgtcgttat gaacctcgta tcgggcttcc  
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt  
601 accgcccgtt tatgggcaag aaatatgggg acgctcattc tgtgtccgt  
651 cctcatcgcc cttttttgcg gtttgatcgg gctgctcatt tcctacaca  
701 tcgaaatccc ttccggcccc gccataagcc tcctgtgcag cgctccttat  
751 cttttttccg tcatactcgg caaagaagcc ggcatcttgc ccaaatgggt  
801 caaaaaacac qcaccaccaca ccacctga

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

g281.ppe

```

1  MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGVGG FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL
101 ISKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSGLTLITL AVIYRPLVLE
151 SIDPLFLKSV NGKGKGLWHVI FLICLVMMNLV SGFQALGILM SVGIMMLPAI
201 TARLWARNMKG TILLSLVLIA LFCGLVLGLLI SYHIEIPSG AIICCSVLYI
251 LFSVILGKEG GILPKWFKNH RHHTT*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEO ID 1159>:

m281.seq (partial)

1	ATGCGCTACG	CCCTCGCATC	CGTCTTCTGC	CTGTCCCTCA	GTGCCGCACC
51	CGTCGGCGTA	TTCCTCGTCA	TGCGCCGTAT	GAGCCTGATA	GGCGACGCAT
101	TGAGCCACGC	CGTCTCTGCC	GGTGC CGCGC	TCGCTACAT	GTTTGCCGGC
151	TTGAGCCTGC	CCGCCATGGG	TTTGGGCGGC	GTAGCCGCAG	GCATGTGATG
201	GCGACTGCTT	CGCGGACTCG	CTACGCGCTT	CACCACCCCTG	AAAGAAGATG
251	CCAACTTTGC	CGCCTTTTAT	CTCAGCAGCG	TCGCCATCGG	CGTAGTCTCT
301	GTCAGCAAAA	ACGGGAGCAG	CGTCGATTTG	CTCCACCTCC	TTTTCGGGTC
351	TGTACTTGCC	GTCGATATTC	CTGCCCTGCA	GCTCATCGCC	GCCGTCTCCA
401	GCCTCAGCTC	CATTACCCCTT	CGCGTCATCT	ACCGCCCGCT	CGTACTCGAA
451	AGCATCGACC	CCCTGTTTCT	CAAACTCCGT	GGCGCCGAAG	CGCGGCTTTG
501	GCACGTCCTC	TTTCTCGTCC	TGGTTCGTAT	GAACCTCGTA	TCGGGCTTTC
551	AAGCCCTCGG	CACACTCATG	TCCGTCGGAC	TCATGATGCT	GCCAGCCATT
601	ACCGCCCGCC	TGTGGGCGAA	GCATATGGGC	GCACTCATCC	TCCTATCCGT
651	TCTGACAGCC	CTCGGTGTGG	CGTTGAGCGG	ACTGCTCAT	TCCTACCACA
701	TCGAAATTCC	TTCCGGTCCC	GCCATCATCC	TCTGTTGCAG	GTCCCTTTAT
751	CTCTTTTCCG	TCATACTCGG	CAAAGAAGGC	GGCACTCTGA	CC

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

m281.pep (partial)

```

1  MRYALASVFC LSLSLAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGVMFAG
51  LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSSLTLTTL AVIYRPLVLE
151 SIDPLFLKSV GKGGLLWHVL FLVLVVMNLV SGFQALGTLM SVGLMMLPAI
201 TARLWAKHMG ALILLSVLA LLCGLSGLLI SYHIETPSGP AILCCSVLY
251 LFSVILKKEG GILT..

```

**Computer analysis of this amino acid sequence gave the following results:**

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

m281/q281

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSL	AAPVGVLV	MRRMSL	IGDALSHAV	LPGA	AVGYMFAGLSLPAMGLGG
	:					
g281	MHYALASVFCLSL	AAPVGVLV	MRRMSL	IGDALSHAV	LPGA	AVGYMFAGLSLPAMGVGG
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGL	VS	RFTTLKEDAN	FAAFYLSS	LAIGVVLV	SKNGSSVDLLHLLFGSVLA
g281	FAAGMLMALLAGL	VS	RFTTLKEDAN	FAAFYLSS	LAIGVILIS	KNSSVDLLHLLFGSVLA
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIAA	VSSSLT	LITLAVIY	RPLVLES	IDPLFLK	SVGGKGLLHWHLVFLVLVVMNL

			:					:		:		:																
g281	VDIPALQLIAAVSGLTLITLAVIYRPLVLESIDPLFLKSVNGKGGLWHVIFLILVMNLV																											
	130				140				150				160				170				180							
					190				200				210				220				230				240			
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTAALLCGLSGLLLISYHIEIPSGP																											
			:			:		:		:		:																
g281	SGFQALGTLMSVGIMMLPAITARLWARNMGTLLILLSVLIALFCGLIGLLISYHIEIPSGP																											
	190				200				210				220				230				240							
					250				260																			
m281.pep	AIILCCSVLYLFVSILGKEGGILT																											
g281	AIILCCSVLYLFVSILGKEGGILPKWFKNHRHHTTX																											
	250				260				270																			

```
a281.seq
  1  ATGCGCTACG  CCCTCGCATC  CGTCTTCTGC  CTGTCCCTCA  GTGCCGCACC
51  CGTCGGCGTA  TTCCTCGTCA  TCGCGCGTAT  GAGCCTGATA  GGCGCAGCAT
101 GTAGCCACGG  CGCTCTTGCC  GGTGGCGCGG  TCGGCTACAT  GTTTGCCGGC
151 TTAAGCCTGC  CCGCCATGGG  TTTGGGCGGC  GTAGCCGAG  GTATGCTGAT
201 GGCAGTGCTT  GCCGGACTCG  TCAGCGGCTT  CACCACCCTG  AAAGAAGATG
251 CCAACTTTGC  CGCCTTTTAT  CTCAGCAGCC  TCGGCATCG  TGTAGTCTCT
301 GTCAGCAAAA  ACGGCAGCAG  CGTCGAGATT  CTCCACCTCC  TTTTTCGGCT
351 CGTACTTGCC  TCGGATATTC  TCGCCTGCA  ACTCATCGCC  GCGGATCCAA
401 CCCTCACACT  GCTTACCCTT  GCCGTCTACT  ACCGCCCCTG  CGTACTCGAA
451 AGCATCTGAC  CCCTGTTTCT  CAAATCTGTC  GCGGCGAAAG  GCGGGCTTTG
501 GCACGTCCTC  TTTCTCGTCT  TGGTGCATAT  GAACTCTGTA  TCCGGCTTTC
551 AAGCCCTCGG  CACATCTATG  TCCGTCGGAC  TTATGATGCT  GCCAGCCATT
601 ACCGCCCCTG  TATGGGCGAA  GCACATGGGC  GCACTCATCC  TCCATCCGCT
651 TCTGACAGCC  CTGCTGTGCG  GCTTGAGCGG  ACTGCTCATT  TCCTACCACA
701 TCGAAATTCC  TCCGCTGCC  GCAATATGCT  TCTGTTGAG  CGTCTTTTAT
751 CTCTTTTCCG  TCACACTCGG  CCAAGAAGCC  GGCATTCTGA  CCAAATGGCT
801 CAAAAACCA  CGCCACCACA  CCACCTGA
```

a281.pap

1	MRYALASVFC	LSLSAAPVGV	FLVMRRMSLI	GDALSHAVLP	GAAVGYMFAG
51	LSLPAMGLGG	VAGCMLMALL	AGLVSRTFTL	KEDANFAAFY	LSSLAIGVVLT
101	VSKNGSSVDL	LHLLFGSVLA	VDIPALQLIA	AVSTLTLLTL	AVIYRPLVLE
151	SIDPLFLKSV	GKGKGLWHVL	FLVLVVMNLV	SGFOALGTLM	SVGLMMLPAI
201	TARLWAKHMG	ALLLSVLTA	LLCGLSGLLI	SYHIEIPSPG	ATILCCSVLY
251	FSVILGKEG	GILTKWLKNH	RHHTT*		

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSLSAAPVGVLVMRRMSLIGDALSHAVLPGA	AVGYMFAGLSLPAMGLGG				
a281	MRYALASVFCLSLSAAPVGVLVMRRMSLIGDALSHAVLPGA	AVGYMFAGLSLPAMGLGG				
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA					
a281	VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIAAVSSLTLITLAVIYRPLVLESIDPLFLKSVGGKGLWHVFLVLVVMNLV					
a281	VDIPALQLIAAVSSLTLITLAVIYRPLVLESIDPLFLKSVGGKGLWHVFLVLVVMNLV					
	130	140	150	160	170	180



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	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1 atgggattgg gtatggaaat cggcaagctg attgtggctc ttttggtgct
51 gatcaatccg tttagcgcgt tgtcgcttta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgac ggcggtgcgc tattgaaggt
201 tttgggcatc agcgtcgggt cgtttcaggt cggcgccggg attttggtgc
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggcgatt gccgtcgtgc ccacgcgat accgatcacc atcggtccgg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgcgc tgattatcgc ggccggtttg gtggtcagtg cgatttgta
501 tgccatttta atcgttgccg ggaaggctcag ccgcctgctg ggccgcagcg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggccggtatc
601 gtggagatta ttgtgtcggg actgaaaacg atattccgcg aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1 MGLGMEIGKL IVALLVLINP FSALSPLYLDL TNGHSTKERR KVARTAATAVAV
51 FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYT
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLR GATGLTILNR IMGMMLAAYS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1 ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51 GATTAATCCG TTTAGCGCGT TGTGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCCG
401 GCGGTATTTC GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTGTGTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGCGCGACGG
551 GGCTGACGAT TTAAACCAGC ATTATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1 MGLGMEIGKL IVAFLVLINP FSALSPLYLDL TNGHSTKERR KVARTAATAVAV
51 FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLR GATGLTILNR IMGMMLAAYS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng)  
from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282.pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
m282.pep	70	80	90	100	110	120
	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
m282.pep	130	140	150	160	170	180
	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRLI					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRLI					
	130	140	150	160	170	180
m282.pep	190	200	210			
	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
g282	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282.seq

1	ATGGGATTGG	GCATGGAAT	CGGCAAGCTG	ATTGTGGCTT	TTTGGTGCT
51	GATTAATCCG	TTTAGCGCGT	TGTCGCTTTA	CCTTGACCTG	ACCAACGGGC
101	ACAGCACGAA	GGAGCGCAGG	AAGGTCGCGC	GGACGGCCGC	CGTTGCCGTG
151	TTTGCCGTGA	TGCGGTATT	TGCGCTGATC	GGCGGTACGC	TGCTGAAGGT
201	TTTGGGCATC	AGCGTCGGTT	CGTTTCAGGT	CGGCGGCGGA	ATTTTGGTGT
251	TGCTGATTGC	CATTTTCGATG	ATGAACGGCA	ACGACAATCC	CGCCAAGCAG
301	AATCTCGGCG	CGCAGCCGGA	AACGGGGCAG	GTGCGCCCCG	CCCCTCAATGC
351	CGGAGCGATT	GCCGTCGTGC	CCATCGCCAT	ACCGATCACC	ATCGGCCCCG
401	GCGGTATTTC	GACCGTGATT	ATTTACGCTT	CGGCGGCTAA	AACATACGGC
451	GACATCGCGT	TGATTATCGC	GGCCGGTTTG	GTGGTCAGTG	CGATTGTGTTA
501	TGCCATTTTA	ATCGTTGCCG	GGAAGGTCAG	CCGCCTGCTG	GGTGCGACGG
551	GGCTGACGAT	TTTAAACCGT	ATCATGGGTA	TGATGCTGGC	GGCGGTATCG
601	GTGGAGATTA	TTGTGTCGGG	ACTGAAAATG	ATATTCCCGC	AACTGGCAGG
651	TTGA				

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282.pep

1	MGLGMEIGKL	IVAFLVLINP	FSALSPLYLDL	TNGHSTKERR	KVARTAAVAV
51	FAVIAVFALI	GGTLLKVLGI	SVGSFQVGGG	ILVLLIAISM	MNGNDNPAKQ
101	NLGAQPETGQ	VRPARNAGAI	AVVPIAIPIT	IGPGGISTVI	IYASAAKTYG
151	DIALIIAAGL	VVSAICYAIL	IVAGKVSRLI	GATGLTILNR	IMGMLAAVS
201	VEIIVSGLKM	IFPQLAG*			

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282.pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
a282	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGOARPARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGOVRPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282.pep	AVVPPIAIPITIGPGGISTVIIYASAAKTYGDIALIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPPIAIPITIGPGGISTVIIYASAAKTYGDIALIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282.pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
a282	GATGLTILNRIMGMLAAVSVEIIVSGLKMIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

```

g283.seq
1   atgaactttg ctttatccgt catcacattt accctcgctt ctttcctgcc
51  cgtcccgctt gccggaaccg ccgtctttac ttggaagac  ggcggcggca
101 acagctattc ggatgtgccg aaacagcttc atcccgacca gagccaaatc
151 ctcaacctgc ggacgctcca aaccaaaccc gcggtcaagc ccaaacctgc
201 cgtcgatacg aatgcggaca gtgcgaagga aaacgaaaag gatatcgccg
251 agaaaaacgg gcagcttgag gaagaaaaga aaaaaattgc cgaaaccgaa
301 cggcagaaca aagaagaaaa ctgccggatt tcaaaaatga acctgaaggg
351 ggtgggaaac tcaaatgcga aaacaagga  tgatttgatc cgtaaatata
401 ataacgccgt aaacaatac  tgccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

```

g283.pep
1   MNFALSVITF TLASFLPVPP AGTAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRLTQTKP AVKPKFAVDN NADSAKENEK DIAEKNGQLE EEKKKIAETE
101 RQNKKEENCR SKMNLKAVGN SNAKNKDDLI RKYNNAVNKY CR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

```

m283.seq
1   ATGAACCTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GCGGCGGGCA
101 ACAGCTATTC GGATGTACCG AACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAACTGCG CGGATTTCAG AAATGAACCT
351 GAAGGCGGTG GGAAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

```

m283.pep
1   MNFALSVIML TLASFLPVPP AGAAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTQTKP AVKPAQADAG KRTDGAAQEN NPDTEKNRQ LEEKKRIAE
101 TERQNKKEEN RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m283/g283  86.1% identity in 144 aa overlap

          10      20      30      40      50      60
m283.pep  MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRLTQTKP
          ||||| :|||||:|||||:|||||:|||||:|||||
g283       MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRLTQTKP
          10      20      30      40      50      60

```

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	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
		:	:	:	:	:
g283	AVKPKPA-VDTNAD-SAKENEKDIAEKNGQLEEEKKRIAETERQNKEENCRISKMNLKAV					
	70	80	90	100	110	
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNVAVNKYCRX					
g283	GNSNAKNKDDLIRKYNNVAVNKYCRX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1173>:

a283.seq

1	ATGAACTTTG	CTTTATCCGT	CATTATGTTG	ACCCTCGCCT	CTTTCCTGCC
51	CGTCCCGCCT	GCCGGAGCCG	CCGTCTTTAC	TTGGAAGGAC	GGCGGCGGCA
101	ACAGCTATTC	GGATGTACCG	AAACAGCTTC	ATCCCGACCA	AAGCCAAATC
151	TTAAACCTGC	GGACGCGCCA	AACCAACCG	GCGGTCAAAC	CCGCCCAAGC
201	CGACGCAGGG	AAGCGCACAG	ACGGCGCGGC	ACAGGAAAAC	AATCCCGACA
251	CTGCCGAGAA	AAACCGGCAG	CTTGAGGAAG	AAAAGAAAAG	AATTGCCGAA
301	ACCGAACGGC	AGAACAAGA	AGAAACTGC	CGGATTTCAA	AAATGAACCT
351	GAAAGCGGTG	GGAATTCAA	ATGCAAAAAA	CAAGGATGAT	TTGATTGGGA
401	AATACAATAA	CGCCGTAAAC	AAATACTGCC	GTTAA	

This corresponds to the amino acid sequence <SEQ ID 1174; ORF 283.a>:

a283.pep

1	MNFALSVIML	TLASFLPVPP	AGAAVFTWKD	GGGNSYSVDP	KQLHPDQSQI
51	LNLRTRQTKP	AVKPAQADAG	KRTDGAQEN	NPDTAEKNRQ	LEEEKKRIAE
101	TERQNKEENC	RISKMNLKAV	GNSNAKNKDD	LIRKYNNAVN	KYCR*

m283/a283 100.0% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSVDPKQLHPDQSQILNLRTRQTKP					
a283	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSVDPKQLHPDQSQILNLRTRQTKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
a283	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
	70	80	90	100	110	120
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNVAVNKYCRX					
a283	GNSNAKNKDDLIRKYNNVAVNKYCRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1175>:

g284.seq.

1	atgccgtctg	aaactcgaaa	tcggtttcag	acggcattgg	tttacgcggc
51	aggttggggc	ttagcgggtc	ttgtaacggc	attcgctttt	gcctgcaaaa
101	gagtcgccgg	ctttgcgttt	gcctttgaag	ccttcgccgg	tttttttgaa
151	actgtctttc	ttaaagcctt	ctttcttgaa	accttcgccg	cgcgttttgc
201	cgccgaagcc	ttctttgccc	ggtttatgat	cgccgcgccg	gccgcgggat
251	ttcctatcgc	cccagccgcc	tttgcctttc	ggcttgccgc	ctgcggattt
301	gcgtttgcgg	gccggctcca	tgccctcgat	ggtcagttcg	ggcagtttgc
351	ggttaatgta	tttttcgatt	ttgtggactt	tgacgtattc	gttcacttcg
401	gcaaacgtaa	tcgcaatacc	cgtgcggcct	gcgcggccgg	tgccgccgat
451	gcggtggacg	tagtcttcgg	cctgtttcgg	caggtcgtag	tttatgacgt

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```

501 gggtaatggt cggtagctca ataccgcgtg cggcaacgtc ggtggcaacc
551 aaaatatttgc agcggccttt acgcaaatcc gtcagcgtgc ggttgcccca
601 gccctgcggc atatcgccgt gcaggcagtt ggcggcgaaa cctttttcgt
651 acaattcatc cgcgatgact tcggtcatcg ctttggtgga cgtgaaaatc
701 acacattggt cgatgttggc atcgcgagg atgtggtcga gcaggcggtt
751 tttgtggcgc atatcgctgc agtacaacaa ctgctcttcg attttgcctt
801 ggccgtccac gcgttcgact tcgataattt cagagtcctt ggtcagtttg
851 cgcgccagtt tgccgactgc gccgtcccaa gtggcggaga acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

```

g284.pep
1 MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
51 TVFLKAFFLE TFAARFAAEA FFARFMIAAP AAGFPIAPAA FAFRLAACGF
101 AFAGRLHAFD GQFGQFAVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDVGNNG RYVNTACGNV GGNQNFAAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHREFG RENHTLVDVG IAQDVVEQAV
251 FVAHIVAVQQ LLFDFAALVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

```

m284.seq..
1 ATGCCGCTCG AAACGCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51 AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTTCGAA
151 ACCGTCTCTC TTAAAGCCTT CTTCTTGAA ACCTTCGCCG CGCGTTTTCG
201 CGCCGAAGCC TTCTTTGCTC GGTATTGAT CGCCGCGCCA ACCGCCGGAT
251 TTACGATCGC CCCAGCGGCC TTGCTTTCG GGCTTGCCGC CTGCGGATTT
301 GCGTTTTCGG GTCGGTTCCA TGCCTTCGAT GGTCAGTTCG GGCAGTTTTC
351 GGTAAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCGGCCT GCGCGGCCGG TCGGCCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACATC GGTGGCAACC
551 AAAATTTTGC AGCGGCCCTT ACGCAATCC ATCAGCGTGC GGTGCGCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT TGCGGCGAAA CCTTTTCGT
651 ACAGTTCATC CGCAATGACT TCGGTCATGG CTTTGGTGGA CGTGAAATC
701 ACGCATGAT CGATATTGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTTCTTCG ATTTTGCCTT
801 GATCGTCCAC GCGTTCGACT TCGATGATT CAGGGTCTTT GGTCAGTTTG
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCG CTCGGCGTTG CTTCCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAAATCAG CACTTCCAAA
1001 CGTTCAAAAT CAACTTGGCC GCTTTCGATC AGGTCCATCA GACGGCCCGG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGCT CAGGGCACGG GTTTGGTAGC
1101 CGAAAGACGC GCCGCCGACG ATGCTGACGG TCGGGAACCA ACGCATATTT
1151 TTGGCATACG CCAGCGCGTT TTTCTCGACT TGAGCCGCCA GTTCGCGGGT
1201 CGGGGTCAAC ACCAAAGCAC GCGGGCCTTT GCCCGGTTT TCGCTGCGTT
1251 TGGTCAGTTT TTGCAAAGTC GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

```

m284.pep
1 MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFHAFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDVGNNG RYVDTACGNI GGNQNFAAAF TQIHQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFEG RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVNQ HFQTFKINFA ALHQVHQTAR
351 RGDNQIDRFA QGTGLVAERR AADDADGAEP THIFGIRQV FLDLSRQFAG
401 RGQHQSTRAF ARFFAAGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

646

	10	20	30	40	50	60
m284 . pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284 . pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAFAGRFHAFDGGQFGQFSVNV					
g284	TFAARFAAEAFFARFMIAAPAAGFPIAPAAFAFRLAACGFAFAGRLHAFDGGQFGQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284 . pep	FFDFVDFDFVHFVHGKRNTRACAAGAPDAVDVVFRLFRQVVVDNVGNRYVDTACGNI					
g284	FFDFVDFDFVHFVHGKRNTRACAAGAPDAVDVVFRLFRQVVVDNVGNRYVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284 . pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNFAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHRFGGRENHTLVDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284 . pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFFRNVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLFFDFALAVHAFDFDNFRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284 . pep	LTVARRCFHGDGFDVVDKAHIQHTVGFVNQHFQTFKINFAALHQVHQTARRGDNQIDRFA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284 . seq
1  ATGCCGCTCG AAACGCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51  AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTGTGAA
151 ACCGTCTCTC TTAAGCCTT CTTCTTGAA ACCTTCGCCG CGCGTTTTGC
201 CGCCGAAGCC TTCTTTGCTC GGTTCATGAT CGCCGCGCCA ACCGCCGGAT
251 TTACGATCGC CCCAGCCGCC TTTCCTTTC GGCTTGCCG CTGCGGATT
301 GCGTTTGGCG GTCGGTTCCA TGCTTCGAT GGTTCAGTCG GGCAGTTTTC
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTCGCGCCT GCGCGGCCGG TCGCCCCGAT
451 GCGGTGGACG TAGTCTTCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACGTC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT GCGCAAATCC ATCAGCGTGC GGTTCGCCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT GCGGCGGAAA CCTTTTTCGT
651 ACAATTCATC CGCGATGACT TCGGTCATGG CTTTGGTGA CGTGAAAATC
701 ACGCATTGAT CGATGTCGGC ATCGCGCAAG ATATGATCGA GCAGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTCTTCG ATTTTGCCTT
801 GGTCGTCCAC GCGTTCGACT TCGATGATTT CAGGGTCTTT GGTCAGTTTG
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCT TCCGGCGTGG CTTTCGACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAAATCAG CACTTCCAAG
1001 CGGGCGAAAT CGACTTTGCC GCTTTCATC AAGTCCATCA GACGGCCCGG
1051 CGTGCGGACA ATCAGATCGA CCGGTTTGCT CAGGGCGCGG GTTGGTAGC
1101 CGAACGATGC ACCACCGACG ATGCTGACGG TACGGAACCA ACGCATATTT
1151 TTGGCATAAC CAGCGCGGTT TTTCTCGACT TGAGCCGCCA ATTCGCGGTT
1201 CGGCGTCAAC ACCAACGCGC GCGGGCCTTT GCCCGGTTTT TCGCTCGGTT
1251 TGGTCAGTCG CTGCAAAGTC GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284 . pep
1  MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE

```

647

```

51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFHAFD GQFGQFSVNV FFDFVDFDVF VHFGKRNNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGFGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNG HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRARAF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

m284.pep	10	20	30	40	50	60
	MPSETRNRFQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFETVSLKAFFLE					
a284	10	20	30	40	50	60
	MPSETRNRFQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFETVSLKAFFLE					
m284.pep	70	80	90	100	110	120
	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
a284	70	80	90	100	110	120
	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
m284.pep	130	140	150	160	170	180
	FFDFVDFDVFVHFGKRNNTRAACAAGAPDAVDVVFRLEFQVVVDNVGNGRYVDTACGNI					
a284	130	140	150	160	170	180
	FFDFVDFDVFVHFGKRNNTRAACAAGAPDAVDVVFRLEFQVVVDNVGNGRYVDTACGNI					
m284.pep	190	200	210	220	230	240
	GGNQNFAAAFTQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDIG					
a284	190	200	210	220	230	240
	GGNQNFAAAFAQIHQRAVAPALRHIAVQAVCGGETFFVQFIRDDFGHGFGGRENHALIDVG					
m284.pep	250	260	270	280	290	300
	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFFDFRVFGQFARQFADRAVPSGGEQQS					
a284	250	260	270	280	290	300
	IAQDMIEQAVFVAHIVAVQQLFFDFALVVHAFDFFDFRVFGQFARQFADRAVPSGGEQQS					
m284.pep	310	320	330	340	350	360
	LTVARRCFHDGFDVVDKAHIQHTVGFVQNGHFQTFKINFAALHQVHQTARRGDNQIDRFA					
a284	310	320	330	340	350	360
	LTVFRRGFDDGFDVVDKAHIQHTVGFVQNGHFQAGEIDFAALHQVHQTARRGDNQIDRFA					
m284.pep	370	380	390	400	410	420
	QGTGLVAERRAADDADGAEPHTHIFGIRQRVFLDLSRQFAGRGQHQSSTRAFARFFAAGQF					
a284	370	380	390	400	410	420
	QGAGLVAERCCTDDADGTEPHTHIFGIRQRVFLDLSRQFAGRRQHQRARAFARFFAAGQS					
m284.pep	LQSRX					
a284	LQSRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

g285.seq
1 atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat tttggcagta

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151 tgtttcctcg gctggatcgc cggtagcgaa gcaggtttgc gtttcgggct  
201 gtaccaaata ccgtcctggt tcggcgtaaa catttcctcc caaaacctca  
251 aaggcacact gctcgacggc ttcgacggcg acaactggtc gatagaaacc  
301 gagggggcag accttaaaat cagccgcttc cgcttcgcgt ggaaaccgtc  
351 cgaactgatg cgccgcagcc tgcacatcac cgacatctcc gccggcgaca  
401 tcgcatcgt aaccaaaccg actccgccta aagaagaacg cccgcctcaa  
451 ggccctgccg acagcataga cctgcccgcc gctgtctatc tcgaccgctt  
501 cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaacctgtc  
551 atctcgaacg cctcaacgcg gcataccgtt acgaccgtaa agggcaccgc  
601 ctcgacctga agggccgccg cagccgctgg agcagttcgt cggggtcagc  
651 ctcgctcgcc ttgaaaaaac cgtttgcctc cgataccgcc atttacacca  
701 aaggcggtt cgaaggcgaa accatacaca gtacggcgcg gctgagcgcg  
751 agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg  
801 cctctcggga aaatcgtca tccaccggtt tgccgaatca ttggataaaa  
851 cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc  
901 gtgccttccc tgcccgatgc cgggtggaat ttcgacctga ccgccatccc  
951 gtcgttttca gacggcatcg cgctggaagg ctcgctcgat ttggaaaaca  
1001 ccaaagcccg ctttgcgcac cgcaacggca tccccgtccg tcaggttttg  
1051 ggcggctttg tcatccggca ggacggcacg gtgcataatc gcaatacgtc  
1101 cgccgccctg ctcggacggg gcggcatcag gctgtcgggc aaaatcgaca  
1151 ccgaaaaaga catccttgat ttaaatatag gcatacaact cgctggcgcg  
1201 gaagacgtgc tgcaaacgcg gttcaaaggc aggttgagcg gcagcatcgg  
1251 catcggcgcc acgaccgcct cgcccaaaat ctcttggaac ctcggcaccg  
1301 gcacggcacg cacggacggc agcctcccca tcgcaagcga ccccgcaaac  
1351 gaacagcgga aactggtgtt cgacacgcgc aacatctccg ccggggaagg  
1401 cagcctgacc gcgcaaggct atctcgagct gtttaaagac cgctgctca  
1451 agctggacat ccgttcccgc gcattcgacc cttcgcgcac cgatccgcaa  
1501 tttccggcag gcaatatcaa cggttcgatt catcttgccg gtgaactggc  
1551 aaaagagaaa tttacgggca aaatgcgttt tttgccgggt acgttcaacg  
1601 gcgtgccgat tgccggcagc gccgacattg tttacgagtc ccgccacctt  
1651 ccgcgcgccg ccgtcgattt gcggttgagg cggaaacatcg tcaaaacaga  
1701 cggcgcttcc ggcaaaaaag gcgacggcgt taacctcaat atcaccgcac  
1751 ccgatttatc ccgttccggt ttcggactcg ccgggtcttt aaatgtacgc  
1801 ggacaccttt ccggcgattt ggacggcgcc atccgaacct ttgaaaccga  
1851 cctttccggc acggcgcgca acttacacat cggcaaaagc gcagacatcc  
1901 gttcgcctca ttttccctc aaaggctcac ccggcacaag ccgcccgatg  
1951 cgcccgata tcaaggcgcg ccgcctttcc ctgtcgggcg gcgcggcggt  
2001 tgtcgatacc gccggcctga cgctggaagg tacggcgcgcg cagcaccgca  
2051 tccgcacaca ccgcccatg acgctggacg gcaaaccggt caaactcgat  
2101 ttggacgctt caggcgcat caacaggga cttaccgat ggaaaggcag  
2151 catcggcatc ctcgacatcg gcggcgcat caacctcaag ctgcaaaacc  
2201 gtatgacgct cgaagccggt gcggaacacg tggcggaag tcgcgcaaat  
2251 tggcaggcaa tggcgggcag cctcaacctg caacactttt cttgggacag  
2301 gaaaaccggc atatcgga aaggcggcgc acgcggcctg cacatcgccg  
2351 agttgcacaa tttcttcaaa ccgcccttcg aacacaatct ggttttaaac  
2401 ggcgactggg atgtgccta cgggcacaa gcgcggcggt acctcaatat  
2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttgggtt  
2501 tgaacgcatt ttccctgaaa acgcgcttcc aaaacgaccg catcggaatc  
2551 ctgcttgacg gcggcgcgcg tttcgacg attaacgccg atttggcat  
2601 cggcaacgcc ttcggcgga atatggcaaa tacaccgctc ggcggcagga  
2651 ttacagcctc ccttcccgc ttggcgcat tgaagccctt tctgcccgcc  
2701 gccgcgcaaa acattaccgg cagcctgaat gcctccgcgc aaatcgcgcg  
2751 acgggtaggc tctccgtccg tcaatgccgc cgtcaacggt agcagcaact  
2801 acgggaaaat caacggcaat atcacgctc ggcaaaagcc ctccttcgat  
2851 accgcacctt tggcgggcag gctcaacctg accgttgccg atgccgaagc  
2901 attccgcaac ttcctaccgg tcggacaaac cgtcaaaggc agcctgaatg  
2951 ccgccgtaac cctcggcgcc agcatcgccg acccgcaact gggcggcagt  
3001 atcaacggcg acaagctcta ttaccgcaac caaacccaag gcatcatctt  
3051 ggacaacggc tcgctcggtt cgcatattgc aggcaggaaa tgggtaatcg  
3101 acagcctgaa attccggcac gaagggacg cggaactctc cggcacggtc  
3151 agcatggaac acagcgtgcc cgatgtcgat atcgcgcgcg tgttcgacaa  
3201 ataccgcatc ctgtcccgc ccaaccgcgc cctgacggtt tccggcaaca  
3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggtatgatt  
3301 aaaactgatc aggggctgtt cggttcgcaa aaatcctcga tgccgtccgt  
3351 cggcgacgat gtcgtcgtat tggcggaagt caagaaagag gcggcgcat  
3401 cgctccccgt caatatgaac ctgactttag acctcaatga cggcatccgc



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3451 ttctccggct acggcgcgga cgttaccata ggccgcaaac tgacctgac
3501 cgcgcaaccg ggccgaaatg tgcgtggggg gggcacggtc cgcgtcatca
3551 aagggcggtta caaagcatatc gggcaggatt tagacattac caaaggcaca
3601 gtctcccttg tcggcccgct caacgacccc aacctgaaca tccgcgccga
3651 acgcccgcctt tcccccgctg gtgcggggcgt ggaaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaanaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcggca gcagcggcga
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctggtg gatgatttgg gctttaccag caagcgcagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accggctgac ccgcgccata
4051 caggcgggtg cccgtatcgg cagccgttcg tcgggcggcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcga
4151 gaaacggcaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

```

g285.pep
1  MTDTPPTDPTD PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51  CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRSLHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLPA AVYLDRFETG KISMGTDFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTFW SSSSGSASVG LKPPFALDTA IYTKGGEFGE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGS LD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFCG RLDGSIGIGG TTASPKISWQ LGTGARTDGL SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRSR AFDPSTRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTGGGF GKKGDRNLNL ITAPDLRFSG FGLAGSLNVR
601 GHLSGDLDDG IRTFETDLTG TARNLHIGKA ADIRSLDFTL KGSPGTSRPM
651 RADIKGGRSL LSGGAADVDT AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKSIGI LDIGGAFNLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSLNL QHFSWDRKTG ISAKGGARGL HIAELHNFFK PPFENHLVLN
801 GDWDVAYGHN ARGYNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNITGSLN ASAQIGGRVG SPSVNAAVNG SSNYKINGN ITVQGSRSFD
951 TAPLGGRNLN TVADAEAFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAEISGTV
1051 SMENSVPDVT IGAVFDDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GGKLTTLTAQP GGNVRGVGTV RVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRLEFGSKK DSAGNGKKG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

```

m285.seq
1  ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACCGG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCCTGAT TTTGGCAGTA
151 TGTTCCTCG GCTGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAACCGTC
351 CGAACTGATG CGCCGACGCC TGCACATTAC CGAAATTTCC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCCTA AAGAAGAAGC CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAGC CTTTGACAAA CAAACCGCTC
551 ATCTGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCGCGCGA CACGCCGTGG AGCAGTTCGT CGGGGCGGCG
651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

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801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA  
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCTTC  
901 GTGCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC  
951 GTCGTTTTCa GACGGCATCG CGCTGGAAGG TTCGCTCGAT TTGGAAAAACA  
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGCTCCG TCAGGTTTAA  
1051 GGCGGCTTTG TCATCCGGCA GGACGGCACG GTGCATATCG GCAATACGTC  
1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTGCGGC AAAATCGACA  
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG  
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG  
1251 CATCGGTGGC ACGACCGCCT CGCCAAAAT CTCTTGCGAA CTCGGCATCG  
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC  
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG  
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA  
1451 AGCTGGACAT CCGTTCCGCG GCATTGACCC CTTGCGCGCAT CGATCCGCAA  
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC  
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG  
1601 CCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT  
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAACACAGA  
1701 CCGCGGCTTC GGCAAAAAG GCGACCGGCT TAACCTCAAT ATCACCGCAC  
1751 CCGATTTATC CCGTTTCGGT TTCGGAATCG CCGGGTCTTT AAATGTACGC  
1801 GGACACCTTT CCGGTGATTT GGACGGCGGC ATCCGAACCT TTGAAACCGA  
1851 CTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC  
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCCGATA  
1951 CGCGCCGACA TCAAAGGCAG CCGCTTTTCG CTGTGCGGCG GAGCGGCGGT  
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGCA  
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAAACGTT CAAATTCGAT  
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAAGGCAG  
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC  
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAAAT  
2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA  
2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG  
2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC  
2401 GGCGACTGGG ATGTGCGCTA CCGGCGCAAC GCGCGCGGCT ACCTCAATAT  
2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT  
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC  
2551 CTGCTTGACG GCGGCGCGCG TTTGCGGCGG ATTAACGCGG ATTTGGGCAT  
2601 CGCCAACGCC TTCGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA  
2651 TTACCGCCTC CTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC  
2701 GCGGCGCAA ACATTACCGG CAGCTGAAT GCCGCGCGC AAATCGGCGG  
2751 ACGGGTAGGC TCTCCGTCCG TCAATGCCCG CGTCAACGGC AGCAGCAACT  
2801 ACGGGAATA CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT  
2851 ACCGCGCCTT TGGGCGGCG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT  
2901 ATTCCGCAAC TTCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG  
2951 CCGCGTAAC CCTCGGCGGC AGCATCGCGC ATCCGCACTT GCGGCGCAGC  
3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT  
3051 GGACAACGGC TCGTGCCTT CGCATATCGC GGGCAGGAAA TGGGTAATCG  
3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CCGAACTCTC CGGTACGGTC  
3151 GGTATGGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTGCAAAA  
3201 ATACCGCATC CTGTCCCGCC CCAACCGCGC CCGTACGGTT TCCGGCAACA  
3251 CCGCCTGCG CTATTCGCGC CAAAAGGCA TATCCGTTAC CCGGATGATT  
3301 AAAACGGATC AGGGGCTGTT CCGTTCGCAA AAATCCTCGA TGCCGTCCGT  
3351 CGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC  
3401 CGCTCCCGCT CAATATGAAC CTGACTTTAG ACCTCAATGA CCGCATCCGC  
3451 TTCGCCGCT ACAGCGCGGA CGTTACCATA GCGGCGAAAC TGACCCGAC  
3501 CGCCCAATCG GCGGGAAGCG TACGGGGCGT GGGCACGGTC CGCGTCATCA  
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG  
3601 GTCTCCTTTG TCGGCCCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA  
3651 ACGCCGCTT TCCCCGTCG GTGCGGGCGT GGAATATTG GGCAGCCTCA  
3701 ACAGCCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAGAGAC  
3751 AAGCTCTCTT GGCTCATCCT CAACCGCGCC GGCAGCGGCA GCAGCGGCGA  
3801 CAATGCCGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAATCA  
3851 ACGACCGCAT CCGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC  
3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCGGAACAGG TGCTGACCGT  
3951 CCGCAAAACA CTGACCGGCA AACTCTACAT CCGCTACGAA TACAGCATCT  
4001 CCAGCGCGGA ACAGTCCGTC AAATGATTT ACCGGCTGAC CCGCGCCATA  
4051 CAGGCGGTTG CCGTATCGG CAGCCGTTTC TCGGCGGCG AGCTGACATA

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG  
4151 GAAACGCGAA AGGAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep  
1 MTDAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV  
51 CFLGWLAGE AGLRFLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET  
101 EGADLKISRF RFAWKPSSELM RRLSHITEIS AGDIAIVTKP TPPKEERPPL  
151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR  
201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG  
251 SLKDVRAELA IDGGNIRLSG KSVIHPPAES LDKTLEEVLV KGFNINPAAF  
301 VPSLPDAGLN FDLTAIPSF S DGIALEGSLD LENTKAGFAD RNGIPVRQVL  
351 GGFVIRQDGT VHIGNTSAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA  
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN  
451 GQRKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ  
501 LPAGNINGSI NLAGE LAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL  
551 PRAAVDLRLG RNIKTGGG KKKGDRNLN ITAPDLRFRG FGLAGSLNVR  
601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI  
651 RADIKSRLS LSGGAAVVDT ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD  
701 LDASGGINRE LTRWKGSGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN  
751 WQAMGGSNL QHFSWDKKTG ISAKGGAHL HIAELHNFFK PPFENLVLN  
801 GDWDVAYGRN ARGYLNISRQ SGDAVLPQQ ALGLNAFSLK TRFQNDRIGI  
851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFLPA  
901 AAQNITGSLN AAAQIGRVS SPSVNAAVNG SSNYGKINGN ITVQSRSEFD  
951 TAPLGGRNL TVADAVERN FLPVGGTVKG SLNAAVTLGG SIADPHLGGG  
1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV  
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI  
1101 KTDQGLFGSQ KSSMPVSGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR  
1151 FAGYGADVTI GKKLTTLAQ S GGSVRGVGT VIKGRYKAY QDLDITKGT  
1201 VSFVGPLNDP NLNIRAERR SPVGAGVEIL GSLNSPRITL TANEPMSKED  
1251 KLSWLILNRA GSGSSGDNA LSAAAGALLA QINDRIGLV DDLGFTSKRS  
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI  
1351 QAVARIGSRS SGGELTYTIR FDRFSGSKK DSAGNGKKG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

m285.pep	10	20	30	40	50	60
	MTDAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
g285	MTDTTPTDPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
m285.pep	70	80	90	100	110	120
	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRF RFAWKPSSELM					
g285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRF RFAWKPSSELM					
	70	80	90	100	110	120
m285.pep	130	140	150	160	170	180
	RRSLHITEISAGDIAIVTKPTPPKEERPPPLSLPDSIDLPAAVYLDRFETGKISMKGAFDK					
g285	RRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDSIDLPAAVYLDRFETGKISMKGTFDK					
	130	140	150	160	170	180
m285.pep	190	200	210	220	230	240
	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
g285	QTVYLERLNAAARYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
m285.pep	250	260	270	280	290	300
	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPPAESLDKTLEEVLVKGFNINPAAF					

g285	TIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIHPPFAESLDKLTLEEVLVKGFNINPSAF	250	260	270	280	290	300
m285.pep	VPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTKAGFADRNGIPVRQVLGGFVIRQDGT	310	320	330	340	350	360
g285	VPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTKAGFADRNGIPVRQVLGGFVIRQDGT	310	320	330	340	350	360
m285.pep	VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGINSVGAEDVLQTAFKGRLDGSIGIGG	370	380	390	400	410	420
g285	VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGINSVGAEDVLQTAFKGRLDGSIGIGG	370	380	390	400	410	420
m285.pep	TTASPKISWQLGIGTARTDGSIAIASDPANGQRKLVLDTVNIAAGGSLTAQGYLELFKD	430	440	450	460	470	480
g285	TTASPKISWQLGTGTARTDGSLPASDPANEQRKLVFDTVNISAGEGSLTAQGYLELFKD	430	440	450	460	470	480
m285.pep	RLCLKDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS	490	500	510	520	530	540
g285	RLCLKDIRSRAFDPSRIDPQFPAGNINGSIHLAGELAKEKFTGKMRFLPGTFNGVPIAGS	490	500	510	520	530	540
m285.pep	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRNLNLNITAPDLSRFGFGLAGSLNVR	550	560	570	580	590	600
g285	ADIVYESRHLPRAAVDLRLGRNIVKTDGGFGKKGDRNLNLNITAPDLSRFGFGLAGSLNVR	550	560	570	580	590	600
m285.pep	GHLSGDLGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGSPTSRPIRADIKGSRLS	610	620	630	640	650	660
g285	GHLSGDLGGIRTFFETDLSGTARNLHIGKAADIRSLDFTLKGSPTSRPMRADIKGGRLS	610	620	630	640	650	660
m285.pep	LSGGAAVVDATDMLDGTGVQHRIRTHAAMTLDGKPKFKDLDDASGGINRELTRWKGSGIGI	670	680	690	700	710	720
g285	LSGGAAVVDATAGLTLEGTGAQHRIRTHAAMTLDGKPKFKDLDDASGGINRELTRWKGSGIGI	670	680	690	700	710	720
m285.pep	LDIGGAFNCLKLQNRMTLEAGAERVAASAANWQAMGGSNLQHFSWDKKTGISAKGGAHGL	730	740	750	760	770	780
g285	LDIGGAFNCLKLQNRMTLEAGAEHVAASAANWQAMGGSNLQHFSWDRKKTGISAKGGARGL	730	740	750	760	770	780
m285.pep	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK	790	800	810	820	830	840
g285	HIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYLNISRQSGDAVLPGGQALGLNAFSLK	790	800	810	820	830	840
m285.pep	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA	850	860	870	880	890	900
g285	TRFQNDRIGILLDGGARFGRINADLGIGNAFGGNMANTPLGGRITASLPDLGALKPFLPA	850	860	870	880	890	900
m285.pep	AAQNITGSLNAAQIGGRVGSVNAAVNGSSNYGKINGNITVGOSRSFDTAPLGGRINNT	910	920	930	940	950	960

g285	AAQNITGSLN	SAQIGGRV	GS	SPSVNA	AVNGSS	NYGKING	NITV	GQSR	SFDTA	PLGGRL	NL
	910	920	930	940	950	960					
m285.pep	TVDAAEVFRN	FLPVGQT	VKGSLN	AAVTL	LGGS	ADPH	LGS	SING	DKLY	YRNQT	QGIILDNG
g285	TVDAAEAFRN	FLPVGQT	VKGSLN	AAVTL	LGGS	ADPH	LGS	SING	DKLY	YRNQT	QGIILDNG
	970	980	990	1000	1010	1020					
m285.pep	SLRSHIAGRK	WVIDSL	KFRHEG	TAEL	SGTV	GMEN	SGPD	VDIG	AVFD	KYRIL	SRPNRLTV
g285	SLRSHIAGRK	WVIDSL	KFRHEG	TAEL	SGTV	SMEN	SVPD	VDIG	AVFD	KYRIL	SRPNRLTV
	1030	1040	1050	1060	1070	1080					
m285.pep	SGNTRLRLY	SPQKG	ISVTG	MIKTD	QGLF	GS	SQKSS	MP	SVGDD	VVVL	GEVKKEAAAPLPVNMN
g285	SGNTRLRLY	SPQKG	ISVTG	MIKTD	QGLF	GS	SQKSS	MP	SVGDD	VVVL	GEVKKEAAASLPVNMN
	1090	1100	1110	1120	1130	1140					
m285.pep	LTLDLNDG	IRFAGY	GADVT	IGGK	LT	TAQ	SGGS	VRG	VGTV	RV	VIKGRYKAYGQDL
g285	LTLDLNDG	IRFAGY	GADVT	IGGK	LT	TAQ	PGGN	VRG	VGTV	RV	VIKGRYKAYGQDL
	1150	1160	1170	1180	1190	1200					
m285.pep	VSFVGP	LN	DPNL	NIRA	ERRL	SPV	GAG	VEIL	GL	SLNS	SPRITLTAN
g285	VSFVGP	LN	DPNL	NIRA	ERRL	SPV	GAG	VEIL	GL	SLNS	SPRITLTAN
	1210	1220	1230	1240	1250	1260					
m285.pep	GSGSSG	DN	AA	LSAA	AG	ALL	AGQ	IND	RIGL	VDDL	GF
g285	GSGSSG	DN	AA	LSAA	AG	ALL	AGQ	IND	RIGL	VDDL	GF
	1270	1280	1290	1300	1310	1320					
m285.pep	LTGKLY	IGYE	YS	ISSA	EQ	SV	KL	LY	RL	TRAI	QAVARIGSRSS
g285	LTGKLY	IGYE	YS	ISSA	EQ	SV	KL	LY	RL	TRAI	QAVARIGSRSS
	1330	1340	1350	1360	1370	1380					
m285.pep	DSAGN	GK	GK	GK							
g285	DSAGN	GK	GK	GK							

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a285.seq
1  ATGACCGATA  CCGCACCGAC  AGATACCGAT  CCGACCGAAA  ACGGCACGCG
51  CAAAATGCGC  TCTGAACACC  GCCCTACCCC  GCCGCGAAAA  AAACGCCGCC
101 CGTGCTGTA  GCTGTCGGCG  GCACTGCTGT  CTGTCTGTAT  TTTGGCAGTA
151 TGTTCCTCG  GCTGGCTCGC  CGGCACGGAA  GCGGGTTTGC  GCTTCGGGCT
201 GTACCAATC  CCGTCTTGTC  TCGGGCGTAA  CATTTCTCTC  CAAAACCTCA
251 AAGGCAGCCT  GCTCAGCGGC  TTCAGCGGCG  ACAACTGGTC  GTAGAAATCC
301 GAGGGGCGAC  ACCTTAAAT  CAGCCGCTTC  CGCTTCGCGT  GGAACCGGTC
351 CGAAGCTGAT  CGCCGCGAGC  TGCACTATAC  CGAAATTTCC  GCCGGCGACA
401 TCGCCATCGT  TACCAAAACG  ACTCGCCTA  AAGAAGAACG  CCCGCGCTC
451 AGCCTTCCC  ACAGCATAGA  CCTGCCTGCC  GCGCTCTATC  TCGACCGGTT
501 CGAGACGGCG  AAAATCAGCA  TGGGCAAAGT  CTTTGACAAA  CAAACCGTCT
551 ATCTCGAAGC  GCTGGATGCT  TCATACCGTT  ACGACCGCAA  AGGACACCGC
601 CTCGACCTGA  AGGCTGCCGA  CACCGCGTGG  AGCAGTTCTG  CGGGGTGAG

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651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA  
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC  
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG  
801 CCTCTCGGGA AAATCCGTCA TCCACCGTT TGCCGAATCA TTGGATAAAA  
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGCCTTC  
901 GTGCCTTCCC TGCCCCGATG CGGGCTGAAT TTCGACCTGA CCGCCATCCC  
951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGAAAAACA  
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCCG TCAGGTTTTA  
1051 GGCAGCTTTG TCATCCGGCA GGACGGCAGG GTGCATATCG GCAATACGTC  
1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTGCGGC AAAATCGACA  
1151 CCGAAAAAGA CATCCTCGAT TTAATATAG GCATCAACTC CGTCGGCGCG  
1201 GAAGACGTAC TGCAAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG  
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGGCAA CTCGGCATCG  
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCCACAAAC  
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG  
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA  
1451 AGCTGGACAT CCGTTCCTCG GCATTGACG CTTGCGGCAT CGATCCGCAA  
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC  
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG  
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT  
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAACACAGA  
1701 CGGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCGCAC  
1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC  
1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA  
1851 CCTTTCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC  
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCGATA  
1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTGCGGCG GAGCGGAGGT  
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGBA  
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT  
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGA CTTACCCGAT GGAAGGCAG  
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC  
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAT  
2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA  
2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG  
2351 AGTTGCACAA TTTCTTCAAA CCGCCTTCG AACACAATCT GGTTTTAAAC  
2401 GCGGACTGGG ATGTGCGCTA CCGGCGAAAC GCGCGCGGCT ACCTCAATAT  
2451 CAGCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT  
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC  
2551 CTGCTTGACG GCGGCGCGCG TTTCGGGCGG ATTAACGCCG ATTTGGACAT  
2601 CCGCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA  
2651 TTACCGCCTC CTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC  
2701 GCCGCGCAA ACATTACCGG CAGCCTGAAT GCCCGCGCGC AAATCGGCGG  
2751 ACGGGTCGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT  
2801 ACGGAAAAAT CAACGCGAAC ATCACCCTCG GGCAAGCCG CTCTTTCGAT  
2851 ACCGCGCCTT TGGGCGGCAG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT  
2901 ATTCCGCAAC TTCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG  
2951 CCGCGGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGCAGC  
3001 ATCAACGGCG ACAAACTCTA TTACCGCAAC CAAACCCAAG GCATCATCTT  
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG  
3101 ACAGCCTGAA ATTCGGGCAC GAAGGGACGG CGGAACCTC CGGTACGGTC  
3151 GGTATGGAAC ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTCCGACAA  
3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA  
3251 CCCGCCTGCG CTATTGCGCG CAAAAGGCA TATCCGTTAC CGGGATGATT  
3301 AAAACGGATC AGGGGCTGTT CGGTTGCGAA AAATCCTCGA TGCCGTCCGT  
3351 CCGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAGAG GCGGCGGCAC  
3401 CGCTCCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCGC  
3451 TTCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCCTGAC  
3501 CGCCCAATCG GCGGGAAGCG TCGGCGGCGT GGGCAGGTC CGCGTCATCA  
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG  
3601 GTCTCCTTTG TCGGCCCGCT CAACGACCCC AACCTCAACA TCCCGGCCGA  
3651 ACGCGCCTT TCCCCGTCTG GTGCGGGCGT GGAAATATTG GGCAGCCTCA  
3701 ACAGTCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAAAAGAC  
3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGGCGA  
3801 CAATGCCGCC CTGTCCGCG CCGCGGCGCG GCTGCTTGCC GGGCAATCA  
3851 ACGACCGCAT CGGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC  
3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT

655

3951 CGGCAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT  
 4001 CCAGCGCGGA ACAGTCCGTC AACTGATTT ACCGGCTGAC CCGCGCCATA  
 4051 CAGGCGGTG CCGTATCGG CAGCCGTTCG TCGGCGGCG AGCTGACATA  
 4101 CACCATACGT TCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG  
 4151 GAAACAGCAA AGGAAATAA

This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

a285.pep  
 1 MTDAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV  
 51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET  
 101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPL  
 151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR  
 201 LDLKAAATPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG  
 251 SLKDVRLELA IDGGNIRLSG KSVIHPPAES LDKTLEEVLV KGFNINPSAF  
 301 VPSLPDAGLN FDLTAIPSF S DGIALEGLSD LENTKAGFAD RNGIPVRQVL  
 351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA  
 401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN  
 451 GQRKLVLDTV NIAAGQGS LT AQYLELEFKD RLLKLDIRSR AFDPSRIDPQ  
 501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL  
 551 PRAAVDLRLG RNIKTDDGGF GKKGDRLNLN ITAPDLSRFG FGLAGSLNVR  
 601 GHLSGDLGG IRTFETDL S AARNLHIGKA ADIRSLDFTL KGSPTDSRPI  
 651 RADIKGSRLS LSGGAEVVD T ADLMLDGTG V QHRIRTHAAM TLDGKPFKFD  
 701 LDASGGINRL LTRWKSGSIGI LDIGGAFLNK LQNRMTLEAG AERVAASAA  
 751 WQAMGGSNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFEHNLVLN  
 801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFLSK TRFQNDRIGI  
 851 LLDGGAREFR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFLPA  
 901 AAQNITGSLN AAAQIGGRV S SPSVNAAVNG SSNYGKINGN ITVGQSRSFD  
 951 TAPLGGRLNL TVADA EVFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGGS  
 1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV  
 1051 GMENSGPDVD IGAVFDKYRI LSRPNRRITV SGNTRLRYSP QKGISVTGMI  
 1101 KTDQGLFGSQ KSSMPVSGDD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR  
 1151 FAGYGADVTI GGLTLTAQS GGSVRGVGT V RVIKGRYKAY GQDLDTIKGT  
 1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSEKD  
 1251 KLSWLILNRA GSGSSGDNA LLSAAAGALLA GQINDRIGLV DDLGFTSKRS  
 1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISSAEQSV KLIYRLTRAI  
 1351 QAVARIGSRS SGEELTYTIR FDRFSGSDKK DSAGNSKKG\*

m285/a285 99.4% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
a285	MTDAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	10	20	30	40	50	60
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRF RFAWKPSSELM					
a285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRF RFAWKPSSELM					
	70	80	90	100	110	120
m285.pep	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDRFETGKISMKGAFDK					
a285	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDRFETGKISMKGAFDK					
	130	140	150	160	170	180
m285.pep	QTVYLERLDASYRYDRKGHRDLKAAATPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
a285	QTVYLERLDASYRYDRKGHRDLKAAATPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK					
	190	200	210	220	230	240
m285.pep	TIHSTARLSGSLKDVRLELAIDGGNIRLSGKSVIHPPAESLDKTLEEVLVKGFNINPAAF					
a285	TIHSTARLSGSLKDVRLELAIDGGNIRLSGKSVIHPPAESLDKTLEEVLVKGFNINPAAF					
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRLELAIDGGNIRLSGKSVIHPPAESLDKTLEEVLVKGFNINPAAF					
a285	TIHSTARLSGSLKDVRLELAIDGGNIRLSGKSVIHPPAESLDKTLEEVLVKGFNINPAAF					

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a285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHFAESLDKTL EEVLVKGFNINPSAF
	250 260 270 280 290 300
	310 320 330 340 350 360
m285.pep	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT
	:     :     :     :     :
a285	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGSFVIRQDGT
	310 320 330 340 350 360
	370 380 390 400 410 420
m285.pep	VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
	:     :     :     :     :
a285	VHIGNTSVALLGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
	370 380 390 400 410 420
	430 440 450 460 470 480
m285.pep	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKVLDTVNIAAGQGS LTAQGYLELFKD
	:     :     :     :     :
a285	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKVLDTVNIAAGQGS LTAQGYLELFKD
	430 440 450 460 470 480
	490 500 510 520 530 540
m285.pep	RLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
	:     :     :     :     :
a285	RLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
	490 500 510 520 530 540
	550 560 570 580 590 600
m285.pep	ADIVYESRHLPRAAVDLRLGRNIIKT DGGFGKKGDRNLNITAPDLSRF GFLAGSLNVR
	:     :     :     :     :
a285	ADIVYESRHLPRAAVDLRLGRNIIKT DGGFGKKGDRNLNITAPDLSRF GFLAGSLNVR
	550 560 570 580 590 600
	610 620 630 640 650 660
m285.pep	GHLSGDL DGGIRT FETDL SGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
	:     :     :     :     :
a285	GHLSGDL DGGIRT FETDL SGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
	610 620 630 640 650 660
	670 680 690 700 710 720
m285.pep	LSGGA VVD TADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSIGI
	:     :     :     :     :
a285	LSGGA EVVD TADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSIGI
	670 680 690 700 710 720
	730 740 750 760 770 780
m285.pep	LDIGGA FNKLQNRMTLEAGAERVAASAANWQAMGGS LNLQHFSWDKKTGISAKGGAHGL
	:     :     :     :     :
a285	LDIGGA FNKLQNRMTLEAGAERVAASAANWQAMGGS LNLQHFSWDKKTGISAKGGAHGL
	730 740 750 760 770 780
	790 800 810 820 830 840
m285.pep	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLP GGQALGLNAFSLK
	:     :     :     :     :
a285	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLP GGQALGLNAFSLK
	790 800 810 820 830 840
	850 860 870 880 890 900
m285.pep	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
	:     :     :     :     :
a285	TRFQNDRIGILLDGGARFGRINADLDIGNAFGGNMANAPLGGRITASLPDLGTLKPFLPA
	850 860 870 880 890 900
	910 920 930 940 950 960
m285.pep	AAQNITGSLNAAAQIGGRVGS PSVNAAVNGSSNYKINGNITVGQSR SFDTAPLGGRNLN
	:     :     :     :     :



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a285      AAQNITGSLNAAQIGGRVGSPSVNAAVNGSSNYGKINGNITVQSRSFDTAPLGGRNLN
           910      920      930      940      950      960

           970      980      990      1000     1010     1020
m285.pep  TVADAEVFRNFLPVGQTVKGSLSNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG
           |||||
a285      TVADAEVFRNFLPVGQTVKGSLSNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG
           970      980      990      1000     1010     1020

           1030     1040     1050     1060     1070     1080
m285.pep  SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRIILSRPNRRLTV
           |||||
a285      SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRIILSRPNRRLTV
           1030     1040     1050     1060     1070     1080

           1090     1100     1110     1120     1130     1140
m285.pep  SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
           |||||
a285      SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
           1090     1100     1110     1120     1130     1140

           1150     1160     1170     1180     1190     1200
m285.pep  LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLITKGT
           |||||
a285      LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLITKGT
           1150     1160     1170     1180     1190     1200

           1210     1220     1230     1240     1250     1260
m285.pep  VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLIILNRA
           |||||
a285      VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLIILNRA
           1210     1220     1230     1240     1250     1260

           1270     1280     1290     1300     1310     1320
m285.pep  GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
           |||||
a285      GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
           1270     1280     1290     1300     1310     1320

           1330     1340     1350     1360     1370     1380
m285.pep  LTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
           |||||
a285      LTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
           1330     1340     1350     1360     1370     1380

           1390
m285.pep  DSAGNGKGKX
           ||||:||||
a285      DSAGNSKGKX
           1390

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

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1   CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAAACATTT CCTCCAAAA CCTCAAAGGC
151 AACTGCTCG ACGGCTTCGA CGGCACAAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCCGCG CAGCCTGCAC ATCACCAGCA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAGGCCT
351 GCCCGACAGC ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAACAAAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGAGCAG TTCGTCGGGG TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC  
601 GGATTCGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT  
651 GAAGGATGTG CGCGCCGAAC TGACGATCGA CGCGGCAAT ATCCGCCTCT  
701 CGGGAATATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG  
751 GAAGAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC  
801 TTCCCTGCCC GATGCCGGGC TGAATTTGCA CCTGACCGCC ATCCCGTCGT  
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAAA  
901 GCGCGGTTTG CCGACCGCAA CGGCATCCCC GTCCGTACGG TTTTGGGCGG  
951 CTTTGTATC CGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCGG  
1001 CCTTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA  
1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTGC GCGCGGAAGA  
1101 CGTGCTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG  
1151 GCGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CACCGGCACG  
1201 GCACGCACGG ACGGCAGCCT cgcCATCGCA AGCGACCCCG CAAACGAACA  
1251 GCGGAAACTG GTGTTGACA CCGTCAACAT CTCGCCCGGG GAAGGCAGCC  
1301 TGACCCGCGA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG  
1351 GACATCCGTT CCGCGCATT CGACCTTCG CGCATCGATC CGCAATTTCC  
1401 GGCAGGCGat atCAACGGTT CGATTCTCT TGCCGGTGAA CTGGCAAAAG  
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTCG CCGGTACGTT CAACGGCGTG  
1501 CCGATTGCCC GCAGCGCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG  
1551 CGCCGCGCTG GATTTGCGGT TGGGGCGGAA CATCGTCAAA ACAGACGGCG  
1601 GCTTCCGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGACCCCGAT  
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA  
1701 CCTTTCGGCG GATTTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT  
1751 CGGCAACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCCGTTTCG  
1801 CTCGATTTTA CCCTCAAAGG CTCACCCGCG ACAAGCGGCC CGATGCGCGC  
1851 CGATATCAAG GCGGCGCGCC TTTCCCTGTC GGGCGGCGCG GCGGTTGTCG  
1901 ATACCGCCGG CCTGACGCTG GAAGGTACGG GCGCGCAGCA CCGCATCCGC  
1951 ACACACGCGC CCATGACGCT GGACGGCAAA CCGTTCAAAC TCGATTTGGA  
2001 CGCTTCAGGC GGCATCAACA GGAAGTTTAC CCGATGGAAG GGCAGCATCG  
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG  
2101 ACGCTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGGCG CAAATTGGCA  
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTTCTTGG GACAGGAAAA  
2201 CCGGCATATC GGCAAAAGGC GCGGCACGCG GCCTGCACAT CGCCGAGTTG  
2251 CACAATTTCT TCAAACCGCC CTTGAAACAC AATCTGTTTT TAAACGCGCA  
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CGGCTACCTC AATATCAGCC  
2351 GGCAAAAGCG CGATGCGGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC  
2401 GCATTTTCTC TGAACACGCG CTTTCAAAC GACCGCATCG GAATCTGTCT  
2451 TGACGGCGGC GCGCGTTTCG GACGGATTAA CGCCGATTTC GGCATCGGCA  
2501 ACGCCTTCGG CCGCAATATG GCAAATACAC CGCTCGGCGG CAGGATTACA  
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCCGCGCG  
2601 GCAAAACATT ACCGGCAGCC TGAATGCCTC CGCGCAAAAT GCGGGACGGG  
2651 TAGGCTCTCC GTCCGTCAAT GCCGCGGTCA ACGGTAGCAG CAACTACGGG  
2701 AAAATCAACG GCAATATCAC CGTCGGGCAA AGCCGCTCCT TCATACCCG  
2751 ACCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTC  
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC  
2851 GTAACCTTCG GCGGCAGCAT CGCCGACCCG CACTTGGGCG GCAGTATCAA  
2901 CGGCGACAAG CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA  
2951 ACGGCTCGCT GCGTTCGCAT ATTGCAGGCA GGAATGGGT AATCGACAGC  
3001 CTGAAATTC GGCACGAAGG GACGGCGGAA CTCTCCGGCA CGGTACGATC  
3051 GGAAAACAGC GTGCCGATG TCGATATCGG GCGGTTGTTT GACAAATACC  
3101 GCATCCTGTC CCGCCCAAC CCGCGCTGTA CGGTTTCCGG CAACACCCGC  
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCAGTA TGATTAACAA  
3201 TGATCAGGGG CTGTTTCGTT CGCAAAAATC CTCGATGCCG TCCGTGCGCG  
3251 AGATGTCGT CGTATTGGGC GAAGTCAAGA AAGAGGCGGC GGCATCGCTC  
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTCTCT  
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCGC  
3401 AACCAGGCGG AATGTGCGT GGGGTGGGCA CGGTCCGCGT CATCAAAGGG  
3451 CGTTACAAAG CATACGGGCA GGATTTAGAC ATTACCAAAG GCACAGTCTC  
3501 CTTTGTCCGG CCGCTCAACG ACCCAACCT GAACATCCCG GCCGAACGCC  
3551 GCCTTTCCCC CGTCGGTGGC GCGGTGGAAT TATTGGGCGC CCTCAACAGC  
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT  
3651 CTCCTGGCTC ATCCTCAACC GTGCCGCGAG CGGCAGCAGC GCGGACAATG  
3701 CGGCCCTGTC CGCAGCCGCA GCGCGCTGCT TTGCCGGGCA AATCAACGAC  
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA  
3801 CGCGCAAAAC GGCGAATCA ACCCGCCGGA ACAGGTGCTG ACCGTGCGCA  
3851 AACAACGTAC CGGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC  
3901 GCGGAACAGT CCGTCAAACCT GATTTACCGG CTGACCCGCG CCATACAGGC  
3951 GGTGCGCCGT ATCGGCAGCC GTTCGTGCGG CCGCGAGCTG ACATACACCA  
4001 TACGTTTCGA CCGCTCTTTC GGTTCGGACA AAAAAGACTC CGCAGGAAAC  
4051 GGCAAGGGA AATAA

This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:  
g285-1.pep

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1  LKLSAALLSV LILAVCFGLW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAYYLD RFETGKISMV KTFDKQTVYL
151 ERLNAAARYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFINI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGTGT
401 ARTDGSIAIA SDPANEQRKL VFDTVNISAG EGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAGL LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVGRHLSG DLDGGIIRTFE TDLSTGARNL HIGKAADIRS
601 LDFTLKGSPG TSRPMRADIK GGRSLSSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAEHVA ASAANWQAMG GSLNLQHFSW DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISROSGDAV LPGGQALGLN
801 AFSLKRFRQF DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAAQNI TGSLSNAAQI GGRVGSFSPV AAVNGSSNYG
901 KINGNITVGQ SRSFDTAPLG GRNLNLTADA EAFRNFLPVG QTVKGSLNAA
951 VTLGGSIAADP HLGGSINGDK LYRNRQTQGI ILDNGLSLRSH IAGRKKWIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAASL
1101 PVNMNLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR GVGTVRVIK
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLF GSDKKDSAGN
1351 GK GK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCCTG TTGGTTCGGC GTAAACATTT CCTCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCAGCAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CGCTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCGCG CGACATCGCC
301 ATCGTATACCA AACCGACTCC GCCTAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCGCT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAAAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG GCGGCCCTCGG
551 TCGGGCTTGA AAAACCGTTT GCCCTCGATA CGCCATTTA CACCAAAGGC
601 GGAATCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAAAAAT CGTCATCCAC CCGTTTGGCG AATCATTTGA TAAAAATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGCGCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGAC TGAATTCGA CCTGACCGCC ATCCCGTCGT
851 TTTACAGACG CATCGCGCTG GAAGGTTTCG TCGATTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGCGCG
951 CTTTGTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCCTGTCTCG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAAATCG GTGCTCGACA CCGTCAACAT CGCCGCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGCGGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GCAAGTCCGA CATTGTTTAC GAGTCCCGCC ACCTTCGCGG
1551 TGCCGCGGTC GATTTCGGGC TGGGGCGGAA CATTATTAAC ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCAGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGGT GATTTCGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCCGTTCC
1801 CTCGATTTCG CGCTCAAAGG TTCGCCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTGCTGTGC GGGCGGAGCG GCGGTTGTCG
1901 ATACCGCCGA CCTGATGCTG GACGGCACGG GCGTGAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAATTTGGCA

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAA
2201 CCGGCATATC GGCAAAAGGC GGCACACACG GTCTGCATAT CGCCGAGTTG
2251 CACAAATTCT TCAAACCGCC CTTGGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GCAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCCCGGC GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGA AAAACGCG CTTTCAAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GCGCGATTAA CGCCGATTGG GGCATCGCCA
2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAATC GCGCGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCCCTC GCGGCAGCAT CGCCGATCCG CACTTGGGCG CGACGATCAA
2901 CGGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT GCGTTCGCAT ATCGCGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTC GGCACGAAGG GACGGCGGAA CTCTCCGTA CGGTCCGTAT
3051 GGAAAACAGC GGACCCGATG TCGATATCGG CGCGGTGTT CACAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCTGA CGGTTTCCGG CAACACCGC
3151 CTGCGCTATT CGCCGAAAA AGGCATATCC GTTACCGGGA TGATTA AAC
3201 GGATCAGGG CTGTTCCGTT CGCAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGG GAAGTCAAAA AAGAGGCGG GGCACCGCTC
3301 CCCGTCATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTACGG GCGGTGGGCA CGGTCCGCGT CATCAAAGG
3451 CGTTATAAGG CATACGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGGC CCGCTCAACG ATCCCAACCT CAACATCCCG GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGG GCGGTGAAA TATTGGGCG CCTCAACAGC
3601 CCGCGCATTG CGCTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCTTGGCTC ATCTCAACG GCGCCGGCAG CGGCAGCAGC GGCAGCAATG
3701 CGCCCTGTC TGCAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGCAACTCA ACCCGCCGGA ACAGGTGCTG ACCGTCGGCA
3851 AACCACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTTACCG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 GGCAAGGAA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pep

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1 LKLSAALLSV LILAVCF LGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGF DGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTFWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAI DGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKG FNI NPAAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGT VHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGS LAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHL SG DL DGGIRTFE TDL SGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA AVVD TADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASAANWQAMG GSNLQHFWS DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGS LNAAQI GGRVGS PSVN AAVNGSSNYG
901 KINGNITVQG SRSFDTAPLG GRLNLT VADA EVFRNLPVG QTVKGS LNAA
951 VTLGGS IADP HLGGSINGDK LYRNTQGI ILDNGLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVMNMLTLDL NDGIRFAGY ADVTIGGKLT LTAQSGGSVR GVGTVRVIK
1151 RYKAYQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSA A GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 GRGK*

```

g285-1/m285-1 96.5% identity in 1354 aa overlap

10 20 30 40 50 60

g285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFLGYQIPSWFGVNISSQNKLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFLGYQIPSWFGVNISSQNKLKGTLLDGFDDGN					
		10	20	30	40	50
		70	80	90	100	110
g285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPSLPDS					
		70	80	90	100	110
		130	140	150	160	170
g285-1.pep	IDLPAAYVLDRFETGKISMGKTFDKQTVYLERLNAAYRYDRKGHRLLDLKAADTPWSSSSG					
m285-1	IDLPAAYVLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRLLDLKAADTPWSSSSG					
		130	140	150	160	170
		190	200	210	220	230
g285-1.pep	SASVGLKKPFALDTAIYTKGGFEGETIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIH					
		190	200	210	220	230
		250	260	270	280	290
g285-1.pep	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTK					
m285-1	PFAESLDKTL EEVLVKGFNINPAAFVPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTK					
		250	260	270	280	290
		310	320	330	340	350
g285-1.pep	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAALLGRGGIRLSGKIDTEKDILDLNIGI					
m285-1	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAALLGRGGIRLSGKIDTEKDILDLNIGI					
		310	320	330	340	350
		370	380	390	400	410
g285-1.pep	NSVGAEDVLQTAFKGRLDGSGIGGTTASPKISWQLGTGTARTDGS LAIASDPANEQRKL					
m285-1	NSVGAEDVLQTAFKGRLDGSGIGGTTASPKISWQLGIGTARTDGS LAIASDPANGQRKL					
		370	380	390	400	410
		430	440	450	460	470
g285-1.pep	VFDTVNISAGEGSLTAQGYLELFKDRLLKLDIRSRADFPSRIDPQFPAGDINGSIHLAGE					
m285-1	VLDTVNIAAGQGS LTAQGYLELFKDRLLKLDIRSRADFPSRIDPQLPAGNINGSINLAGE					
		430	440	450	460	470
		490	500	510	520	530
g285-1.pep	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIVKTDGGFGKKGD					
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIVKTDGGFGKKGD					
		490	500	510	520	530
		550	560	570	580	590
g285-1.pep	RLNLNITAPDLSRFGFLAGSLNVRGHLSGDLGGIRT FETDLSGTARNLHIGKAADIRS					
m285-1	RLNLNITAPDLSRFGFLAGSLNVRGHLSGDLGGIRT FETDLSGAARNLHIGKAADIRS					
		550	560	570	580	590
		610	620	630	640	650
g285-1.pep	LDFTLKGSPGTSRPMRADIKGGRLSLGGAAVVDTAGLTLEGTGAQHRIRTHAAMTLDGK					
m285-1	LDFTLKGSPDTSRPIRADIKGSRLSLGGAAVVDADLMLDGTGVQHRIRTHAAMTLDGK					
		610	620	630	640	650
		670	680	690	700	710
g285-1.pep	PFKLDLDASGGINRELTRWKGSIGILDIGGAFNLKLQNRMTLEAGAEHVAA SAANWQAMG					
m285-1	PFKFDLDASGGINRELTRWKGSIGILDIGGAFNLKLQNRMTLEAGAEVAA SAANWQAMG					
		670	680	690	700	710
		730	740	750	760	770
g285-1.pep	GSLNLQHFSWDRKGTGISAKGGAGRLHIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYL					
m285-1	GSLNLQHFSWDKGTGISAKGGAGRLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL					

662

	730	740	750	760	770	780
	790	800	810	820	830	840
g285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGRITASLPDLGALKPFLPAAAQNTGSLNAAQIGGRVGSPSVNAAVNGSSNYG					
m285-1	ANAPLGGRITASLPDLGALKPFLPAAAQNTGSLNAAAQIGGRVGSPSVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVQSRSFDTAPLGGRLNLTVADAEAFRNFPLVPGQTVKGSLNAAVTLGGSIADP					
m285-1	KINGNITVQSRSFDTAPLGGRLNLTVADAEVFRNFPLVPGQTVKGSLNAAVTLGGSIADP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVGIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVGIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVTIGGKLTTLTAQPGGNVR					
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRFLFGSDKKDSAGNGKGK					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

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1  CTGAAGCTGT CGCGGCACT GCTGTCTGTT CTGATTTTGG CAGTATGTTT
51  CCTCGCGCTGG CTCGCCGCA CGAAGCGGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATT CCTCCCAAAA CCTCAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATCGCGCG CAGCCTGCAC ATTACCGAAA TTTCGCGCGG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCCAGACG ATAGACCTGC CTGCGCCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGACGCTT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCTT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTTGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCGG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCTA CCGTACCGCC ATCCGCTCGT
851 TTTGAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTTGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTACAG TTTTAGGCAG
951 CTTTGTCTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCTG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAACCGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAG
1451 AGAAATTAC AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG CGAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGCTC GATTTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCCGGC GATTTGAGCG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCGA CATCCGTTCTG
1801 CTCGATTTCG CGCTCAAAGG TTCGCCGAC ACAAGCCGCC CGATACGCGC
1851 CGCATCAAAA GGCAGCCGCC TTTGCTGTC GGGCGGAGCG GAGGTTGTCTG
1901 ATACCGCGCA CCGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGATGGCAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCCTGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAATTTGGCA
2151 GGCATAGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTTGG GATAAAAAAA
2201 CCGCATATC GGCAAAAGGC GGCACACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAAACGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAACACGCG CTTTCAAAC GACCGTATCG GAATCCTGCT
2451 TGACGGGCGG GCGGTTTTCG GCGGATTAA CGCCGATTG GACATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAATGACG CGCTCGGCGG CAGGATTACC
2551 GCGTCCCTTC CCGACTTGGG CACATTGAAG CCCTTCTCTG CCGCGCGCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAATC GCGGACGCGG
2651 TCGGCTCTCC GTCCGTCAAT GCCGCCGTC ACGGCAGCAG CAATACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTT ACCGGTCCGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTTCG GCGGAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTCCGAT ATCGCGGCGA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTCGGTAT
3051 GGAAAACAGC GGACCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCCTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAC
3201 GGATCAGGGG CTGTTCCGTT CGCAAAAATC CTCGATGCGG TCCGTGCGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGCGCG AAGCGTGGCG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGC CCGCTCAACG ACCCAAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCCGTGCG GCGGTGGAAA TATTGGGCGG CCTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCTTGCTC ATCTCAACC GCGCCGCGAG TGGCAGCAGC GGCACAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGTC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAACC GCGGAATCA ACCCCGCCGA ACAGGTGCTG ACCGTGCGCA
3851 AACCACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTGCGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCTG CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 AGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

## a285-1.pep

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1  LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGDN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGTTASP KISWQLGIGT
401 ARTDGSIAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLGAARNL HIGKAADIRS
601 LDFTLKGSPP TSRRIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIIGLDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWQAMG GSLNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNEFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPPGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGMM ANAPLGGGRIT
851 ASLPDLGTLK PFLPAAQNI TGSLNAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGG SRSFDTAPLG GRLNLTVADA EVFRNPLPVG QTVKGS LNAA
951 VTLLGGSIAPI HLGGSSINGDK LYRNRQTQGI ILDNGSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDDVVVLG EVKKEA AAPL
1101 PVMNMLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSSVR GVGTVRVIKG
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAG GALLAQIIND
1251 RIGLVDDLGF TSKRSRQAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 SKGK*

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a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
	70	80	90	100	110	120
	130	140	150	160	170	180
a285-1.pep	IDLPAAYLDRFETGKISMKGAFDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG					
m285-1	IDLPAAYLDRFETGKISMKGAFDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a285-1.pep	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	190	200	210	220	230	240
	250	260	270	280	290	300
a285-1.pep	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTK					
m285-1	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDLNIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDLNIGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
a285-1.pep	NSVGAEDVLQTAFKGRLDGSIGIGTTASPKISWQLGIGTARTDGS LAIASDPANGQRKL					
m285-1	NSVGAEDVLQTAFKGRLDGSIGIGTTASPKISWQLGIGTARTDGS LAIASDPANGQRKL					
	370	380	390	400	410	420
	430	440	450	460	470	480



665

a285-1.pep	VLDTVNIAAGQGS	LTAAQGYLE	FKDRLLK	LDIRSF	ADPSRIDP	QLPAGNINGS	INLAGE
m285-1	VLDTVNIAAGQGS	LTAAQGYLE	FKDRLLK	LDIRSF	ADPSRIDP	QLPAGNINGS	INLAGE
	430	440	450	460	470	480	
a285-1.pep	490	500	510	520	530	540	
a285-1.pep	LAKEKFTG	KMRFLPG	TFGVPI	AGSADIV	YESRHL	PRAAVDL	RRLGRNIIKT
m285-1	LAKEKFTG	KMRFLPG	TFGVPI	AGSADIV	YESRHL	PRAAVDL	RRLGRNIIKT
	490	500	510	520	530	540	
a285-1.pep	550	560	570	580	590	600	
a285-1.pep	RLNLNIT	APDLSR	FGFGL	AGSLNVR	GHLSGD	LDGGIRT	FETDLSGA
m285-1	RLNLNIT	APDLSR	FGFGL	AGSLNVR	GHLSGD	LDGGIRT	FETDLSGA
	550	560	570	580	590	600	
a285-1.pep	610	620	630	640	650	660	
a285-1.pep	LDFTLK	GSPDTS	RP	IRADIK	GSRLS	LSGGAE	VVDATDML
m285-1	LDFTLK	GSPDTS	RP	IRADIK	GSRLS	LSGGAE	VVDATDML
	610	620	630	640	650	660	
a285-1.pep	670	680	690	700	710	720	
a285-1.pep	PFKFDL	DASGGI	NRELTR	WKGSIG	ILDIGG	AFNLKL	QNRMTLE
m285-1	PFKFDL	DASGGI	NRELTR	WKGSIG	ILDIGG	AFNLKL	QNRMTLE
	670	680	690	700	710	720	
a285-1.pep	730	740	750	760	770	780	
a285-1.pep	GSLNLQ	HFSWDK	KTGIS	AKGGAH	GLHIAE	LHNFFK	PPFEHNL
m285-1	GSLNLQ	HFSWDK	KTGIS	AKGGAH	GLHIAE	LHNFFK	PPFEHNL
	730	740	750	760	770	780	
a285-1.pep	790	800	810	820	830	840	
a285-1.pep	NISRQSG	DAVLP	GGQAL	GLNAF	SLKTRF	QNDRI	GILLDGG
m285-1	NISRQSG	DAVLP	GGQAL	GLNAF	SLKTRF	QNDRI	GILLDGG
	790	800	810	820	830	840	
a285-1.pep	850	860	870	880	890	900	
a285-1.pep	ANAPL	GGRIT	ASLPD	LGTLP	KPFLP	AAQNI	TGSLNAA
m285-1	ANAPL	GGRIT	ASLPD	LGTLP	KPFLP	AAQNI	TGSLNAA
	850	860	870	880	890	900	
a285-1.pep	910	920	930	940	950	960	
a285-1.pep	KINGNIT	VGQSR	SFDTA	PLGGRL	NLTVA	DAEVR	NFLPVGQ
m285-1	KINGNIT	VGQSR	SFDTA	PLGGRL	NLTVA	DAEVR	NFLPVGQ
	910	920	930	940	950	960	
a285-1.pep	970	980	990	1000	1010	1020	
a285-1.pep	HLGGS	INGDK	LYYRN	QTQGI	ILDNG	SLRSHI	AGRKWID
m285-1	HLGGS	INGDK	LYYRN	QTQGI	ILDNG	SLRSHI	AGRKWID
	970	980	990	1000	1010	1020	
a285-1.pep	1030	1040	1050	1060	1070	1080	
a285-1.pep	GPDVD	IGAVF	DKYR	ILSRP	NRRLT	VSGNTR	LRYSPO
m285-1	GPDVD	IGAVF	DKYR	ILSRP	NRRLT	VSGNTR	LRYSPO
	1030	1040	1050	1060	1070	1080	
a285-1.pep	1090	1100	1110	1120	1130	1140	
a285-1.pep	SVGDD	VVVL	GEVKE	AAAPL	PVNMN	LTL	DLNDG
m285-1	SVGDD	VVVL	GEVKE	AAAPL	PVNMN	LTL	DLNDG
	1090	1100	1110	1120	1130	1140	
a285-1.pep	1150	1160	1170	1180	1190	1200	
a285-1.pep	GVGT	VRVIK	GRYK	AYGQ	DL	DITK	GTVSF
m285-1	GVGT	VRVIK	GRYK	AYGQ	DL	DITK	GTVSF

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	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTAN	EPSEKDKLSWL	ILNRAGSGSSGDNAAL	SAAAGALLAGQINDRIGL	VDDDLGF	
m285-1	PRITLTAN	EPSEKDKLSWL	ILNRAGSGSGDNAAL	SAAAGALLAGQINDRIGL	VDDDLGF	
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSRNAQTGELNPAEQVLT	VGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR				
m285-1	TSKRSRNAQTGELNPAEQVLT	VGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR				
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNSKGKX					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNSKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

g286.seq

```

1 atgcagaaca ccggtaccat gatgatcaaa ccgaccgccc tgctcctgcc
51 ggctttatatt ttctttccgc acgcatacgc gcctgcccgc gacctttccg
101 aaaacaaggc ggcggttttc gcattgttca aaagcaaaag ccccgacacc
151 gaatcagtca aattaaaacc caaatcccc gtccgcatcg acacgcagga
201 cagtgaatc aaagatatgg tcgaagaaca cctgcccgtc atcacgcagc
251 agcaggaaga ggttttgat aaggaacaga cgggattcct tgcccagaag
301 gcaccggaca acgttaaaac aatgctccgc agcaaaaggct atttcagcag
351 caaggtcagc ctgacggaaa aagacggagc ttatacggtg cacatcacac
401 cgggcccgcg caccaaaatc gccaacgtcg gcgtcgccat cctcgccgac
451 atcctttcag acggcaacct cgccgaatac taccgcaacg cgctgaaaaa
501 ctggcagcag ccggtaggca gcgatttcga tcaggacagt tgggaaaaca
551 gcaaaacttc cgtcctcggc gcggtaacgc gcaaaggcta cccgcttgcc
601 aagctcgga acaccgggc ggccgtcaac cccgataccg ccaccgcga
651 tttgaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701 aaatcaccgg cacacagcgt taccgccaac aaaccgtctc cggcctggcg
751 cgcttccaac cgggcacgcc ctacgacctc gacctgctgc tcgacttcca
801 acaggcgctc gaacaaaacg ggcatattc cggcgcgctc gtacaagccg
851 acttcgaccg cctcccaagg ggaccgcgtc cccgtcaaa tcagcgtaac
901 cgaggtcaaa cgccacaaac tcgaaaccgg catccgcctc gattcggaat
951 acggtttggg cggcaaaatc gcctacgact attacaacct cttcaacaaa
1001 ggctatatcg gctcggtcgt ctgggatatg gacaataacg aaaccacgct
1051 tgccgcggc atcagccagc cgcgcaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaaccgt tcgaccaccc aaaacctcga aaaaacgccc
1151 ttctccggcg gcatctggtg tgtgcgcgac cgcgcgggca tcgatgccag
1201 gctggggcg gaatttctcg cagaaggccg gaaaatcccc ggctcggatg
1251 tcgatttggg caacagccac gccacgatgc tgaccgcctc ttggaacgc
1301 cagctgctca acaacgtgct gcaccccgaa aacggccatt acctcgacgg
1351 caaaatcggg acgactttgg gcacattcct gtctccacc gcgctaattc
1401 gcacctctgc ccgcgcaggt tatttcttca cgcccgaaaa caaaaaactc
1451 ggcacgttca tcatacgcgg acaagcgggt tacaccgttg cacgcgacaa
1501 tgccgatgtc ccctcggggc tgatgttccg cagcggcggc gcgtcttccg
1551 tgcgcggtta cgaacttga

```

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

g286.pep

```

1 MONTGTMNIK PTALLLPALF FFPAYAPAA DLSENKAAGF ALFKSKSPDT
51 ESVKLKPFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFIAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAIVT HITPGPRTKI ANVGVAIGLD
151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201 KLGNTAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQTVSGLA
251 RFQPGTPYDL DLLLDFQQAL EQNGHYS GAS VQADFRLPR GPRPRQSQRN
301 RGQTPQTRNR HPPRFGIRFG RQNRLLRLQ LQRLYRLGR LGYQIRNHA
351 CRRHQPAQL SGQLLDKQRF LQPFDPKPR KTRLLRRHLV CARPRGHRCQ
401 AGGGISRRRP ENPRLGCRFG QPRHDAADRL LETPAAQORA APRKRPLPRR

```

451 QNRDDFGHIP VLHRANPHLC PRRLFLHARK QKTRHVHHTR TSGLHRCTRQ  
501 CRCPLGADVP QRRRVFRARL RT\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

```
m286.seq
1   ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
51  GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GCGGGGTTC GCATTGTCA AAAACAAAAG CCCCACACCC
151 GAATCAGTCA AATTAAAACC CAAATCCCC GTCCTCATCG ACACGCAGGA
201 CAGTGAAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCACGCAGC
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCGCCGACA ACGTTAAAC GATGCTCCG AGCAAAGGCT ATTCAGCAG
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCGCG CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAATA
501 CTGGCAGCAG CCGGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAAACA
551 GCAAACTTTC CGTCCTCGGC GCGGTAAACG GCAAAGCCTA CCGCTTGCC
601 AAGCTCGGCA ATACGCAGGC GGCCGTCAAC CCCGATACCG CCACGCCGGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GGCGACTTTG
701 AAATCACCGG CACACAGCGT TACCCGAAC AAATCGTCTC CGGCCTTGCG
751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA
801 ACAGGCGCTC GAACAAAACG GGCATTATTC CGGCGCGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
901 AAGGTCAAAC GCCACAAACT CGAAACCGGC ATCCGCTCG ATTTCGGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAAATACGA AACCACGCTT
1051 GCCGCCGGCA TCAGCCAGCC GCGCAACTAT CGGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCCGCT
1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
1201 CTGGGGGCGG AATTTCTCGC AGAAGGCCGG AAAATCCCCG GCTCGGCTGT
1251 CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCTCT TGGAAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCGAAA ACGGCCATTA CCTCGACGGC
1351 AAAATCGGTA CGACTTTGGG CACATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CATACCGGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCGACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTCCGT
1551 GCGCGGTTAC GAACGCGACA GCATCGGACT TGCCGCGCCG AACGGATCGG
1601 TCCTGCCCGA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTT CACGATATGG GCGATGCCGC
1701 CGCCAATTTT AAACGTATGA AGCTGAAACA CGGTCGGGCA CTGGGCGTGC
1751 GCTGGTTTCA CCCGCTTGGC CCGTTTCTCT TCGACATCGC CTACGGGCAC
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA
```

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

```
m286.pep
1   MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51  ESVKLPKFP VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLEAE
101 APDNVKTMLR SKGYFSSKVS LTEKDGYTV HITPGPRTKI ANVGVAIGD
151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTQAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGMPYDL DLLLDFQQAL EQNGHYSYGAS VQADFDRLOQ DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAIDYYNL FNKGYIGSVV WMDMKYETTL
351 AAGISQPRNY RGNYWTSNVS YNRSTQNLK KRAFSGGVWY VRDRAGIDAR
401 LGAEFLAEGR KIPGSVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLGTFL SSTALIRTS RAGYFTFEN KKLGTFIIRG QAGYTVARDN
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTLGSAVF HMDGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*
```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap



668

m286.pep	10	20	30	40	50	60
	MHDTRTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKN	KS	PD	TESV	KLKPKFP
g286	10	20	30	40	50	60
	MQNTGTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKS	KS	PD	TESV	KLKPKFP
m286.pep	70	80	90	100	110	120
	VLIDTQDSEIKDMVEEHLPLIT	QQQEEVL	DKEQTGF	LAE	APDNV	KTMLRSKGYFSSKVS
g286	70	80	90	100	110	120
	VRIDTQDSEIKDMVEEHLPLIT	QQQEEVL	DKEQTGF	LAE	APDNV	KTMLRSKGYFSSKVS
m286.pep	130	140	150	160	170	180
	LTEKDGAYTVHITPGPR	TKIANVGVAILGDIL	SDGNLAEYYRNA	LENWQQ	PVGS	DFDQDS
g286	130	140	150	160	170	180
	LTEKDGAYTVHITPGPR	TKIANVGVAILGDIL	SDGNLAEYYRNA	LENWQQ	PVGS	DFDQDS
m286.pep	190	200	210	220	230	240
	WENSKTSVLGAVTRKAY	PLAKLGNTQAAVN	PD	TATADLN	VVVD	SGRPIAFGDFEITGTQR
g286	190	200	210	220	230	240
	WENSKTSVLGAVTRKGY	PLAKLGNTRAAVN	PD	TATADLN	VVVD	SGRPIAFGDFEITGTQR
m286.pep	250	260	270	280	290	299
	YPEQIVSGLARFQPGMPY	DLDDLDFQ	QALEQNGHYS	GASVQAD	FDRL	-QGDRV
g286	250	260	270	280	290	299
	YPEQTVSGLARFQPGT	PYDLDDLDFQ	QALEQNGHYS	GASVQAD	FDRL	PRGPRPRQSQRN
m286.pep	300	310	320	330	340	359
	TEV	KRHKLETGIRL	DSEYGLGGK	IAYDYYN	LFNKG	YIGSVVWMDKYETTLAAGISQPRN
g286	300	310	320	330	340	359
	RGQTPQ	TRNRHPPR	FGIRFGRQ	NRLRLQLQ	RLYRLGR	LYGYQIRNHACRRHQPA

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1197>:

```

a286.seq
1 ATGCACGACA CCCGTACCAT GATGATTAAA CCGACCGCCC TGCTCTGTCC
51 GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GCGGGTTTTC GCATTGTTCA AAAACAAAGC CCCCAGACCA
151 GAATCAGTTA AATTAAAACC CAAATTCCCC TCCGCATCGC ACACGCAGGA
201 TAGTGAAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCACGCAGC
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGTTCCTT CGCCGAAGAA
301 GCACCGGACA ACGTTAAAAC AATGCTCCGC AGCAAAGGCT ATTTCCAGCA
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CATCATCAC
401 CGGGCCCGCG CACCAAAATC GCCAACGTCG CGCTGCCCAT CCTCGCGCAG
451 ATCCTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA
501 CTGGCAGCAG CCGGTAGGCA GTGATTTCGA TCAGGACAGT TGGGAAAAACA
551 GCAAACTTTC CGTCTCTGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC
601 AAGCTCGGCA ACACCCGGGC GGGCGTCAAC CCGGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCCC CATCGCCTTC GGCAGCTTTG
701 AAATTACCGG CACGCAGCGT TACCCCGAAC AAATCGTCTC CGGCTTGGCG
751 CGCTTCCAAC CGGGCAGCCG CTACGACCTC GACCTGCTGC TCGACTTTCCA
801 ACAGGCGCTC GAACAACACG GGCATTATTC CGGCGCGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAAGT CAGCGTFAAC
901 GAGGTCAAC GCCACAAGCT CGAAACCGGC ATCCGCGCTC ATTCCGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGGTCTGC TGGGATATGG ACAAATACGA AACCACGCTT
1051 GCCGCCGGCG TACGCCACGC GCGCAACTAT CGGGGCAACT ATCGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AACGCGCCT
1151 TCTCCGGCGG CATCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
1201 CTGGGGGCGG AGTTTCTCGC AGAAGGCGCG AAAATCCCCG TCTCGGATAT
1251 CGATTTTGGC AACTAGCCAG CCACAGTGCT GACCGCCTCT TGGAACACGC
1301 AGCTGCTCAA CAACGTGCTG CATCCGAAA ACGGCCATTA CCTCGACGG

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1351 AAAATCGGTA CGACTTTGGG CGCATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTACGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCG ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTT CACGATATGG GCGACGCCCG
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTTCGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTTCCT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

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This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

```

a286.pep
1 MHDTRTMMIK PTALLLPALF FFPAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFIAEE
101 APDNVKTMLR SKGYFSSKVS LTKDGAYTV HITPGPRTKI ANVGVAAILGD
151 ILSGDNLAAY YRNALENWQQ PVGSDFDQDS WENKTSVLG AVTRKAYPLA
201 KLGNTAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLLDFQQAL EQNGHYS GASVQADFRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKG YIGSVV WMDMKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTQNLE KRAFSGGIYV VRDRAGIDAR
401 LGAEFLAAGR KIPGSDIDL NSHATMLTAS WKRLNNVL HPENHYLDG
451 KIGTTLGAFL SSTALIRTS RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRLGSAVF HMDGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

```

m286/a286 98.7% identity in 615 aa overlap

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPKFP					
a286	MHDTRTMMIKPTALLLPALFFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPKFP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFIAEEAPDNVKTMLRSKGYFSSKVS					
a286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFIAEEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m286.pep	LTEKDGYTVHITPGPRTKIANVGVAAILGDILSDGNLAEYRNALENWQQPVGSDFDQDS					
a286	LTEKDGYTVHITPGPRTKIANVGVAAILGDILSDGNLAEYRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m286.pep	WENKTSVLGAVTRKAYPLAKLGNTQAAVNPDATADLNVVDSGRPIAFGDFEITGTQR					
a286	WENKTSVLGAVTRKAYPLAKLGNTAAVNPDATADLNVVDSGRPIAFGDFEITGTQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m286.pep	YPEQIVSGLARFQPGMPYDLDLLLDFQQALEQNGHYS GASVQADFRLQGDRVPVKVSVT					
a286	YPEQIVSGLARFQPGTPYDLDLLLDFQQALEQNGHYS GASVQADFRLQGDRVPVKVSVT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m286.pep	EVKRHKLETGIRLDSEYGLGGKIAYDYNNLFNKG YIGSVVWMDMKYETTLAAGISQPRNY					
a286	EVKRHKLETGIRLDSEYGLGGKIAYDYNNLFNKG YIGSVVWMDMKYETTLAAGISQPRNY					
	310	320	330	340	350	360
	370	380	390	400	410	420

670

m286.pep	RGNYWTSNVSYNRSTTQNLKRAFSGGVWYVRDRAGIDARLGAEFLAEGRKIPGSAVDLG
a286	RGNYWTSNVSYNRSTTQNLKRAFSGGIWIYVRDRAGIDARLGAEFLAEGRKIPGSDIDLG
	370 380 390 400 410 420
m286.pep	NSHATMLTASWKRQLNNVLHPENGHYLDGKIGTTTLGTFLSSTALIRTSARAGYFFTPEN
a286	NSHATMLTASWKRQLNNVLHPENGHYLDGKIGTTTLGAFLSSTALIRTSARAGYFFTPEN
	430 440 450 460 470 480
m286.pep	KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
a286	KKLGTFIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
	490 500 510 520 530 540
m286.pep	LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPAPFSDIAYGH
a286	LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPAPFSDIAYGH
	550 560 570 580 590 600
m286.pep	SDKKIRWHISLGTREFX
a286	SDKKIRWHISLGTREFX
	610

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

g287.seq

1	atgtttaaac	gcagtgat	tgcaatggct	tgtatttttc	ccctttcagc
51	ctgtgggggc	ggcgggtggcg	gatcgcccgga	tgtcaagtcg	gcggaacacgc
101	cgtcaaaacc	ggccgcccc	gttggtgctg	aaaatgccgg	ggaaggggtg
151	ctgccgaaaag	aaaagaaaaga	tgaggaggca	gcgggcggtg	cgccgcaagc
201	cgatacgag	gacgcaaccg	ccggagaagg	cagccaagat	atggcgccag
251	tttcggcaga	aaatacaggc	aatggcggtg	cggcaacaac	ggacaacccc
301	aaaaatgaag	acgcgggggc	gcaaaatgat	atgccgcaaa	atgccgccga
351	atccgcaaat	caaacaggga	acaaccaacc	cgccggttct	tcagattccg
401	cccccgctc	aaaccctgcc	cctgcgaatg	gcggtagcga	ttttggaagg
451	acgaacgtgg	gcaattctgt	tgtgattgac	ggaccgtcgc	aaaatataac
501	gttgaccac	tgtaaaaggc	attcttgtaa	tggtgataat	ttattggatg
551	aagaagcacc	gtcaaaatca	gaatttgaaa	aattaagtga	tgaagaaaaa
601	attaagcgat	ataaaaaaga	cgagcaacgg	gagaattttg	tcggtttggt
651	tgctgacagg	gtaaaaaagg	atggaactaa	caaatatata	atcttctata
701	cggacaaaacc	acctactcgt	tctgcacggt	cgaggaggtc	gcttccggcc
751	gagattccgc	tgattcccgt	caatcaggcc	gatacgctga	ttgtggatgg
801	ggaagcggtc	agcctgacgg	ggcattccgg	caatatcttc	gcgccgaag
851	ggaattaccg	gtatctgact	tacggggcgg	aaaaattgcc	cggcgatcg
901	tatgccctcc	gtgtgcaagg	cgaaccggca	aaaggcgaaa	tgcttggttg
951	cacggccgtg	tacaacggcg	aagtgtgca	ttcccatatg	gaaaacggcc
1001	gtccgtaccc	gtccggaggc	aggtttgccg	caaaagtcga	tttcggcagc
1051	aaatctgtgg	acggcattat	cgacagcggc	gatgatttgc	atatgggtac
1101	gcaaaaattc	aaagccgcca	tcgatggaaa	cggctttaag	gggacttgga
1151	cggaaaaatg	cggcggggat	gtttccggaa	ggttttacgg	cccggccggc
1201	gaggaaagtg	cgggaaaata	cagctatcgc	ccgacagatg	ctgaaaaagg
1251	cggattcggc	gtgtttgccc	gcaaaaaaga	tcgggattga	

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

g287.pep

1	MFKRSVIAMA	CIFPLSACGG	GGGGSPDVKS	ADTPSKPAAP	VVAENAGEGV
51	LPKEKKDEEA	AGGAPQADTQ	DATAGEGSQD	MAAVSAENTG	NGGAATTDNF
101	KNEDAGAQND	MPQNAAESAN	QTGNNQPAGS	SDSAPASNPA	PANGGSDFGF

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```

151 TNVGNVSVVID GPSQNITLTH CKGDSCNGDN LLDEEAPSKS EFEKLSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGTNKYI IFYTDKPPTR SARSRRLSPA
251 EIPLIPVNQA DTLIVDGEAV SLTGHSGNIF APEGNYRYLT YGAEKLPGGS
301 YALRVQGEPA KGEMLVGTA VNGEVLHFHM ENGRPYPSGG RFAAKVDFGS
351 KSDVGIIIDSG DDLHMGTKKF KAAIDGNFKE GTWTENGGGD VSGRFYGPAG
401 EEVAGKYSYR PTDAEKGFGF VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1 ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTGT CCCTTTCAGC
51 CTGCGGGGGC GCGGGTGGCG GATCGCCCGA TGTCAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTTCCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGTTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGGCA GCGGGGCAAA ATGCGCGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGGTT
551 CTTCAGATCC CATCCCCGCG TCAAACCTG CACCTGCGAA TGGCGGTAGC
601 AATTTTGAA GGGTTGATTT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGGA TGAAGAAGTA CAGCTAAAAT CAGAATTGTA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCGGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCCGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCGGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCAGG
1201 TTTGCCGCAA AAGTCGATTT CGGCAGCAAA TCTGTGGACG GCATTATCGA
1251 CAGCGGCGAT GATTTGCATA TGGGTACGCA AAAATTCAAA GCCGCCATCG
1301 ATGGAACCGG CTTTAAGGGG ACTTGGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTTGCCGGCA
1451 AAAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1 MFKRSVIAMA CIFALSACGG GGGSPDVKS ADTLSPKPAAP VVSEKETEAK
51 EDAPQAGSQG QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMANAA
151 DGMQGGDDPSA GGQNAAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFRVLDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRRS
301 ARSRRLPAE MPLIPVNQAD TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIIDSG DLHMGTKQFK AADGNFKEG TWTENGSGDV
451 SGKIFYGPAGE EVAGKYSYRPT TDAEKGFGFV FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

          10      20      30      40      49
m287.pep MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSE-----KETE
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287      MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEVLPKEKKDEEA
          10      20      30      40      50      60

```

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	50	60	70	80	90	100	109
m287.pep	KEDAPQAGSQGQAPSAGGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMDMPQNAAGT						
	:   ::             :						
g287	AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQNMDMPQNA--						
	70	80	90	100	110		
m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDFNMLAGNMENQATDAGESSQPANQPDMANAADMGGDDPSAGGQNAGNTA						
g287	-----						
m287.pep	170	180	190	200	210	220	229
	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQINITLTHCKGDS						
	::   :                :    : : :						
g287	-ESANQTGNNQPAGSSDSAPASNPAPANGGSDFGRTNVGNSSVIDGPSQINITLTHCKGDS						
	120	130	140	150	160	170	
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEVQLKSEFEKLSDADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP						
	: : :    :        : :     :  : :         :   :						
g287	CNGDNLLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVKKDGTNKYIIFYTD						
	180	190	200	210	220	230	
m287.pep	290	300	310	320	330	340	349
	KPTSFARFRRSARRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNRYRLT						
	:            :						
g287	KPPT-----RSARRSLPAEIPVNPQADTLIVDGEAVSLTGHSGNIFAPEGNRYRLT						
	240	250	260	270	280	290	
m287.pep	350	360	370	380	390	400	409
	YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTGRFRAAKVDFGS						
	: :             :						
g287	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHFMENGRPYPSGGRFRAAKVDFGS						
	300	310	320	330	340	350	
m287.pep	410	420	430	440	450	460	469
	KSVDDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGSGDVSFGKFGPAGEEVAGKYSYR						
g287	KSVDDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGSGDVSFGKFGPAGEEVAGKYSYR						
	360	370	380	390	400	410	
m287.pep	470	480	489				
	PTDAEKGFGVFAGKKEQDX						
	:						
g287	PTDAEKGFGVFAGKKDRDX						
	420	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1203>:

a287.seq

1	ATGTTTAAAC	GCAGTGTGAT	TGCAATGGCT	TGTATTGTTG	CCCTTTCAGC
51	CTGTGGGGGC	GGCGGTGGCG	GATCGCCCGA	TGTTAAGTCG	GCGGACACGC
101	TGTCAAAACC	TGCCGCCCTT	GTTGTTACTG	AAGATGTCGG	GGAAGAGGTG
151	CTGCCGAAAG	AAAAGAAAGA	TGAGGAGGCG	GTGAGTGGTG	CGCCGCAAGC
201	CGATACGCAG	GACGCAACCG	CCGAAAAGG	CGGTCAAGAT	ATGGCGCAG
251	TTTCGCGAGA	AAATACAGGC	AATGGCGGTG	CGGCAACAAC	GGATAATCCC
301	GAAAATAAAG	ACGAGGGACC	GCAAAATGAT	ATGCCGCAAA	ATGCCGCCGA
351	TACAGATAGT	TCGACACCGA	ATCACACCCC	TGCACCGAAT	ATGCCAACCA
401	GAGATATGGG	AAACCAAGCA	CCGGATGCCG	GGGAATCGGC	ACAACCGCA
451	AACCAACCGG	ATATGGCAAA	TGCGGCGGAC	GGAATGCAGG	GGGACGATCC
501	GTCGGCAGGG	GAAAATGCCG	GCAATACGGC	AGATCAAGCT	GCAAATCAAG
551	CTGAAAACAA	TCAAGTCGGC	GGCTCTCAAA	ATCCTGCCTC	TTCAACCAAT
601	CCTAACGCCA	CGAATGGCGG	CAGCGATTTT	GGAAGGATAA	ATGTAGCTAA
651	TGGCATCAAG	CTTGACAGCG	GTTCCGAAAA	TGTAACGTTG	ACACATTGTA
701	AAGACAAAGT	ATGCGATAGA	GATTTCTTAG	ATGAAGAAGC	ACCACCAAAA
751	TCAGAATTTG	AAAAATTAAG	TGATGAAGAA	AAAAATAATA	AATATAAAAA



a287.pcp

m287/a287 77.2% identity in 501 aa overlap

		10	20	30	40	49
m287.pep		MFKRSVIAMACIFALSACGGGGGSPDVKSADTL SKPAAPVVSE-----KETE				
a287		MFKRSVIAMACIVAL SACGGGGGSPDVKSADTL SKPAAPVVTE DVGEEVLPKEKKDEEA				
		10	20	30	40	60
	50	60	70	80	90	100
m287.pep		KEDAPQAGSQGGAPS AQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQN DMPQNAAGT				109
		:     : : :				
a287		VSGAPQADTQ--DATA GKGQDMAAVSAENTGNGGAATT DN PENKDEGPQNDMPQNAADT				
		70	80	90	100	110
	110	120	130	140	150	160
m287.pep		DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGDDPSAGGQNAAGNTA				169
		: :				
a287		DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGDDPSAG-ENAGNTA				
	120	130	140	150	160	170
	170	180	190	200	210	220
m287.pep		AQGANQAGNNQAAGSSDPIASNPAPANGGSNFGRVDLANGVLIDGPSQNTITLTHCKGDS				229
		:                 :     :                     :   :				
a287		DQAANQAENNQVGSQNPASSTNPNATNGGSDFGGRINVANGIKLDSGSENVTLTHCKDKV				
	180	190	200	210	220	230
	230	240	250	260	270	280
m287.pep		CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP				289
		: :         :               :     :       : :               :         :				
a287		CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVKNGTINKYVIYIKD				
	240	250	260	270	280	290
	290	300	310	320	330	340
m287.pep		KP--TSFARFRRSARSRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRY				
		: :				
a287		KSASSSARFRRSARSRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRY				
	300	310	320	330	340	350

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	350	360	370	380	390	400
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287.pep	GSKSVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS					
a287	GSKSVDGIIDSGDDLHMGTKQFKAVIDGNGFKGTWTENGSGDVSGRFGYPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287.pep	YRPTDAEKGGFGVFAGKKEQDX					
a287	YRPTDAEKGGFGVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1   atgcacaccg gacaggcggg aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgtcaag caacctacc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcgggt cgcccttacc gcaccttttc
201 acccttgccg gtgctgccaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccg cgcccgccg ttaaccggca ttctaccctg
301 cggagcccgg actttcctcc ccgtatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgcgg cgcggtatt aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacagggt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgct caagtcgccc tccaatacgg
501 ctttgtggtt gccgacttcg tagcctgtac gcaagtcttt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288.pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288.seq
1   ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTCGGTCT TGCTCCGAAT GGGGTTCGGC
151 CTGCCGCATA TTGTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCGGTTTTC CTTTCTGTTC
251 CACTTTCCTG CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288.pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFAVACTQVF					
g288	PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADFAVACTQVF					
	130	140	150	160	170	180
m288.pep	DTX					
	:					
g288	DAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

a288.seq

1	ATGCACACCG	GACAGGCGGT	AAGCCGGGTT	CTGTCTCGGA	CAGTCATTCC
51	TCTAGGCATA	CCGTTGCCGG	TATGCTCAAG	CAACCTACCC	GAACGCTCGG
101	CGGGCAGCGT	CATTGCGTTC	TGTTTGGTCT	TGCTCCGAAT	GGGGTTTGGC
151	CTGCCGCATA	TTGTTACCAA	ATGCGCGGTG	CGCCCTTACC	GCACCTTTTC
201	ACCCCTGCCT	GTGCTGCCAA	AGCAGCCATC	GGCGGTTTTC	CTTCTGTTC
251	CACTTTCCTG	CGCGTTACCG	CGCCCGGCCG	TTAACCGGCA	TTCTACCCTG
301	CGGAGCCCGG	ACTTTCCTCC	CCGTATGCCT	TACGCGATAC	GCGGCGACTG
351	TCTGCCCGTC	CCGTGTGCGG	CGCGGATTAT	AACACGAAAC	GCAAAAATGC
401	CGTCTGAAAC	GGTACAGGTT	TCAGACGGCA	TACAGCCTAA	ACTACACGCC
451	CTGTTTCAGG	CTGGCTTCGA	TAAAGCCGTC	CAAGTCGCCG	TCCAATACGG
501	CTTTGGTGTT	GCCGACTTCG	TAGCCTGTGC	GCAAGTCTTT	AATGCGTGA

This corresponds to the amino acid sequence &lt;SEQ ID 1210; ORF 288.a&gt;:

a288.pep

1	MHTGQAVSRV	LSRTVIPLGI	PLPVCSSNLP	ERSAGSVIAF	CLVLLRMGFG
51	LPHIVTKCAV	RPYRTFSPLP	VLPKQPSAVL	LSVPLSVALP	RPAVNRHSTL
101	RSPDFPPRMP	YAIRGDCLPV	PCAARIITRN	AKMPSETVQV	SDGIQPKLHA
151	LFQAGFDKAV	QVAVQYGFV	ADFAVACQVF	NA*	

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFAVACTQVF					

676

a288 PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADFAVACAQVF  
 130 140 150 160 170 180

m288.pep DTX  
 ::  
 a288 NAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

g290.seq  
 1 atggcaaaaa tgatgaaatg ggcggtctgtt gcggcggtcg cggcggcagc  
 51 ggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata  
 101 ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg  
 151 ggcgagattt cgccgtccaa cctggtatcg gtcggcgcgc aggcttcggg  
 201 gcagattaaa aagctttatg tcaaaactcg gcaacaggtc aaaaagggcg  
 251 atttgattgc ggaaatcaat tcgaccacgc agaccaacac gatcgatatg  
 301 gaaaaatcca aattggaaac gtatcaggcg aagctggtgt ccgcacagat  
 351 tgcattgggc agcgcgga aaatataaa gcgtcaggcg gcgttggtga  
 401 aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt  
 451 gccgcccga aagccaatgt tgccgagttg aaggctttaa tcagacagag  
 501 caaaatttcc atcaataacc cggagtcgga tttgggctac acgcgcatta  
 551 ccgcgacgat ggacggcacg gtggtggcga ttcccggtga agagggcgag  
 601 actgtgaacg cggcgcgatc tacgccgacg attgtccaat tggcgaatct  
 651 ggatatgatg ttgaacaaaa tcgagattgc cgaggcgat attaccaagg  
 701 tgaaggcggg gcaggatatt tcgtttacga tttgtccga accggatacg  
 751 ccgattaagg cgaagctcga cagcgtcgac cccgggctga ccacgatgtc  
 801 gtcggggcgc tacaacagca gtacggatac ggcttccaat gcggtctatt  
 851 attatgcccg ttcgtttgtg ccgaatccg acggcaaat cgccacgggg  
 901 atgacgacg agaatacggg tgaatcgac ggtgtgaaaa atgtgttgc  
 951 tattccgtcg ctgaccgtga aaaatcgcg cggcaaggcg ttcgtacgcg  
 1001 tgttgggtgc ggacggcaag gcagtggaac gcgaaatccg gaccggtatg  
 1051 aaagacagta tgaataccga agtgaaaagc ggggtgaaag agggggacaa  
 1101 agtggtcac tccgaaataa ccgcgcgcca gcagcaggaa agcggcgaa  
 1151 gcgccttagg cggcccgcg cgccgataa

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

g290.pep  
 1 MAKMMKWA AVAAAVWG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT  
 51 GEISPSNLVS VQAQASGQIK KLYVKLGQV KKGDLIAEIN STTQNTIDM  
 101 ESKKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATSK EDLESAQDAL  
 151 AAAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEGQ  
 201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT  
 251 PIKAKLDSVD PGLTTMSSSG YNSSTDASN AVYYIYARFV PNPDGKLTG  
 301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM  
 351 KDSMNTVEKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

m290.seq (partial)  
 1 ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA  
 51 ACTCGGGCAA CAGGTTAAAA AGGGCGATTT GATTGCGGAA ATCAATTCGA  
 101 CCTCGCAGAC CAATACGCTC AATACGAAA AATCCAAGTT GGAACGTAT  
 151 CAGGCCAAGC TGGTGTCCGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA  
 201 ATATAAGCGT CAGGCGCGCT TATGGAAGGA AAACGCGACT TCCAAAGAGG  
 251 ATTTGGAAG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC  
 301 GAGCTGAAGG CTTTAATCAG ACAGAGCAA ATTTCCATCA ATACCGCCGA  
 351 GTCGGAATTG GGCTACACGC GCATTACGCG AACGATGGAC GGCACGGTGG  
 401 TGGCGATTCT CGTGGAAGAG GGCAGACTG TGAACGCGGC GCAGTCTACG  
 451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAAATGCA  
 501 GATTGCCGAG GCGATATTA CCAAGGTGAA GGCGGGGCAG GATATTTCGT  
 551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC  
 601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GGCGGTTACA ACAGCAGTAC  
 651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCGTTCT TTTGTGCCGA

677

```

701 ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGAATAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TCGCGGTGTT GGGTGGCGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
  1  ..VSVGAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
 51  QAKLVSAQIA LGSAEKYKQR QAALWKENAT SKEDLESAQD AFAAAKANVA
101  ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151  PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201  VDPGLTTMSS GGYNSSDTA SNAVYYYARS FVPNPDGKLA TGMTTQNTVE
251  IDGVKNVLII PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTEV
301  KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

m290.pep                                10      20      30
                                      VSVGAQASGQIKILYVKLGQVKKGDLIAE
g290                                PQAAYITEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQVKKGDLIAE
30      40      50      60      70      80

m290.pep                                40      50      60      70      80      90
INSTSQNTNLNTEKSKLETYQAKLVSAQIALGSAEKYKQRQAALWKENATSKEDLESAQD
g290                                INSTTQNTNIDMEKSKLETYQAKLVSAQIALGSAEKYKQRQAALWKDDATSKEDLESAQD
90      100     110     120     130     140

m290.pep                                100     110     120     130     140     150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
g290                                ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPVEEGQTVNAAQST
150     160     170     180     190     200

m290.pep                                160     170     180     190     200     210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
g290                                PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
210     220     230     240     250     260

m290.pep                                220     230     240     250     260     270
GGYNSSDTASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIIPSLTVKNRGG
g290                                GGYNSSDTASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
270     280     290     300     310     320

m290.pep                                280     290     300     310     320     330
KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
g290                                KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
330     340     350     360     370     380

m290.pep                                PPRRX
g290                                PPRRX
390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1  ATGGCAAAAA TGATGAAATG GCGGGCTGTT GCGGCGGTCG CGGCGGCAGC
51  GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAC GGTCAAGCGC GCGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAA GAACTTTATG TCAAACCTCG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTGGA AAAGCGCACA GGATGCGCTT
451 GCGCGCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATT
551 CCGCAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGGA AGAGGGGCAG
601 ACTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGCGGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTGTCCGA ACCGGATACG
751 CGGATTAAGG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TTCGTTTGTG CCGAATCCGG ACGGCAAACG CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAATCGAC GGTGTGAAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CGGCAGGGCG TTTGTGCGCG
1001 TGTGGGTGCG AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCGGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1  MAKMMKWAAY AAVAAAAVWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDLIAEIN STSQTNTLNT
101 EKSLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEQ
201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSG YNSSTDASN AVYYYARFV PNPDGKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTGM
351 RDSMNTEVKS GLKEGDKVVI SEITAEQQE SGERALGGPP RR*
```

m290/a290 98.2% identity in 334 aa overlap

m290.pep				10	20	30
				VSVGAQASGQIK	KLYVKLGQOV	KKGDLIAE
a290						
	30	40	50	60	70	80
m290.pep		40	50	60	70	80
		INSTSQTNTLN	TEKSKLETYQ	AKLVSAQIAL	GSAEKKYKRQ	AALWKENATS
a290						
	90	100	110	120	130	140
m290.pep		100	110	120	130	140
		AFAAAKANVA	ELKALIRQSK	ISINTAESEL	GYTRITATMD	GTVVAILVEE
a290						
	150	160	170	180	190	200
m290.pep		160	170	180	190	200
		PTIVQLANLDM	MLNMQIAEGD	ITKVKAGQDI	SFTILSEPDT	PIKAKLDSVD
a290						
	210	220	230	240	250	260
m290.pep		220	230	240	250	260
		PTIVQLANLDM	MLNMQIAEGD	ITKVKAGQDI	SFTILSEPDT	PIKAKLDSVD
a290						
	270					

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```

m290.pep      GGYNSSTDASNAVYYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               |||||||
a290          GGYNSSTDASNAVYYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               270      280      290      300      310      320

               280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTSEVKSGLKEGDKVVISSEITAAEQQESGERALGG
               :|||||
a290          RAFVRVLGADGKAAEREIRTGMRDSMNTSEVKSGLKEGDKVVISSEITAAEQQESGERALGG
               330      340      350      360      370      380

m290.pep      PPRRX
               ||||
a290          PPRRX
               390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51  gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttgacaaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaatctt atgggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atgcgtaaa gcaaatcccc ggctcggcggc agcatctgcg acaatcccgt
651 cgcgaaacc acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tccccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaac cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSVASLKR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRNGNKLKV AVFSDPDCCF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQGFN GTPTLRLPQR AHPKRLQPD
251 PTGGNHPQKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGACAAA AGCCATCAAA GAAGTGC GCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCATTG CCGGCCTGCA CCCCAGTGCC GCGCGCAAGG
551 CGCAATCTT ATGGTGTGAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAAATCCC GGTCGGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCAACGGG GCGAGCCAAA GCGGCTACAG CCCGATGCC

```

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751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

This corresponds to the amino acid sequence &lt;SEQ ID 1220; ORF 292&gt;:

```

m292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAASLKAR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFGVGLIN
101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151  CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251  QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

m292.pep	10	20	30	40	50	60
	MKTKLIKILTPFTVLPLLACGQTPVSNANAEP	PAVKAESAGKSVAAASLKARLEKTYSAQDL				
g292	MKTKLIKILTPFTVLPLLACGQTPVSNANAES	AVKAESAGKSVAAASLKARLEKTYSAQDL				
	10	20	30	40	50	60
m292.pep	70	80	90	100	110	120
	KVLVSSETFPVKGIYEVVVSQRQIIYTDAEGGYM	FGVGLINIDTRKNLTEERAADLNKIDF				
g292	KVLVSSETFPVKGIYEVVVSQRQIIYTDAEGGYM	FGVGLINIDTRKNLTEERAADLNKIDF				
	70	80	90	100	110	120
m292.pep	130	140	150	160	170	180
	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKR	LEHEFEKMTDVTVYSFMMPIAGLHPDA				
g292	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKR	LEHEFEKMTDVTVYSFMMPIAGLHPDA				
	130	140	150	160	170	180
m292.pep	190	200	210	220	230	240
	ARKAQILWCQPDRAKAWTDWMRKGFVPVGG	SICDNPVAETTSLGEQFGFNGTPTLVFPNG				
g292	ARKAQILWCQPDRAKAWTDWMRKGFVPVGG	SICDNPVAETTSLGEQFGFNGTPTLRLPQR				
	190	200	210	220	230	240
m292.pep	250	260				
	RSQSGYSPMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHPQKPAVNPQX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1  ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101  TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151  TTGGAAAAAA CCTATTCCGC CCAAGATTTG AAAGTGTTGA GCGTCAGCGA
201  AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251  TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301  ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351  AATCGACTTC GCCTCCCTGC CTTTGACAA AGCCATCAAA GAAGTGCGCG
401  GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451  TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501  CAGCTTTATG ATGCCCATTT CCGGCCTGCA CCCCATGCCG GCGCGCAAGG
551  CGCAAATCTT ATGGTGTCAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601  ATGCGTAAAG GCAAATTTCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651  CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701  CCTCGTCTT CCCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC
751  CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

```



This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLAKAR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSFMP
251 QLEEIIRKNQ *

m292/a292    100.0% identity in 260 aa overlap

              10      20      30      40      50      60
m292.pep      MKTKLIKILTPFTVLPLLACGQTPVSNANAEP AVKAESAGKSVASLAKARLEKTYSAQDL
              |||||||
a292           MKTKLIKILTPFTVLPLLACGQTPVSNANAEP AVKAESAGKSVASLAKARLEKTYSAQDL
              10      20      30      40      50      60

              70      80      90     100     110     120
m292.pep      KVLVSSETPVKGIYEVVVSQ RQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
              |||||||
a292           KVLVSSETPVKGIYEVVVSQ RQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
              70      80      90     100     110     120

              130     140     150     160     170     180
m292.pep      ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
              |||||||
a292           ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
              130     140     150     160     170     180

              190     200     210     220     230     240
m292.pep      ARKAQILWCQPDRAKAWTDWMRKGFVPVGG SICDNPVAETTS LGEQFGFNGTPTLVFPNG
              |||||||
a292           ARKAQILWCQPDRAKAWTDWMRKGFVPVGG SICDNPVAETTS LGEQFGFNGTPTLVFPNG
              190     200     210     220     230     240

              250     260
m292.pep      RSQSGYSFMPQLEEIIRKNQX
              |||||||
a292           RSQSGYSFMPQLEEIIRKNQX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtctggtc
51  ggttcgggct gtcagaacat catcgaaccg ctttctcgcg gcgttacgac
101 gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151 tggcatcggg tgccggcggt caagtcgaat cggcggagcg gtggcgtgaa
201 gccgttgaaa aaaccttatac tggcgagggg ggcggaatgc agatgcaggc
251 gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301 ccgagggcgt gcgggaagcg gtatgcggac atcggggggc atagtgtatac
351 aatccgtatc cgagttttcc ggttggagca tcgtatgagt atttatgccg
401 tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcggcggtg
451 ttttttgaag tgctggtttt gtccgtcctg catacgggac ggggtgtcgcg
501 cgaggcgcg cgcgaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
551 tgatgccgtt tgcggtcgga ctgctgttcg ccagggaac tctagagtcg
601 actgcagcag catgccctc...

```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
1  MRITCAPMSL LSAAVWSVRA VRTSSNRFFA ALRRYSAPRP TIFPKPAGTP
51  WHRVRRFKSN RRTRGVKPLK KPYLARGAEC RCRRRAWTALS HNIAERARES
101 PRRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151 FFEVLVLSVL HTGRVSRREAR REVEKAMSYR AVRVMFPAVG LLFARGTLES
201 TAAACP....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

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## m294.seq

```

1  ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
51  GATTCGGGTT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
151 TGGCATCGGG TCGGGCGGTT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC
351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG
451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCGCG
501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTC CCAGCGGCAT CGTGATGGCG
601 GCAAACCGCT ATCTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCCG
651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC GGTCCGTTGG
751 TCGAAATACA TACACGCCGT CGTCTTACC CATATGCTGC TGATTGTCTT
801 TTGGCAAAA GCGATGTTT ATATCAGCTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

## m294.pep

```

1  MRITCAPMSL LSAAVWSIRV VRTSSNRFP AFRRYSAFQ TIFPKPADTP
51  WHRVRREKSN RMRGGKPLK KPYRPRGGC RCRRRAWTALS HNIAERARES
101 PRRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIVHL YCAIAFVGGV
151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFPVVG LLEFASGIVMA
201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
251 SKYIHAVVET HMLLIVFLAK AMFYISW*

```

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSA	AVWSVRAVRTSS	NRFPALRRYSA	FRPTIFPKPAG	TPWHRVRREKSN	
m294	MRITCAPMSLLSA	AVWSIRVVRTSS	NRFPAAFRRYSA	FQPTIFPKPAD	TPWHRVRREKSN	
	10	20	30	40	50	60
g294.pep	RRTRGVKPLKPY	LARGAECRCRR	AWTALSHNIAE	RARESPRRCGK	RYADIGGDSDT	IRI
m294	RRMRGGKPLKPY	RPRGGCRCRR	AWTALSHNIAE	RARESPRRCGK	RYADIGGDSDT	IRI
	70	80	90	100	110	120
g294.pep	RVRLEHRMSIYA	VAHIHLYCAT	AFVGVFFEV	LVLSVLHTGR	VSREARREVEK	AMSYR
m294	RVRLEHRMSIYA	VAHIHLYCAI	AFVGVFFEV	LVLSVLHTGR	VSREARREVEK	AMSYR
	130	140	150	160	170	180
g294.pep	AVRVMFPFAVGL	LFARGTLESTA	AACP			
m294	AVRVMFPVVG	LLFASGIVMA	ANRYLSILGE	PFATSFGTML	TLKILLAFSV	LAHFAIAVVK
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

## a294.seq

```

1  ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
51  GATTCGGGCT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT
151 TGGCATCGGG TCGGGCGGTT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
201 GCCGTTGAAA AAAACTTATC GTCCGAGGAG GCGGGAATGC AGATGCAGGC
251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
351 AATCCGTATC CGAGTTTTC GGTGGAGTA CCGTATGAGT ATTTATGCCG
401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTTGT CGGCGGCGTG
451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCGCG
501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTC CCAGCGGCAT CGTGATGGCG
601 GCAAACCGCT ATCTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCCG
651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

```

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701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG  
 751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT  
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294.pep  
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAFRP TIFPKPAGTP  
 51 WHRVRRFKSN RRTRGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES  
 101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV  
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMFVVG LFFASGIVMA  
 201 ANRYSILGE PFATSFGTML TLKILLAFSV LAHFIAVVK MARSTLTVGW  
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW\*

m294/a294 94.9% identity in 277 aa overlap

m294.pep	10	20	30	40	50	60
	MRITCAPMSLLSAAVWSIRVVRTSSNRFPAAFRYSAFQPTIFPKPADTPWHRVRRFKSN					
a294	MRITCAPMSLLSAAVWSIRAVRTSSNRFPAAFRYSAFRPTIFPKPAGTPWHRVRRFKSN					
	10	20	30	40	50	60
m294.pep	70	80	90	100	110	120
	RRMRGGKPLKKPYRPRGGCRRRAWTALSHNIAERARESPRCGKRYADIGGDSDTIRI					
a294	RRTRGGKPLKTYRPRRAECRRARTALSHNIAERARESPRRYGKRYADIGGDSDTIRI					
	70	80	90	100	110	120
m294.pep	130	140	150	160	170	180
	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFFEVLLSVLHTGRVSREARREVEKAMSYR					
a294	RVFRLEYRMSIYAVAHIVHLYCAIAFVGGVFFEVLLSVLHTGRVSCEARREVEKAMSYR					
	130	140	150	160	170	180
m294.pep	190	200	210	220	230	240
	AVRVMFVVGLLFASGIVMAANRYSILGEPFATSFGTMLTLKILLAFSVLAHFIAVVK					
a294	AVRVMFVVGLLFASGIVMAANRYSILGEPFATSFGTMLTLKILLAFSVLAHFIAVVK					
	190	200	210	220	230	240
m294.pep	250	260	270			
	MARSTLTVGWSKYIHAVVFTHMLLIVFLAKAMFYISWX					
a294	MARSTLTVGWSKYIHTVVFTHMLLIVFLAKAMFYISWX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295.seq  
 1 atgctcggga tggcgcggca cgacggccag caggcgcacg ccgcgatatt  
 51 gttgccacgc cgccagcagt tttccgcct cgtcttcgcc ccgataaacg  
 101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gtttttcaaa  
 151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg  
 201 tattccgcga cactgcacg gatgccgcgc ccaatttcgc caaccgcgcc  
 251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg  
 301 acggatcagg cggcggactt tcagataacc gttcagcgaat tttccgaca  
 351 gccgcgcatt cgccaaaaac agcggcacac ccgctcgcgc gcattccttc  
 401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcgggcy  
 451 gtgttcgcgc aaaaactgcc gtaccacagt tttttgtca tacggaagat  
 501 agcggcattg cgcacgcgga aacagaactt gcgcggttcc ccgtcccgtc  
 551 ggggtcatct gcgtcatcag cagcggcgca tcgggaaaac gccgcgcgaa  
 601 ctccggtatc aagggctggg cggcacgcgt ttctccgacc gaaacggcgt  
 651 gtatccaaac cgcgcgggta acgggattcg gatgcggcgt gccgaaacgc  
 701 tcgtccctat gcgcccggta tgcgggggca cttccggagc gtttgcctaa  
 751 ataacgcgt atccatctcg gcgcaagcag ccacaataca tcataaagcc  
 801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacgggtc  
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

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## g295.pep

```

1  MLGMARHDDGQ QGIAAILLPR RQOFFRLVFA PINARAAAHG NRPASDAFFK
51  LPRQRFHVFR RHQVVFGLAA HLHGCRAQFR QPRRIRLRLR QTARQSRGCG
101 TDQAADFQIT VQREFFRQPRI RQQRHTRSP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

## m295.seq

```

1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCGGCCGG CCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCGC AGCGTTTTC TCTGTTCCGA CGGTATGATG TCGTATTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTGAGCGAAG CGCGCGCAGG
301 ACGGATCAGG CGGCGGACTT TCAGATAACC GTTCAACGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGCGCGCCG GCATTCCCTC
401 ATCAGGTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTCCGCGC AAAAAGTCC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG CGCATCGGGA AACAGAACTT GCGCGGTTT CCGCCCCGTC
551 GGGGTATCT GCGTCATCAG CAGCGGCGCA TCGGAAAAC GCCGCCGCAA
601 CTCGCGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGTA ACGGGATTCG GATACGGCTT GCCGAAACGC
701 TCGTCCCGAT GCGCCCGATA TGCCGGGGCA CTTCGGGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTCTATTT CCTGCAAAAC AAATGCCGTC TGAACGGTTC
851 AGACGGCATT TCGGCAACGG AATCAATAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

## m295.pep

```

1  MLGMARHDDQ QRIAAILLPR RQOFFRLVFT PINARAAAHG NRPASDAFFK
51  LPRQRFHLFR RYDVVFGLAA HLHGCRAQFR QPRRIRLCLR QTPRQRSGGR
101 TDQAADFQIT VQREFFRQPRI RQQRHTRAP AFPHQVGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PPRRGLRHQ QRRIGKTPPQ
201 LAYQGLGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV XTQVTAFRQR NQIS*

```

m295/g295 93.9% identity in 294 aa overlap

m295.pep	10	20	30	40	50	60
	MLGMARHDDQRIAAILLPRRQOFFRLVTFPINARAAAHGNRPASDAFFKLPQRQFHLFR					
g295	MLGMARHDDGQGGIAAILLPRRQOFFRLVFA PINARAAAHGNRPASDAFFKLPQRQFHVFR					
m295.pep	10	20	30	40	50	60
	RYDVVFGLAAHLHGCRAQFRQPRRIRLCLRQTPRQRSGGRDQAADFQITVQREFFRQPRI					
g295	RHQVVFGLAAHLHGCRAQFRQPRRIRLRLRQTARQSRGCGTDQAADFQITVQREFFRQPRI					
m295.pep	70	80	90	100	110	120
	RQQRHTRAPAFPHQVGPDFGFHQNAEHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
g295	RQQRHTRSPAFHLHQIGPDFGFHQNAEHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
m295.pep	130	140	150	160	170	180
	PPRRGHLRHQRRIGKTPPQLAYQGLGTRFSDRNGVYPNRAGNGIRIRLAETLVPMRPI					
g295	PSRRGHLRHQRRIGKTPPQLAYQGLGTRFSDRNGVYPNRAGNGIRMRLAETLVPMRPV					
m295.pep	190	200	210	220	230	240
	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTQVTAFRQRNQISX					
g295	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVRTVRTAFRQRNQIS					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1 ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51 GTTGCCACGC CGCCAGCAGT TTTCCGCCT CGTCTTACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTCAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGCATCAGG TCGTATTG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGTGCGCCG GCATTCCTTC
401 ATCAGATTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTCCGCG AAAAAGTCC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTT CCGTCCCGTC
551 GGGGTATCT GCGTCATCAG CAGCGGCGCA TCGGAAAAC GCTGCCGCAA
601 CTCGCGTATC AAAGTTGGG CGGCACGCGT TTCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCGATA TGCAGGGGCA CTTCCGGAGC GTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTCTATTT CTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGCAACGG AATCAAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1 MLGMARHDDQ QGIAAILLPR ROQFFRLVFT PINARAAAHG NLPVSDAFFK
51 LPRQRFHLFR RHQVVFQIAA HLHGCRAQFR QPRRIRLRLC QTARQSSGGR
101 TDQAADFQIT V*RFFRQPRI RQKQRHTRAP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL CIRKQNLRF PSRRGHLRHQ QRRIGKTLPO
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQ	RIAAILPR	ROQFFRLVFT	PINARAAAHG	NRPASDAFFK	LPRQRFHLFR
a295	MLGMARHDDQ	QIAAILPR	ROQFFRLVFT	PINARAAAHG	NLPVSDAFFK	LPRQRFHLFR
	70	80	90	100	110	120
m295.pep	RYDVVFQIAA	HLHGCRAQFR	QPRRIRLRLC	QRTARQSSGGR	TDQAADFQIT	VQRFRRQPRI
a295	RHQVVFQIAA	HLHGCRAQFR	QPRRIRLRLC	QRTARQSSGGR	TDQAADFQIT	VXRFFRQPRI
	130	140	150	160	170	180
m295.pep	RQKQRHTRAP	AFPHQVGFDF	GFHQNAEHR	AVFAQKLPYPR	FFVIRKIAAL	RIGKQNLRF
a295	RQKQRHTRAP	AFPHQVGFDF	GFHQNAEHR	AVFAQKLPYPR	FFVIRKIAAL	CIRKQNLRF
	190	200	210	220	230	240
m295.pep	PPRRGHLRHQ	QRRIGKTL	PQLAYQGL	GGTRFSDR	NGVYPN	RAGNGIRIRL
a295	PSRRGHLRHQ	QRRIGKTL	PQLAYQGL	GGTRFSDR	NGVYPN	RAGNGIRIRL
	250	260	270	280	290	
m295.pep	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	XTVQTA	FRQRNQISX
a295	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	RTVRTA	FRQRNQISX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1 ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
```

```

51  GCTTGCCGTT TCGATTATTC TGGTGtcgGC GGCATACATT Gcttcgacag
101 aggggaccga ggcggtcaga ccgcAGCGCG Tggaacaaa ACTGCCGCCG
151 CTGTCTTGGg gcggcaacgg CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGgcatt tGCGTGCCGA CCAGTCGGTT CATGTTTGG TCGGCGGCGA
351 CGGCAGTGCG CGCGAAGTGC AGTTTTttac CGACGAAGAC GGCAGGCGCA
401 aTctGGTCGC TTTGGAAAAA AAAGGCGGCA TATGGCGCGC GTCGGCTTCT
451 GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 CAAGGTGGCG GCGGGCGATA TTTGGCGCG GGAAGTTGTC AAGGGCGGCA
701 CAACCCATCA GCGTTCCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCgaG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCA
1051 CAAGGCAATG TGCAGCGCGG CGAGGTCATC GGTTTTGTG GTTCGACAGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGGAATT GACGCGGGC
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

```

g297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PORVEQKLPP
51  LSWGNGVQQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGS A REVQFTDED GERNLVALEK KGGIWRRSAS
151 DADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRELSLGI AGRFSLDGLK
201 EGDVRLLYD SLYFHQQOVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNYDEDGRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGTTPVRA SADGVITFKG RKGyGNAVM IRHANGVETL YAHLSAFSQA
351 QGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPVNPVS ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

```

m297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
51  GCTTGCCGTT TCGATTATTT TGGTGTCGCG GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGAACAAAAA TCTCCGCCCG
151 CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCAGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TGCCTGCCGA CCAGTCGGTT CATGTTTGG TCGGCGGCGA
351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCAGGCGCA
401 ATCTGGTCGC TTTGGAAAAG AAAGGCGGCA TATGGCGCGC GTCGGCTTCT
451 GAGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTGGCGCG TGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCG
1051 GAAGGCAATG TGCAGCGCGG CGAGGTCATC GGTTTTGTG GTTCGACCGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGGAATT GACGCGGGC
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

```

m297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERVR PORVEQNLPP
51  LSWGSGVQQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGS A REVQFTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRELSLGI AGRFSLDGLK

```

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201 EGDVRLMYD SLYFHGQQA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG  
 251 GNYDDEGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY  
 301 AAPQGTVPRA SADGVITFKG RKGyGNAVM IRHANGVETL YAHLSAFSQA  
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA  
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD \*

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERVPRQVEQNLPPLSWGSGVQT					
g297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTEGTERVPRQVEQKLPPLSWGNGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA					
g297	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTTDEDGERNLVALEKKGGIWRRSASEADMKVLPPLRSVVVKTSARGSLARAEVVP					
g297	REVQFFTTDEDGERNLVALEKKGGIWRRSASDADMKVLPPLRSVVVKTSARGSLARAEVVP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQQAAGDILAAEVVKGTRHQAFY					
g297	EIRESLSGIFAGRFSLDGLKEGDAVRLLYDSLYFHGQQAAGDILAAEVVKGTTHQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGGNYDDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGGNYDDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTVPVASADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTVPVASADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVGSTGRSTGPHLHYEARINGQPVNPVSVVALPTPELTQADKAFAAQKQKADALLARLR					
g297	GFVGSTGRSTGPHLHYEARINGQPVNPVSVVALPTPELTQADKAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1 ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC  
 51 GCTTGCCGTT TCGATTATTT TGGTGTCGGC GGCATACATT GCTTCGACAG  
 101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAAACAAA ACTGCCGCCG  
 151 CTGTCTTGGG GCGGCAGCGG TGTTCAGACG GCATATTGGG TGCAGGAGGC  
 201 GGTGCAGCCA GGCGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG  
 251 CGCGGGACGA AATTGCCCGA ATAACGAAA AATATGGCGG CGAAGCCGAT  
 301 TTGCGGCATT TCGTGCCGA CCAGTCGGT CATGTTTGG TCGCGGCGA  
 351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCGAGCGCA  
 401 ATCTGGTCGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT  
 451 GAGGCGGATA TGAAGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC  
 501 GTCGCGCGC GGTTCGCTGG CGCGGCGGCA AGTGCCCGTC GAAATTCGCG

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551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGCG
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACTTGCGCGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTACGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TCGCGGCGCG CGAGGTCATC GGTTTTGTCG GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GGCGCGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

```

a297.pep
1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTVRV PQRVEQKLPP
51 LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGGA REVQFTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQQVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
251 GNYDEDGRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGPVRA SADGVITFKG RKGyGNAVM IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPNVPSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/a297 99.3% identity in 430 aa overlap

```

          10      20      30      40      50      60
m297.pep  MAVFPLSAKHKRYALRALAVSIILVSAAYIASTERTVRVPQRVEQNLPLPSWGGSGVQT
          |||
a297      MAVFPLSAKHKRYALRALAVSIILVSAAYIASTERTVRVPQRVEQKLPLPSWGGSGVQT
          10      20      30      40      50      60

          70      80      90      100     110     120
m297.pep  AYWVQEAQVPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA
          |||
a297      AYWVQEAQVPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA
          70      80      90      100     110     120

          130     140     150     160     170     180
m297.pep  REVQFTDEDGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEVPV
          |||
a297      REVQFTDEDGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEVPV
          130     140     150     160     170     180

          190     200     210     220     230     240
m297.pep  EIRESLSGIFAGRFSLDGLKEGDVRLMYDSLYFHGQQVAAGDILAAEVVKGGTRHQAFY
          |||
a297      EIRESLSGIFAGRFSLDGLKEGDVRLIYDSLYFHGQQVAAGDILAAEVVKGGTRHQAFY
          190     200     210     220     230     240

          250     260     270     280     290     300
m297.pep  YRSDKEGGGGNYDEDGKVLQEKGGFNIEPLVYTRISSPFGyRMHPILHTWRLHTGIDY
          |||
a297      YRSDKEGGGGNYDEDGRVLQEKGGFNIEPLVYTRISSPFGyRMHPILHTWRLHTGIDY
          250     260     270     280     290     300

          310     320     330     340     350     360
m297.pep  AAPQGPVRA SADGVITFKGRKGyGNAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
          |||
a297      AAPQGPVRA SADGVITFKGRKGyGNAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
          310     320     330     340     350     360

```



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	370	380	390	400	410	420
m297.pep	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298.seq

```

1 ATGAAAACT TTCTTCCCT TTTCGCCTCC ATACTGATGT CTGCCCTGAT
51 TGCCGTGTGG TTCAGCCAAA ACCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCCTG TCCGGCGAAA cgcgcgcac ggCTCAAGAC GGCAGTTCGG
251 CAGATATGCC GCCTGAAGCC GCCGCATCCG AAGCCGCCCC GCCGCGCGGC
301 GGAACAGAAT GGAACAAGG CACCGAAGCC GCCGCCGTCC GCAGCGCGCA
351 CAAAGTCTTT TTCGCCGAG ATTCTGCTGAT GCAGGGCGTT GCGCTTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCTTGAAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCC GAACGACCCG TGGGATTTC CCGTCGGCAA ACGTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCGCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAATGCTTT CGGAACACTT GAAAGGCAA ATCATCTGA TTCCCAACGC
801 GCAAACACTG AGCGGCGGGA AAGgccGCTA CACGATTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAATAATA ATGGAATAA TCGTTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298.pep

```

1 MKNFLSLFAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51 SGAALQENAY ALSDGIKTFL SGETPPTAQD GGSADMPPEA AASEAAPPA
101 GTEWKQGETA AAVRSGDKVF FAGDSLMOGV APFVKSLKQ QYGI SANLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201 KFASDEWAQE YLKRVDRIE AAHTRVQVV WLGI PYMKKV KLDGQMR YLD
251 KLLSEHLKGI ILIPTAQL SGGKGRYVDS VNVNGKPVRY RSKDGIHFTA
301 EQQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298.seq

```

1 ATGAAAACT TTCTTCCCT TTCTCCTCC ATACTGATGT CTGCCCTGAT
51 TGCCGTGTGG TTCAGCCAAA ACCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCGGAC GGCTCAAGAC GGCAGTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCCGTCCC TCAAACCGGT
301 GAAACAGAAT GGAACAAGA CACCGAAGCC GCCGCCGTCC GCAGCGCGCA
351 CAAAGTCTTT TTGTGCGCG ACTCGCTGAT GCAGGGCGTT GCCCCTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGCAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCGCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAATGCTTT CGGAACATTT GAAAGGCAA ATCATCTGA TTCCACCAC
801 GCACACCCTG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGCAATAATA ATGGAATAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep

```
1 MKNFLSLFSS IILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51 SGAALQENAY ALSDGIKAPL SGETPPTAQD GGSADMPSEA AASEAVPQTG
101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL
201 KFASDEWAQE YLKRVDRIE AAHTRVQVW WLGIPYMKKA KLDGQMRVLD
251 KLLSEHLKKG IILPTHTL SGGKDRYTDV VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*
```

m298/g298 94.8% identity in 327 aa overlap

m298.pep	10	20	30	40	50	60
	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
g298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
m298.pep	70	80	90	100	110	120
	ALSDGIKAPLSGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
g298	ALSDGIKTFLSGETPPTAQDGGSDMPPEAAASEAAPAGTEWKQGTETAAAVRSGDKVF					
	70	80	90	100	110	120
m298.pep	130	140	150	160	170	180
	FVGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	FAGDSLMOGVAPFVQKSLKQQYGIESANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
m298.pep	190	200	210	220	230	240
	LAVFLGPNDPWDFPVGKLYLKPFASDEWAQEYLKRVDRIEAAHTRVQVWVLGIPYMKKA					
g298	LAVFLGPNDPWDFPVGKRYLKPFASDEWAQEYLKRVDRIEAAHTRVQVWVLGIPYMKKV					
	190	200	210	220	230	240
m298.pep	250	260	270	280	290	300
	KLDGQMRVLDKLLSEHLKKGKIIILPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
g298	KLDGQMRVLDKLLSEHLKKGKIIILPTAQTLSGGKGRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
m298.pep	310	320				
	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	EGQKLLAEKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq

```
1 ATGAAAACT TTCTTCCCT TTTGCCTCC ATACTGATGT CTGCCCTGAT
51 TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCCTACGG ATGGTGGCGG
151 AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GCGGTTCCGG
251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAAGTGGC
301 GAAACAGAAT GGAAACAAA CACCGAAGCC GCCGCCGTCC GAACAGGGGA
351 CAAAGTCTTT TTCGCCGCG ACTCGCTGAT GCAGGCGGTT GCACCTCTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGCTGTC CTACCCCTCA TTCTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGAAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT
551 TCCTCGGTCC GAACGACCCG TGGGATTTC CCGTTGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
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751  AAACGCTTT  CGGAATATTT  GAAAGGCAAA  ATCATCCTGA  TTCCCACCGC
801  GCACACCCTG  AGCGGCGGGA  AAGACCGCTA  CACCGACTCC  GTCAACGTCA
851  ACGGCAAACC  CGTCCGCTAC  CGCAGCAAGG  ACGGCATACA  CTTTACCGCC
901  GAAGGACAAA  AACTGCTGGC  GGCAAAAATA  ATGGAAAAAA  TCGTTTTTGA
951  ACCAAGTACG  CAACCATCAA  GTACACAGCC  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
1  MKNFLSLFAS  ILSALIAVW  FSQNPINAYW  QQTYHRNSPL  EPLAAYGWWR
51  SGAALQENAY  ALSDGIKAF  LSGETPPTAQD  GGSADMPSEA  AAPETAPQTG
101 ETEWKQNTA  AAVRTGDKVF  FAGDSLMOGV  APFVQKSLKQ  QYGIESVNLS
151 KQSTGLSYPS  FFDWPKTIEE  TLKKHPEISV  LAVFLGPNDP  WDFPVGKRYL
201 KFASDEWAE  YLKRVDRIE  AAHTHYVQVW  WLGIPLYMKA  KLDGQMRYL
251 KLLSEYLGK  ILIPTAHTL  SGGKDRYTD  VNVNGKPVRY  RSKDGIHFTA
301 EGQKLLAAKI  MEKIVFEPST  QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFESSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFLSGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAFLSGETPPTAQDGGSDMPSEAAAPETAPQTGETEWKQNTAEEAVRTGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDLSMQGVAPFVQKSLKQYQYIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDLSMQGVAPFVQKSLKQYQYIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWFDFPVGKLYLKFADEWAEYLKRVDRIEAAHTRVQVWVWLGIPLYMKA					
a298	LAVFLGPNDPWFDFPVGKRYLKFADEWAEYLKRVDRIEAAHTHYVQVWVWLGIPLYMKA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLKLLSEHLKGKILIPHTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
a298	KLDGQMRYLKLLSEYLGKILIPHTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
a298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
1  ATGAACCCCA  AACACTTCAT  CGCATTTTCC  GCCCTGTTCC  CCGCCACGCA
51  GGCGAAGCC  CTGCCCCTCG  CCTCCGTCAG  CCCCAGACCC  GTTACCGTTT
101 CCCCCTCCG  CCCCTACACC  GATACAAACG  GGCTGCTGAC  CGACTACGGC
151 AACGCCGCC  CCTCGCCTTG  GATGAAAAAA  CTCGATCCG  TCGCACAAGG
201 CAGCGCGAG  GCCTTCCGCA  TCCTGCAAA  CGGCGACTCG  CATACCGCCG
251 GCGACTTCT  TACCGACGCC  CTGCGCAAA  GCCTGCAAAA  AACATGGGGC
301 GACGGCGCA  TAGGCTGGT  TTACCCCGCC  AACGTCAAAG  GGCAGCGCAT
351 GCGGCGCGT  CGTCACAGCG  GCAACTGGCA  AAGCTTCACC  AGCAGGAACA
401 ATACCGGAGA  TTTCCCCTC  GCGGCGATCC  TCGCCCAAC  CGGCGCGGC
451 GCGGCGATGA  CCCTGACCG  GTCTGACGG  AAAACCGGCA  AACAGCGCGT

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```

501 TTCCCTGTTT GCCAAACCGC TGCTCGCCGA ACAAACCTTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCTGGCCAT ACAGACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTGACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCT TTCAACAACA ACATCGACAT TGCCGATACC GAACAAAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCCGC CGCCGGCATC
901 CTCATCATCG GCGCGCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACGCGCCCC GTCTCTCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCC
1001 CCCGTCAGGG GCAGACGATG TTTTGGTCTT GGCAAAACGC AATGGGCGGC
1051 ATATGCAGCA TGAAAACTG GCTCAACCAA GGATGGGCGC CCAAGACGG
1101 CGTACACTTC TCCGCCAAG GCTACCGCG CGCGGCGGAA ATGCTTGCCG
1151 ACAGCCTCGA AGAACTCGTC CGCGCGCGC CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1248; ORF 299.ng>:

g299.pep

```

1 MNPKEHIAFS ALFAATQAEA LPVASVSPDT VTVSPSAPYT DTNGLLTDYG
51 NAAASPWMKK LRSVAQGSSE AFRILQIGDS HTAGDFFTD LKRRLQKTWG
101 DGGIGWVYPA NVKGQMAAV RHSGNWQSFT SRNNTGDFPL GGILAQTGSG
151 GGMTLTASDG KTGKQVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201 AALPLAIQTE MPWDIGFINI ENPAGGITS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGRTP VLLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKNWLNQ GWAAKDGVHF SAQGYRRAE MLADSLLELV RAAAIQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1249>:

m299.seq

```

1 ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTCC CCGCCACGCA
51 GGCAGAAGCC CTACCTGTGC CCTCCGTGAG CCTCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAA CTCCAATCCG TCGCACAAGG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAAT CGGCGACTCG CATACGCGCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTGCAAAA AACTTGGGGC
301 GACGCGCGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GCGCGCGGTC CGGCACAACG GTAAGTGGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCTCGTC GCGCGCATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCTTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTCG CCCAAACCGG CGCCGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCT TTCAACAACA ACATCGACAT TGCCGACACC GAACAAAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCTGC CGCCGGCATC
901 CTCATCATCG GCGCACCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCC
1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC CATGGGCGGC
1051 ATATGCAGCA TGAAAACTG GCTCAACCAA GGATGGGCGC CCAAGACGG
1101 CGTACACTTC TCCGCCAAG GCTACCGCG CGCGGCGGAA ATGCTGCGCG
1151 ACAGCCTCGA AGAACTCGTC CGCTCGCTG CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1250; ORF 299>:

m299.pep

```

1 MNPKEHIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
51 NASASPWMKK LQSVAGGSSE TFRILQIGDS HTAGDFFTDS LKRRLQKTWG
101 DGGIGWVYPA NVKGQMAAV RHNGNWQSLT SRNNTGDFPL GGILAHGTSG
151 GGMTLTASDG IASKQVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201 AALPLTIHTE MPWDIGFINI ENPAGGITS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGRTP VRLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKNWLNQ GWAAKDGVHF SAKGYRRAE MLADSLLELV RAAAIQ*

```

m299/g299 95.5% identity in 397 aa overlap

```

10 20 30 40 50 60
m299.pep MNPKEHIAFSALFAATQAEALPVASVSLDTVTVPSPAPYDTNGLLTDYGNASASPWMKK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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g299	MNPKHFIAFSALPAATQAEALPVASVSPDVTVTSPSAPYTDNGLLTDYGNAASPWMKK
	10 20 30 40 50 60
m299 . pep	LQSV AQSGSETFRILQIGDSHTAGDFFDTS LRKRLQKTWGDGGIGWVYPANVKGQRM AAV
g299	LRSV AQSGSEAFRILQIGDSHTAGDFFDTS LRKRLQKTWGDGGIGWVYPANVKGQRM AAV
	70 80 90 100 110 120
m299 . pep	RHNGNWQSLTSRNN TGDFPLGGILAHTGSGGSMILTASDGIASKQRVSLFAKPLLA EQTL
g299	RHSGNWQSFTSRNN TGDFPLGGILAHTGSGGSMILTASDGTGKQRVSLFAKPLLA EQTL
	130 140 150 160 170 180
m299 . pep	TVNGNTVSANGGGWQVLDTG AALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
g299	TVNGNTVSANGGGWQVLDTG AALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299 . pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADEQKWLDTVRQIRDSLPAAGI
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299 . pep	LIIGAPESLKNLTGVCGRTPVRLTEVQQMORRVARQGQTMFWSWQNAMGGICSMKNWLNQ
g299	LIIGAPESLKNLTGVCGRTPVRLTEVQQMORRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299 . pep	GWA AKDGVHFSAGYRRAAEMLADSL EELVRSAAIRQX
g299	GWA AKDGVHFSAGYRRAAEMLADSL EELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

a299.seq

1	ATGAACCCCA	AACACCTCAT	CGCATTTTCC	GCCCTATTCC	CCGCCACGCA
51	GGCAGAAGCC	CTACCTGTCT	CCTCAGTCAG	CCTCGACACC	GTTACCGTTT
101	CCCGTCCGCG	CCCCTACACC	GATACAAACG	GGCTGCTGAC	CGACTACGGC
151	AACGCCTCCG	CCTCGCCTTG	GATGAAAAAA	CTCCAATCCG	TCCGACAAGG
201	CAGCGGCGAG	ACCTTCCGTA	TCCTGCAAAT	CGGCGACTCG	CATACCGCCG
251	GCGACTTCTT	TACCGACAGC	CTGCGCAAAC	GCCTACAAAA	AACTTGGGGC
301	GACGGCGGCA	TAGGCTGGGT	TTACCCCGCC	AACGTCAAAG	GGCAGCGCAT
351	GGCGGCCGTC	CGGCACAACG	GTAAC TG GCA	AAGCCTCACC	AGCAGGAACA
401	ACACCGGAGA	CTTCCCGCTC	GGCGGCATCC	TCGCCCACAC	CGGCAGCGGC
451	GGCAGCATGA	CCCTGACCGC	ATCGGACGGC	ATAGCAAGCA	AGCAGCGCGT
501	TTCCCTGTTT	GCCAAACCCC	TGCTTGCCGA	ACAAACCCCTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	GCGGCACTGC	CCCTGACCAT	ACACACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATC	GAAATCCCG	CCGCGCGCAT	TACCGTTTCC	GCGATGGGCA
701	TCAACGGCGC	ACAATTAACC	CAGTGGTCGA	AATGGCGTGC	CGACCGTATG
751	AACGACCTTG	CCCAAACCGG	CGCCGATCTA	GTATCCTTG	CCTACGGTAC
801	CAACGAAGCC	TTCCGGCGACA	ACATCGACAT	TGCCGATACC	GAACAGAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCGCGACA	GCCTACCTGC	CGCCGGCATC
901	CTCATCATCG	GCGCGCCCGA	ATCCCTGAAA	AACACGCTCG	GCGTATGCGG
951	CACACGCCCC	GTCCGCCTGA	CCGAAGTCCA	ACAGATGCAG	CGGCGCATCG
1001	CCCGTCAGGG	GCAGACGATG	TTCTGGTCTT	GGCAAAACGC	GATGGGCGGC
1051	GTTTGACGCA	TGAAAACTG	GCTCAACCAC	GGATGGGCCG	CCAAAGACGG
1101	CGTACACTTT	TCCGCCAAAG	GCTACCAACG	GTCGGCGGAA	ATGCTCGCCG
1151	ACAGCCTCGA	AGAACTCGTC	CGCTCCGCTG	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
  1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
 51  NASASPWMKK LQSVAGGSSE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101  DGGIGWVYPA NVKGQORMAAV RHNGNWQSLT SRNNTGDFPL GGILAHGTSG
151  GSMTLTASDG IASKQRVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201  AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251  NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRQ IRDSLPAAGI
301  LIIGAPESLK NTLGVCGRTP VRLTEVQQMQ RRIARQGQTM FWSWQNAMGG
351  VCSMKNWLNH GWAADGVHF SAKGYQSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

m299.pep	10	20	30	40	50	60
	MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
a299	MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
	10	20	30	40	50	60
m299.pep	70	80	90	100	110	120
	LQSVAGGSGETFRILQIGDSHTAGDFFTDSLRLQKTWGDGGIGWVYPANVKQORMAAV					
a299	LQSVAGGSGETFRILQIGDSHTAGDFFTDSLRLQKTWGDGGIGWVYPANVKQORMAAV					
	70	80	90	100	110	120
m299.pep	130	140	150	160	170	180
	RHNGNWQSLTSRNNTGDFPLGGILAHGTSGGSMTLTASDGIASKQRVSLFAKPLLAETL					
a299	RHNGNWQSLTSRNNTGDFPLGGILAHGTSGGSMTLTASDGIASKQRVSLFAKPLLAETL					
	130	140	150	160	170	180
m299.pep	190	200	210	220	230	240
	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
a299	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
	190	200	210	220	230	240
m299.pep	250	260	270	280	290	300
	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI					
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIDIADTEQKWLDTVRQIRDSLPAAGI					
	250	260	270	280	290	300
m299.pep	310	320	330	340	350	360
	LIIGAPESLKNTLGVCGRTPVRLTEVQQMQRRVARQGQTMFWSWQNAMGGICSMKNWLNQ					
a299	LIIGAPESLKNTLGVCGRTPVRLTEVQQMQRRRIARQGQTMFWSWQNAMGGVCSMKNWLNH					
	310	320	330	340	350	360
m299.pep	370	380	390			
	GWAADGVHFSAGYRRAEMLADSLEELVRSAAIRQX					
a299	GWAADGVHFSAGYQRSAEMLADSLEELVRSAAIRQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
  1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
 51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101  TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151  GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGTCC
201  TGTGGGGCG AAAGGACGTG CCGATGACGG TTTGATTAC GTTGTCAGCC
251  TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301  TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGGCGT
```

```

351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCGTC ATCTTTTATT CGCTCGGCCG CCATCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAA
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACAGG TTTTATATGG
701 CAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGT CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCCTGAAA CAGGATTGGT
951 TGCCGGTTTC CCGTTTTTAA AATCGATTGT TGTTTTTAT TTCTGTGTGT
1001 TTGCGCTGCC GGGCATTGTT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTTCGA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGCGGCAG TGTGTTGTTT ATCGGTTTAA TTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCTT ATGCTGATGT TGGCCGGCTA CGCGCCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCACGGTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATT CTATGATGTT GCCGTATTCC
1501 GCTTTCTTCT TAATTGCATG GATCGCCTTA TTCTGCATT GGGTATTTGT
1551 TTTGGGTCTG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1  MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTKSPRK LTTFMVVFTG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGAVFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPQ
451 VIQAAYRIGD SVTNIITPMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLVGL PVGPPTPTFY PVP*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTTACGCTT TTTATTATT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCCGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTGTTGTGC AAAGGACGTG CCGATGACGG TTTGATTTAC ATGTCTAGCC
251 TGCTCAATGC CGACGGTTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTTATT CCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAAATC ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCTG
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGATTGG TTATTTTGT ACTGAAAAA TCGTCGAACC GCAATTGGGC
751 CTTTATCAAT CAGATTGTG ACAAGAAGAA AAAGACATTC GGCATTCCAA
801 TGAAATCACG CCTTTGGAAT ATAAAGGATT AATTGGGCT GCGGTGGTGT
851 TTGTTGCCTT ATCCGCCCTA TTGGCTTGA GCATCGTCCC TGCCGACGGT
901 ATTTTGCCTC ATCCTGAAAC AGGATTGGT TCCGGTTCGC CGTTTTTAAA
951 ATCGATTGTT GTTTTTATTT TCTTGTGTT TGCATGyCG GGCmTTGTTT
1001 ATGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

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1051 ATGCCCGAAT CGATGAGTAC TCTGGsGCTT TmTTTGswCA kcATCTTTTT
1101 TGCCGCACAG TTGTTCGCAT TTTTAAATG GACGAATATT GGGCAATATA
1151 TTGCCGTAA AGGGCGCAGC TTCTTAAAG AAGTCGGCTT GGGCGGCAGC
1201 GTGTTGTTTA TCGGTTTTAT TTTAATTGT GCTTTTATCA ATCTGATGAT
1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAAC TCGCCCGATT TTCGTCCCTA
1301 TGCTGATGTT GGCCGGCTAC GCGCCGAAG TCATTCAAGC CGCTTACCGC
1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTTCGG
1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GCGGTGGGTA
1451 CGCTGATTTC TATGATGTTG CCGTATTCCG CTTTCTTCTT GATTGCGTGG
1501 ATTGCCTTAT TCTGCATTG GGTATTTGTT TTGGGCTGC CCGTCGGTCC
1551 CGGCGCGCCC ACATTCTATC CCGCACCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

m302.pep

```

1 MHSIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVPDPRVGA KGRADDGLIY IVSLLNADGF IKILTHTVKN
101 FTGFAPLGTV LVSL LGVIA EKSLISALM RLLTKSPRK LTFMVVFTG
151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 STIDPLLACI THQAAVVGPE ANWFFMVAST FVIALIGYFV TEKIVEPQLG
251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVVVALSAL LAWSIVPADG
301 ILRHPTGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA
351 MAESMSTLXL XLXIXFFAAQ FVAFFNWTNI GQYIAVKGAT FLKEVGLGGS
401 VLFIGFILIC AFINLMIGSA SAQWAVTAPI FVPMMLLAGY APEVIQAAAYR
451 IGDSVTNIIT PMMSYFGLIM ATVIKYKKA GVGTLISMML PYSAFFLIAW
501 IALFCIWVVFV LGLPVGPGAP TFYPAP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng) from *N. gonorrhoeae*:

m302/g302

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTDTRDGRFLRTVEWLG NMLPHPVTLFII FIVLLLIASAVGAYFGL					
g302	MHSIYFFKEKQMSQTDARRSGRFLRTVEWLG NMLPHPVTLFII FIVLLLIASAVGAYFGL					
	10	20	30	40	50	60
m302.pep	SVPDPRVGA KGRADDGLIYIVSLLNADGFI KILTHTVKNFTGFAPLGTVLVSL LGVIA					
g302	SVPDPRVGA KGRADDGLIHVVSLLDADGLIKILTHTVKNFTGFAPLGTVLVSL LGVIA					
	70	80	90	100	110	120
m302.pep	EKSGLISALMRLLLTKSPRKLTTFMVVFTGILSNTASELGYVVLIPLSAI IFHSLGRHPL					
g302	EKSGLISALMRLLLTKSPRKLTTFMVVFTGILSNTASELGYVVLIPLSA VIFHSLGRHPL					
	130	140	150	160	170	180
m302.pep	AGLAAAFAGVSGGYSANLFLSTIDPLLACI THQAA-----VVGPEANWFFMVASTFVI					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQAAQIIHPDYVVGPEANWFFMAASTFVI					
	190	200	210	220	230	240
m302.pep	ALIGYFVTEKIVEPQLG PYQSDLSQEEKDIRHSNEITPLEYKGLI WAGVVVVALSALLAW					
g302	ALIGYFVTEKIVEPQLG PYQSDLSQEEKDIRHSNEITPLEYKGLI WAGVVVVALSALLAW					
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEPQLG PYQSDLSQEEKDIRHSNEITPLEYKGLI WAGVVVVALSALLAW					
g302	ALIGYFVTEKIVEPQLG PYQSDLSQEEKDIRHSNEITPLEYKGLI WAGVVVVALSALLAW					
	250	260	270	280	290	300
	300	310	320	330	340	350



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m302.pep  SIVPADGILRHPETGLVSGSPFLKSI VVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      SIVPADGILRHPETGLVAGSPFLKSI VVFIFLLFALPGIVYGRITRSLRGEREVVNAMAE
          310      320      330      340      350      360

          360      370      380      390      400      410
m302.pep  SMSTLXLXLXIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGILICAFI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGAFLKEVGLGGSVLFIFIGILICAFI
          370      380      390      400      410      420

          420      430      440      450      460      470
m302.pep  NLMIGSASAQWAVTAPIFVPMMLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      NLMIGSASAQWAVTAPIFVPMMLAGYAQVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          430      440      450      460      470      480

          480      490      500      510      520
m302.pep  IKYKKDAGVGTLSMMLPYSAFFLI AWIALFCIWVFLGLPVGPAPTFFYPAPX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      IKYKKDAGVGTLSMMLPYSAFFLI AWIALFCIWVFLGLPVGPPTPTFFYPVPX
          490      500      510      520      530

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTCAC GTTGTCAGCC
251 TGCTCGATGC TGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGCGCT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 TTCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGCTCTGG
551 CTGCGGCTTT CGCGCGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCT TAGGCCCTGA AGCCAACCTG TTTTTTATGG
701 TAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTGGGCG TGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCTGAAA CAGGATTGGT
951 TTCCGGTTTC CCGTTTAA AATCAATTGT TGTTTTATT TTCTTGTGT
1001 TTGCACTGCC GGGCATTGTT TATGGCCGGG TAACCCGAAG TTTGCGCGG
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTAAATT
1151 GGACGAATAT TGGCAATAT ATTGCCGTTA AAGGGCGCAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTGTTT ATCGGTTTAT TTTTAAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCCCGGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCACGGTG ATCAAAATCA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATT GGGTATTTGT
1551 TTTGGGCTG CCCGTCGGTC CCGGCGGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1  MHSIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLISALM RLLTKSPRK LTTFMVFTG

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151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMEE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASQAQ WAVTAPIFVP MMLLAGYAPE
451 VIQAAYRIGD SVTNIITPM SYFGLIMATV IKYKKGAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

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m302/a302 96.1% identity in 533 aa overlap

```

          10      20      30      40      50      60
m302.pep  MHSIYFFKEKQMSQTDQDGRFLRTVEWLGNNMLPHPVTLFIIFIVLLLIASAVGAYFGL
          |||||||
a302      MHSIYFFKEKQMSQTDQDGRFLRTVEWLGNNMLPHPVTLFIIFIVLLLIASAAGAYFGL
          10      20      30      40      50      60

          70      80      90     100     110     120
m302.pep  SVPDPRPVGAKGRADDGLIYIVSLLNADGFIKILHTVKNFTGFAPLGTVLVSLGVLGIA
          |||||||
a302      SVPDPRPVGAKGRADDGLIHVVSLLDADGLIKILHTVKNFTGFAPLGTVLVSLGVLGIA
          70      80      90     100     110     120

          130     140     150     160     170     180
m302.pep  EKSGLSALMRLLLTKSPRKLTFMVVFTGILSNTASELGYVVLIPLSAIIHSLGRHPL
          |||||||
a302      EKSGLSALMRLLLTKSPRKLTFMVVFTGILSNTASELGYVVLIPLSAIIHSLGRHPL
          130     140     150     160     170     180

          190     200     210     220     230
m302.pep  AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI
          |||||||
a302      AGLAAAFAGVSGGYSANLFLGTLIDPLLAGITQQAQIIHPDYVVGPEANWFFMVASTFVI
          190     200     210     220     230     240

          240     250     260     270     280     290
m302.pep  ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVVALSALLAW
          |||||||
a302      ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVVALSALLAW
          250     260     270     280     290     300

          300     310     320     330     340     350
m302.pep  SIVPADGILRHPETGLVSGSPFLKSIVVFI FLLFALXGXVYGRVTRSLRGEQEVVNAMEE
          |||||||
a302      SIVPADGILRHPETGLVSGSPFLKSIVVFI FLLFALPGIVYGRVTRSLRGEQEVVNAMEE
          310     320     330     340     350     360

          360     370     380     390     400     410
m302.pep  SMSTLXLXLIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI
          |||||||
a302      SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI
          370     380     390     400     410     420

          420     430     440     450     460     470
m302.pep  NLMIGSASQAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          |||||||
a302      NLMIGSASQAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          430     440     450     460     470     480

          480     490     500     510     520
m302.pep  IKYKKGAGVGTLSMMLPYS AFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX
          |||||||
a302      IKYKKGAGVGTLSMMLPYS AFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX
          490     500     510     520     530

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

g305.seq

```

1 ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
101 GCAATCTGAT TGGTTTTTAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CGGTTTTTGGC GGTAGTGTTT GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GACAAACAAA TCAAAGAGTA TCTGTTTAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GTGTTGCCCA AGTGTTTGCA CTGGTTCCGG GTACGTCCCG
501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGCCCG TCCGATGAT GGTTCAGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATAGGCT TTATTGCCGC TTTTGTTTCC GGTTCGGTAG
701 CGGTTAAAGC ACTGCTGAAG TTGTTTCCA AGAAAACTA TATCCCGTTT
751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGGTTGTC
801 GGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep

```

1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51 QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAIAP IPAAVMGLLF
101 QKQIKEXLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TVMGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
251 AYYRIVFGIV IILWLSGWI SWE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)

```

1 AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
101 GCAATCTGAT TGGTTTTTAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CAGTTTTTGGC GGTAGTGTTT GAATACCGGC AACGTTTCAG
201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GGCawACAAA TCAAAGAGyA TCTGTTTAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTtyTG GrCGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GCGTTGCCCA AGTGTTTGCA CTGGTTCCGG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGAAAAA
551 CTGCGACAGA ATTCTCGTTT TTCTTGCGTG TGCCGATGAT GGTTCGCCCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTTCCTA GGCTTGGTAG
701 CGGTAAAAGC GTTGCTGAGG TTTGTTTCGG GTAC...

```

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)

```

1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51 QLGAVLAVVF EYRQRFNSVL HGLGKDRKAN RFVLNLAIAP IPAAVMGLLF
101 GXQIKEXLFN PLSVAVMLVL XGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHNKVFIEIAIQLGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHNKVFIEIAIQLGAVLAVVF					
	10	20	30	40	50	60

700

	70	80	90	100	110	120
g305.pep	BYRQRF	SNVLHG	VGKDRK	ANRFVL	NLAIAFI	PAAVMGL
	70	80	90	100	110	120
m305	BYRQRF	SNVLHG	LGLKDR	KANRFVL	NLAIAFI	PAAVMGL
	70	80	90	100	110	120
g305.pep	GGFFIL	WVEKRQ	SRAEPK	IAVDAL	RPIDAL	MIGVAQ
	130	140	150	160	170	180
m305	XGFXIL	WVEKRQ	SRAEPK	IAVDAL	RPIDAL	MIGVAQ
	130	140	150	160	170	180
g305.pep	ERKTATE	FSFFLA	VPMVA	AATAYD	VLDKHY	RFFTLH
	190	200	210	220	230	240
m305	ERKTATE	FSFFLA	VPMVA	AATAYD	VLDKHY	RFFTLH
	190	200	210	220	230	240
g305.pep	FVSKKN	YIPFAY	YRIVFG	IVIIIL	WLSGW	ISWEX
	250	260	270			
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1  ATGGATTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTCG
101 GCAATCTGAT TGATTTTCAC AGCAATCACA AGGTTTTGA AATTACCATC
151 CAGCTCGGTG CGGTTTGGC GGTAGTGTG GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGG GCTGTGTTC
301 GGCAAACAAA TCAAAGAGTA TCTGTTTAA CCCTTGAGT TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTT TTATTTTGT GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAATTTGTC GATGTTGATG CATGCGTCC GATTGATGCG
451 TTGATGATCG GCGTTGCCCA AGTGTGTCGA CTGGTCCAG GTACGTCGCC
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTGGCCG TTCCGATGAT GGTGTCAGCA
601 ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTGTTTCA GGCTTGGTGG
701 CGGTCAAAGC GTTGCTGAGG TTTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVLAVVF EYRQRF SNVL HGVGKDRKAN RFLNLAIAF IPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFFILWVEK RQSRAPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKAL	MMGLVEGFTE	FLPISSSTGHL	IVFGNLIDFH	SNHKVFEI	IAIQLGAVLAVVF
	10	20	30	40	50	60
a305	MDFLIVLKAL	MMGLVEGFTE	FLPISSSTGHL	IVFGNLIDFH	SNHKVFEI	IAIQLGAVLAVVF
	10	20	30	40	50	60
m305.pep	EYRQRF	SNVLHG	LGLKDR	KANRFVL	NLAIAFI	PAAVMGL
	70	80	90	100	110	120
a305	EYRQRF	SNVLHG	VGKDRK	ANRFVL	NLAIAFI	PAAVMGL

701

	70	80	90	100	110	120
m305.pep	130	140	150	160	170	180
	XGFXILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
a305	GGFFILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
	130	140	150	160	170	180
m305.pep	190	200	210	220	230	240
	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAFVSGLVAVKALLR					
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

g306.seq

```

1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCGGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAGGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGGCGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TGCGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAGA
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGCAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAGA  AAATGAAAAA  CTTTGGGCAA  GCGGGAAGCC  AACGCATTAT
651 CTGCAAATGG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTTCCGA  AGTGGTCGGC  TATCAGCGCG
751 GACATAAAAC  GCTTTACCGC  GTGCAAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

g306.pep

```

1  MFMNKSQSG  KGLSGFFFL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREEDP  GQAVRKKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMKNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

m306.seq (partial)

```

1  ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCGmAwAA  CCAGCYTAAG
151 GAAGACATCC  AACCTGAwCC  GGCCGATCAA  AACGCCTTGT  CCGAACCAGG
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAawGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGGTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGGACGG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAAGCT
451 TCAAAGAAG  AGAAAAAGGC  GCGGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCTCAACA  GCGGCAGCAT  CGAAAAGCG  CGCAGTGCCG
551 CCGCCAAAGA  AGTGCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```

702

601 ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG  
 651 CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGTTATCA  
 701 GCGGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG  
 751 ATGCGGTGA

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

m306.pep (partial)  
 1 ..GLFFGLILAT VIIAGILFYL NQSGQNAFKI PASSKQPAET EILKPXNQXK  
 51 EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP  
 101 EREEPDQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA  
 151 SKEEKKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR  
 201 IICKWARMPT VRARKGSVPN WQSWAYLPRW SVIRIRDIKRF TGCKAAICLP  
 251 MR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

m306/g306

m306.pep	10	20	30	40
	GLFFGLILATVIIAGILFYL NQSGQNAFKI PASSKQPAET EILKPX			
g306	:     :     :     :     :     :     :     :     :     :			
	10	20	30	40
	MFMNKFSQSGKLSGFFGLILATVIIAGILLYLNQGGQNAFKI PAPSQPAET EILKLK			
	10	20	30	40
m306.pep	50	60	70	80
	NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKA DEVEEKAGEPEREEDP			
g306	:     :     :     :     :     :     :     :     :     :			
	50	60	70	80
	NQPKEDIQPEPADQNALSEPDAEAEQSDAEXAADKQPVADKA DEVEEKAGEPEREEDP			
	70	80	90	100
m306.pep	110	120	130	140
	GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKAAKEKVAPKP			
g306	:     :     :     :     :     :     :     :     :     :			
	110	120	130	140
	GQAVRKKALTEEREQTVREKAQKKDAETVKKKAVKPSKETEKKASKEEKAAKEKVAPKP			
	130	140	150	160
m306.pep	170	180	190	200
	TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSVPNWQSWA			
g306	:     :     :     :     :     :     :     :     :     :			
	170	180	190	200
	TPEQILNSRSIEKARSAAAKEVQKMNFGGGSQRIICKWARMPNPGARKGSVPNWQSWA			
	190	200	210	220
m306.pep	230	240	250	
	YLPRWSVIRIRDIKFTGCKAAICLPMRX			
g306	:     :     :     :     :     :     :     :     :			
	YLPKWSAIRIRDIKFTACKAAICPPMRX			
	230	240	250	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

a306.seq  
 1 ATGTTTATGA ACAAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTT  
 51 CTTGCGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTTATC  
 101 TGAACCAGAG CGGTCAAAT GCGTTCAAAA TCCCGGTTCC GTCGAAGCAG  
 151 CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCTA AGGAAGACAT  
 201 CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA  
 251 AAGAGGCAGA GCAGTCGAT GCGGAAAAAG CTGCCGACAA GCAGCCGTT  
 301 GCCGACAAAG CCGACGAGT TGAGGAAAAG GCGGACGAGC CGGAGCGGGA  
 351 AAAGTCGGAC GGACAGGCAG TCGCAAGAA AGCACTGACG GAAGAGCGTG  
 401 AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA  
 451 AAACAAGCGG TAAAAACATC TAAAGAAACA GAGAAAAAG CTTCAAAGA  
 501 AGAGAAAAAG GCGGAGAAG AAAAAGTTGC ACCCAAACCG ACCCGGAAC  
 551 AAATCTCAA CAGCGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

```

601 GAAGTGCAGA AAATGAAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
701 ACTGGCAATC TTGGGCATAT CTCCAAGGT GGTCTGTTAT CAGGCGGGAC
751 ATAAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
801 A

```

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```

a306.pep
1 MFMNKFSQSG KGLSGFFFL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
51 PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD GQAVRKALTE EEREQTVGEK AQKKAETVK
151 KQAVKPSKET EKKASKEKK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

m306/a306 93.7% identity in 252 aa overlap

```

m306.pep          10      20      30      40
                  GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPKX
a306              10      20      30      40      50      60
                  MFMNKFSQSGKGLSGFFFLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK
                  10      20      30      40      50      60

m306.pep          50      60      70      80      90      100
                  NOXKEDIQXPADQNALSEPDAATEAEQSDAEKXADKQPVADKADEVEEKAGEPEREEDP
a306              50      60      70      80      90      100      110      120
                  NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD
                  70      80      90      100      110      120

m306.pep          110     120     130     140     150     160
                  GQAVRKALTEEREQTVREKAQKKAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
a306              110     120     130     140     150     160     170     180
                  GQAVRKALTEEREQTVGEKAQKKAETVKKQAVKPSKETEKKASKEEKKAEKEKVAPKP
                  130     140     150     160     170     180

m306.pep          170     180     190     200     210     220
                  TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTVRARKGSVFNWQSWAY
a306              170     180     190     200     210     220     230     240
                  TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTAGARKGSVFNWQSWAY
                  190     200     210     220     230     240

m306.pep          230     240     250
                  LPRWSVIRRDIKRFTGCKAAICLPMRX
a306              230     240     250
                  LPRWSVIRRDIKRFTGCKAAICLPMRX
                  250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

```

g307.seq
1 atgaaaacct tcttcaaaac cctttcgacc gcgtcactcg cgctcatcct
51 cgcagcctgc ggcgggtcaaa aagacagcgc gccgcagcc tctgcccgcg
101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
151 accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201 ggagaaaaaa ggctacaccg tcaattggt cgaatttacc gactatgtgc
251 gccggaatct ggcattggcg gagggcgagt tggacatcaa cgtcttccaa
301 cacaaaccct atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351 cgaagccttc caagtgccga ccgcgccttt gggactgtat ccgggcaaac
401 tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgccaac
451 gacccttcca acttcgcacg cgccttggtg atgctgaacg aactgggttg
501 gatcaaatc aaagacggca tcaatccgct gaccgatcc aaagccgaca
551 tcgcggaata cctgaaaaac atcaaatcgc tcgagcttga agccgcacaa
601 ctgccgcgca gccgcgcgca cgtggatttt gccgtcgta acggcaacta
651 cgccataagc agcggcatga agctgaccga agccctgttc caagagccga

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704

701 gctttgccta tgtcaactgg tctgccgtca aaaccgccga caaagacagc  
 751 caatggccta aagacgtaac cgaggcctat aactccgacg cgttcaaagc  
 801 ctacgcgcac aaacgcttcg agggctacaa ataccctgcc gcatggaatg  
 851 aaggcgagc caaataa

This corresponds to the amino acid sequence <SEQ ID 1272; ORF 307.ng>:

g307.pep

1 MKTFFKTLST ASLALILAAC GGQKDSAPAA SAAAPSADNG AAKKEIVFGT  
 51 TVGDFGDMVK EIQAELEKK GYTVKLVEFT DYVRPNLALA EGELDINVFQ  
 101 HKPYLDDFKK EHNLDITEAF QVPTAPLGLY PGKLKSLEEV KDGSTVSAPN  
 151 DPSNFARALV MLNELGWIKL KGINPLTAS KADIAENLKN IKIVELEAAQ  
 201 LPRSRADVDF AVVNGNYAIS SGMKLTEALF QEPSFAYVNW SAVKTADKDS  
 251 QWLKDVTEAY NSDAFKAYAH KRFEGYKYP A WNEGAAK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1273>:

m307.seq (partial)

1 ..CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC  
 51 CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCTGCC GCATGGAATG  
 101 AAGGCGCAGC CAAATAA

This corresponds to the amino acid sequence <SEQ ID 1274; ORF 307>:

m307.pep (partial)

1 ..QWLKDVTEAY NSDAFKAYAH KRFEGYKSPA A WNEGAAK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 307 shows 97.4% identity over a 38 aa overlap with a predicted ORF (ORF 307.ng) from *N. gonorrhoeae*:

m307/g307

m307.pep				10	20	30
				QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA		
g307	SGMKLTEALFQEPSFAYVNW	SAVKTADKDS	QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA			
	230	240	250	260	270	280

  

m307.pep		39
	AWNEGAAKX	
g307	AWNEGAAKX	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1275>:

a307.seq

1 ATGAAAACCT TCTTCAAAC CCTTCCGCC GCCGCACTCG CGCTCATCCT  
 51 CGCCGCCTGC GGCGGTCAA AAGATAGCGC GCCCGCCGCA TCCGCTTCTG  
 101 CCGCGCCGCA CAACGCGCGC GCGAAAAAG NAATCGTCTT CGGCACGACC  
 151 GTCGGCGACT TCGGCGATAT GGTCAAAGAA CAAATCCAAC CCGAGCTGGA  
 201 GAAAAAAGGC TACACCGTCA AACTGGTCGA GTTTACCGAC TATGTGCGCC  
 251 CGAATCTGGC ATTGGCTGAG GCGGAGTNGG ACATCAACGT CTTCACACAC  
 301 AAACCCATC TTGACGACTT CAAAAAGAA CACAATCTGG ACATCACCGA  
 351 AGTCTTCCAA GTGCCGACCG CGCCTTTGGG ACTGTACCGG GGCAAGCTGA  
 401 AATCGCTGGA AGAAGTCAA GACGGCAGCA CCGTATCCGC GCCCAACGAC  
 451 CCGTCCAAC TCGCCCGCGT CTTGGTGATG CTCGACGAAC TGGGTTGGAT  
 501 CAAACTCAA GANGGCATCA ATCCGCTGAC CGCATCCAAA GCGGACATTG  
 551 CCGAAAAACCT GAAAAACATC AAAATCGTCG AGCTTGAAGC CGCGCAACTG  
 601 CCGCGTAGCC GCGCCGACGT GGATTTTGN C GTCGTCAACG GCAANTACGC  
 651 CATAAGCAGC GGCATGAAGC TGACCGAAGC CCTGTTCCAA GAACCGAGCT  
 701 TTGCCTATGT CAACTGGTCT GCCGTCAAAA CCGCGACAA AGACAGCCAA  
 751 TGGCTTAAAG ACGTAACCGA GGCCTATAAC TCCGACGCGT TCAAAGCCTA  
 801 CGCGCACAAA CGCTTCGAGG GCTACAAATC CCCTGCCGCA TGAATGAAG  
 851 GCGCAGCCAA ATAA

This corresponds to the amino acid sequence <SEQ ID 1276; ORF 307.a>:

a307.pep

1 MKTFFKTLA AALALILAAC GGQKDSAPAA SASAAADNGA AKKXIVFGTT



```

51  VGDFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFOH
101 KPYLDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLKN  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEGYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                      QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
          220      230      240      250      260      270

                                39
m307.pep      AWNEGAAX
              |||||
a307          AWNEGAAX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTCTT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGAAC
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGCGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCGGA
401 CGCTTGCTTC  TGTCGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAGCCGCG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTGCTGTT
651 CGGAATCGAT  ACGCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVFYRIL  GVADNLYPCL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTCTT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGAAC
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTTC  TGTCGCGCAC  GGCTTCGGCG  ACAATCTGCT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GwAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  gcG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

m308.pep (partial)

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTTIA  GLPLQAVLWE  RRMVRRLLI
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADVFHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNMR  XTEMGGVVFP  PVPAMYRKPQ
201 TADDIVAHSV  AHALSFGID  TPDSA EWQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADVFHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLNMR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLNMR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPAMYRKPQTADDIVAHSAHALSLFGIDTPDSA EWQGM					
g308	VTEMGGVVFPVPAMYRKPQTADDIVAHSAHTLSLFGIDTPDLA EWQGMAD					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGATATTA  TCGGATTCT  GTTTTTTAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTTC  GGTCGTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCAG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTCG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTTIA  GLPLQAVLWE  RRMVRRLLI
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXIARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNMR  VTEMGGVVFP  PVPAMYRKPQ
201 TADDIVAHSV  AHALSFGID  TPDSA EWQGM  AD*

```

**m308/a308 95.7% identity in 231 aa overlap**

	10	20	30	40	50	60
m308.pep	MLNRV	FYRIL	GVADN	LYPRL	SDFCFF	TIAGL
a308	MLNRIF	YRILGV	ADNLYP	YLSDFC	FFTIAG	LPLQAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALE	LLRAQD	VETHLV	VSKGAEM	ARSETAY	ARDEVY
a308	GVKALX	LLRAQDI	ETHLVV	SKAEMAR	SETXYAR	DXVYAL
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGML	VAPCSMR	TLASVA	HGFGDN	LLTRAAD	VVLKERR
a308	KTDGML	VAPCSMR	TLASV	VHGFGDN	LLTRAAD	VVLKERR
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGG	VVFPVP	PAMYRK	PQTADD	IVAHSV	AHALSL
a308	VTEMGG	VVFPVP	PAMYRK	PQTADD	IVAHSV	AHALSL
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

**g308-1.seq**

```

1  ATGTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGTGTTTA TCGGATTTC TTTTTCAC TATAATAGCC GGTGTTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGTGAAGG CTTTGAACT
201 TTTGCGCGCG CAAGATGTGC AAACGCACCT TGTGGTATCG AAAGCGCGCG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTCTG TCGATGCGGA
401 CGCTTGCCCTC TGTGCGGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGC CGGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGCGGCGGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAGCCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

**g308-1.pep**

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFIIA GLPLQAVLWE RRMVRRLLII
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADEVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
151 ADVVLKERRR LVLVRETPPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

**m308-1.seq**

```

1  ATGTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTTC TTTTTCAC TATAATAGCC GGTGTTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGTGAAGG CTTTGAACT
201 TTTGCGCGCG CAAGATGTGC AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCCTC TGTGCGGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGC CGGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGCGGCGGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

**m308-1.pep**

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFIIA GLPLQAVLWE RRMVRRLLII

```

708

51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA  
 101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA  
 151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRK PQ  
 201 TADDIVAHSV AHALSLFGID TPDSA EWQGM AD\*

m308-1/g308-1 97.0% identity in 232 aa overlap

	10	20	30	40	50	60
m308-1.pep	MLNRV	FYRILGVADNLYPRLSDFCFF	FTIIAGLPLQAVLWERRMMVRR	LIIGISGASGFQY		
g308-1	MLNRV	FYRILGVADNLYPCLSDFCFF	FTIIAGLPLQAVLWERRMMVRR	LIIGISGASGFQY		
	10	20	30	40	50	60
	70	80	90	100	110	120
m308-1.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADVFHPIGNIGACIASGTF				
g308-1	GVKALELLRAQDVETHLVVSKGAEMARASE	TDYTKDEVYALADVFHPIGNIGACIASGTF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m308-1.pep	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308-1	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308-1.pep	VTEMGGVVFPVPAMYRK PQ	TADDIVAHSVAHALSLFGIDTPDSA EWQGMADX				
g308-1	VTEMGGVVFPVPAMYRK PQ	TADDIVAHSLAHTLSLFGIDTPDLA EWQGMADX				
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA  
 51 TCCGATTATTA TCGGATTCTT GTTTTTTCAC TATAATAGCC GGTTCGCCGT  
 101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC  
 151 GGCATCAATG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGANCT  
 201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGATATCG AAAGGTGCGG  
 251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC  
 301 TTGGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG  
 351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCGGA  
 401 CGCTTGCCCT GGTGCTGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG  
 451 CCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA  
 501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA  
 551 TGGCGGCGGT GGTGTTTCCC CCTGTTCCCTG CGATGTACCG CAAACCGCAG  
 601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTGCTGTT  
 651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1288; ORF 308-1.a&gt;:

a308-1.pep

1 MLNRIFYRIL GVADNLYPYL SDFCFFTTII GLPLQAVLWE RRMVRRLLII  
 51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA  
 101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVVH GFGDNLLTRA  
 151 ADVVLKERRR LVLVRETPL NLAHLDNMXR VTEMGGVVFP PVPAMYRK PQ  
 201 TADDIVAHSV AHALSLFGID TPDSA EWQGM AD\*

a308-1/m308-1 96.1% identity in 232 aa overlap

	10	20	30	40	50	60
a308-1	MLNRIFYRILGVADNLYPYLSDFCFF	TTIIAGLPLQAVLWERRMMVRR	LIIGISGASGFQY			
m308-1	MLNRIFYRILGVADNLYPRLSDFCFF	TTIIAGLPLQAVLWERRMMVRR	LIIGISGASGFQY			
	10	20	30	40	50	60
	70	80	90	100	110	120
a308-1	GVKALXLLRAQDIETHLVVSKGAEMARASE	TXYARDXVYALADXVHPIGNIGACIASGTF				
m308-1	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADVFHPIGNIGACIASGTF				
	70	80	90	100	110	120
	130	140	150	160	170	180
a308-1	KTDGMLVAPCSMRTLASVVHGF	GDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR				

```

m308-1      KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLHLNDNMKR
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSAEOGMADX
              |||||
m308-1      VTEMGGVVFPPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSAEOGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

```

g311.seq
1   atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgcgtgcgc gcgcgctttg ggtgttttgg
101 gtttggaac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggcg gcattctgat tgaaacagtc agggcgggcg gtaaaccggt
201 tgccgtgggc ggtatcgcca tcaatttcgt gctgcccaag gaagtggaaa
251 acgccgcttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgtgtgt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggtaaaaggc gtggacggac gaggcgttct
501 gcacttgga aacggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
601 gaacgttttt tgctgttggg aggcgggaac agccggctca agtgggcgtg
651 ggtggaacaa ggcacgttcg caaccgtggg cagcgccgctg taccgcgatt
701 tgcgcctttt gggcgcgagg tggcggaaga aggcggatgg aaatgtccgc
751 atcgtcgggt gcgccgtgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgcca caggctttgg
851 gcatacgcaa ccaactaccg caccgcgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct cgcgtcgtcg
951 cagttgcggc acggcggtta cggttgacgc gctcaccgat gacggacatt
1001 atctcgcgcg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaaact caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggtt
1151 gcggctcgat aatgatgatg caccggcgtt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggcggcgcgcg cgaaagtccg
1251 cgaagccctg ccgcctgcat ttttgcgga aaataccgtg cgcgtggcg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

```

g311.pep
1   MFSFGWAFDR POYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGGILITV RAGGKTAVV GIGINFVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLET LAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVKG VDGRGVHLHLE TAEGEQTVVS GEISLRPDNR SVSVPKRPDS
201 ERFLLEGGN SRLKWAVVEN GTFATVGSAP YRDLSPLGAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNR AGKRYPFPTT TGNASGMM DAVCGSIMM HGRLKEKNGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

```

m311.seq (partial)
1   ATGTTCAAGT TTGCTGGGT GTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTCGCCT GTTGCGGCAG TGGCGTTCG GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCATATTAG TGGCCCAATG ATTTGGTTGT CCGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTGT CCTGCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCTGA CGGCATCGCG GCGGGGCAAT
301 CCGCATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAT
351 CAGCCTGCGG TCCGACnACA GGCCGGTTTC CGTGnCGAAG CGGCGGGATT

```

710

```

401 CGGAACGTTT TCTGCTGTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAG ACGGCACGTT CGCAACCGTC GGTCAGCGGC CGTACCgCGA
501 TTTGTGCGCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TGCGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCCGACC
701 GCTGGTTCAA CGCCTTGGGC AGCCGCCGCT TCAGCCGCAA CGCyTGCgTC
751 GTCGTAGTTC GCGGCACGGC GGTAACGGTT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrgGAACCA TCATGCCCGG TTTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTCGCGC TCGGTTATGA TGATGCACGG GCGTTTGAAG GAAAAAACCG
1001 GGGCGGGCAA GCCTGTGCGT GTCATCATT CCGGCGCGCG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGG GCGGAAAATA CCGTGCgCGT
1101 GCGGACAAC CTCGTCATT ACggGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGAATA TGAACAT....

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
  1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
 51 KLGGILIETV RTGGKTAVV GIGINFLPX EVENAASVQS LFQTASRRGN
101 ADAVLLXXX XXXXEISLR SDXRPVSXK RRDSEFLLL DGGNSRLKWA
151 WVENGTATV GSAPYRDLSP LGAEWAEKAD GNVRIVCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPPEH GSDRWFNALG SRRFSRNACV
251 VVSCGTATVT DALTDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTGNV AVSGMMDAVCG SVMMHGRLEK EKTGAGKPD VIITGGGAAG
351 VAEALPPAFL AENTVRVADN LVIYGLNMI AAEGREYEH....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311

      10      20      30      40      50      60
m311.pep MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311      MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPNDLVVGRDKLGGILIETV
          10      20      30      40      50      60

      70      80      90      100     110
m311.pep RTGGKTAVVVGIGINFLPXEVENAASVQSLFQTASRRGNADAAVLLXXX-----
          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      RAGGKTAVVVGIGINFLPKEVENAASVQSLFQTASRRGNADAAVLLLETLLAELGAVLEQ
          70      80      90      100     110     120

m311.pep -----XXXX
g311      YAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDGRGVLHLETAEGEQTVVS
          130     140     150     160     170     180

      120     130     140     150     160     170
m311.pep XEISLRSDXRPVSXKRRDSEFLLLDGGNSRLKWAWVENGTFATVGSAPYRDLSPLGAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      GEISLRPDNRSVSVKRPDSEFLLLEGGNSRLKWAWVENGTFATVGSAPYRDLSPLGAE
          190     200     210     220     230     240

      180     190     200     210     220     230
m311.pep WAEKADGNVRIVGCVCGEFKAQVQEQELARKIEWLPSSAQALFGIRNHYRHPPEHGS DR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      WAEKADGNVRIVGCVCGESKKAQVKEQLARKIEWLPSSAQAL-GIRNHYRHPPEHGS DR
          250     260     270     280     290

```

711

	240	250	260	270	280	290
m311.pep	WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR					
g311	WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPVVDVITGGGAAKVAEA					
g311	PAGKRYPFPTTTGNAVASGMMDAVCGSIMMHGRLEKKTGAGKPVVDVITGGGAAKVAEA					
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEH					
g311	LPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1   ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTTC
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGAAAAC GCAAATCAAG TGGCCAAACG ATTTGGTCGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAACCGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTCGT GCTGCCCAAG GAAGTGGAAA
251 ACGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGAAAT
301 GCCGATGCCG CCGTGTGCT GGAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTGCAA TATGCGCGGG ACGGATTGTC GCCTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGCG
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC GTGGACGGAC AAGGCGTCTT
501 GCACTTGGA ACGGCAGAGG GCAAACAGAC GGTCGTCAGC GGCGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTCCG TGCCGAAGCG GCGGGATTCTG
601 GAACGTTTTC TGCTGTGGA CGGCGGCAAC AGCCGGCTCA AGTGGGCGTG
651 GGTGGAAC GGCACGTTG CAACCGTCGG TAGCGCGCCG TACCGCGATT
701 TGTCGCCTTT GGGCGCGGAG TGGGCGGAAA AGGTGGATGG AAATGTCCGC
751 ATCGTCGTT GCGCCGTGTG CGGAGAATTC AAAAAGGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAATCG AGTGGCTGCC GTCTTCGCA CAGGCTTTGG
851 GCATACGCAA CCACTACCGC CACCCGAAG AACACGGTTC CGACCGCTGG
901 TTCAACGCCT TGGGCAGCCG CCGCTTCAGC CGCAACGCCT GCGTCGTCGT
951 CAGTTGCGGC ACGGCGGTAA CGGTTGACGC GCTACCGGAT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGGTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCCGAA CCGCAACCT CAACCGGCAC CGCGGTAAGC GTTATCCTTT
1101 CCCGACCACA ACGGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 GCGGCTCGGT TATGATGATG CACGGGCGTT TGAAAGAAA AACCAGGGCG
1201 GGCAAGCCTG TCGATGTCAT CATTACCGGC GGCGGCGCGG CAAAAGTTGC
1251 CGAAGCCTG CCGCTGCAT TTTTGCGGGA AAATACCGTG CGCGTGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTGCCG CGAAGGCGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1   MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGILIVTV RTGKTVAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVILETL LAELDAVLLQ YARDGFAPFV AEYQAANRDH GKAVLLLRDG
151 ETVFEGTVKG VDGQGVHLLE TAEGKQTVVS GEISLRSDDR PVSVPKRRDS
201 ERFLLDGGN SRLKWAVVEN GTFATVGSAP YRDLSPGAE WAEKVDGNVR
251 IVGCAVCGEF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRFRS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRH AGKRYPFPTT TGNASGMM DAVCGSVMM HGRLEKKTGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

	10	20	30	40	50	60
m311.pep	MFSFGWVFDRPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV					
a311	MFSFGWVFDRPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGILIETV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADAVALXXXXXX----					
a311	RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADAVALLETLLAELDAVLLQ					
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVDGQGVLLHLETAEGKQTVVS					
	130	140	150	160	170	180
	120	130	140	150	160	170
m311.pep	-EISLRSDXRPVSVXKRRDSEFLLLDGGNSRLKWAWVNGTFATVGSAPYRDLSPLGAE					
a311	GEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAWVNGTFATVGSAPYRDLSPLGAE					
	190	200	210	220	230	240
	180	190	200	210	220	230
m311.pep	WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYRHPPEHGS DR					
a311	WAEKV DGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQAL-GIRNHYRHPPEHGS DR					
	250	260	270	280	290	
	240	250	260	270	280	290
m311.pep	WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLG GTIMPGFHLMKESLAVRTANLNR					
a311	WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLG GTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPV DVIITGGGAAKVAEA					
a311	HAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPV DVIITGGGAAKVAEA					
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPFAFLAENTVRVADNLVIYGLLN MIAAEGREYEH					
a311	LPFAFLAENTVRVADNLVIHGLLN LIAAEGGESEHTX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGCGGTT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GAAAAGGTCT GGTTCAGAG
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACCGACGAGT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGCG TGACCCACCT
351 GCAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAGTGGTCT CACCGTTTGG
401 GCGAGTGCCT GATGTTCACT TTCGGCTGGG CGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA CTGCGTGCC GCGCGCTTT
501 GGGGTGTTTG GGTTCGAAA CGCAATCAA GTGCCAAAC GATTGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAAACCGG TTGCCGTGGT CGGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTGGA AAGCCGCTT CCGTGAGTC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTATTGC TGGAAACATT GCTTGCGGAA
751 CTGGGCGCGG TGTGGAACA ATATGCGGAA GAAGGTTCTG CGCCATTTT

```



```

801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGGCGGACGG CGAAACCGTG TGGCAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGGTT TGCACCTGGA AACGGCAGaa ggCGAACAGA cggtcGtcag
951 cggcGaaaTC AGccTGCGGC CCGacaacag gtcggtttcc GTgccaagc
1001 gGccggaTTC GgaacgttTT tTGCTgttgg aaggcgggaa cagccggctc
1051 aAGTGGcggt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGcGCC
1101 gtaCCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAAAT CAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TGGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACC GA
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCCTT TCCCGACCAC AACGGGCAAC GCCGTCGCAA CGGCATGAT
1551 GGACGCGGTT TCGGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGCGCG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1  MTLVKPSHWR VLAELADGLP QHVSQAREA DMKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWAFDRPOY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVRDRKLG GILITVRAG
201 GKTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVDDG
301 RGVHLHLETAE GEQTVVSGEI SLRPDNRSVS VPKRPDSERF LLEGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLFPSSAQL GIRNHYRHE EHSGDRWFNA LGSRRFRSNA
451 CVVUSCGTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRPAK
501 RYFPPTTGN AVASGMMDAV CGSIMMHGR LKEKNGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1  ATGACGTTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGGCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACCGGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGGCGC CATTGGCGGT
201 TTTGATGATC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTCCTAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACCGACGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTGACCG CCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA GTGGCGGTGC GCGCGGCTT
501 GTCGCGTTTA GGTGTTGATG TGCAGATTAA GTGGCCCAAT GATTGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGGTT TGCACCTGGA AACGGCAGAG GGCAACAGA CGGTCGTCAG
951 CGCGGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTTC GTGCCGAAGC
1001 GCGGGGATTC GGAACGTTTT CTGCTGTTGG ACGCGGCGAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCCTGTGTG GCGGAGAAAT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TGGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACC GA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACCGGCA CGCCGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCGA CGGCATGAT
1551 GATGCGGTTT TCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACGGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACCG GTTGTGAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1298; ORF 311-1&gt;:

m311-1.pep

```

1  MTVLKLSHWR VLAELADGLP QHVSQALARM DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVDRPQY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILIETVRTG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVGDG
301 QGVHLHLETAE GKQTVVSGEI SLRSDDRPSV VPKRRDSERF LLLDGGNSRL
351 KWAWVENGTF ATVGSAFYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQLARKI EWLPSAQAAL GIRNHYRHPE EHGSDRWFNA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*

```

m311-1/g311-1 93.9% identity in 591 aa overlap

	10	20	30	40	50	60
m311-1.pep	MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRG	LLRQHDGYWR				
g311-1	MTVLKPSHWRVLAELADGLPQHVSQALAREADMKPQQLNGFWQOMPAHIRG	LLRQHDGYWR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m311-1.pep	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
g311-1	LVRPLAVFDAEGLRDLGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m311-1.pep	GRGRQGRKWSHRLGECLMFSFGWVDRPQYELGSLSPVAACRRALSRLGLDVQIKWPN					
g311-1	GRGRQGRKWSHRLGECLMFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m311-1.pep	DLVVGRDKLGGILLETVRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
g311-1	DLVVGRDKLGGILLETVRAGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m311-1.pep	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
g311-1	AVLLETLLAELGAVLEQYAEAGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVGDG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m311-1.pep	QGVHLHLETAEGKQTVVSGEISLRSDDRPSVVPKRRDSERFLLDGGNSRLKWAWVENGTF					
g311-1	RGVLHLETAEGEQTVVSGEISLRPDNRSVVPKRPDSERFLLLEGGNSRLKWAWVENGTF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m311-1.pep	ATVGSAFYRDLSPPLGAEWAEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSAQAAL					
g311-1	ATVGSAFYRDLSPPLGAEWAEKADGNVRIVGCAVCGESKKAQVQEQLARKIEWLPSAQAAL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m311-1.pep	GIRNHYRHPEEHGSDRWFNALGSRRFSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGF					
g311-1	GIRNHYRHPEEHGSDRWFNALGSRRFSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGF					
	430	440	450	460	470	480
	490	500	510	520	530	540
m311-1.pep	HLMKESLAVRTANLNRHAGKRYFPFTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
g311-1	HLMKESLAVRTANLNRHAGKRYFPFTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
	490	500	510	520	530	540
	550	560	570	580	590	

```

m311-1.pep  VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEHIX
              |||
g311-1      VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHAX
              550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1  ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGCGCGA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAGGTTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTTGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTGCGC TGTTCGCGCA GTGGCGTGCC GGCGCGCCTT
501 GTCGCGTTTG GGTTTGAAAA CGCAAATCAA GTGGCCAAAC GATTGGGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGAAA TGCCGATGCC GCCGTGTGTC TGGAACGCTT GTTGGCGGAA
751 CTTGATGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGACGCG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGACGCGA
901 CAAGGCGTTC TGCACTTGGG AACGCGAGAG GGCAACAGA CGGTCGTCAG
951 CCGCGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GCGCGGATTG GGAACGTTTT CTGCTGTTGG ACGCGGCGAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCTT TGGGCGCGGA GTGGGCGGAA AAGTGGATG
1151 GAAATGTCGG CATCGTCGGT TCGCGCGTGT GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACGCGTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACTGTATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTCGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACGCG GCTGTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1  MTVLKPSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECMLFS FGWVFDPRQY
151 ELGSLSPVAA VACRRALSRL GLKTOIKWPN DLVVGDRDLG GILLETVRTG
201 GRTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVILLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVVDG
301 QGVHLHETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KVDGNVRIVG CAVCGEFKKA
401 QVQEQALKRK EWLPSAQAAL GIRNHYRHEP EHGSDRWANA LGSRRFRSNA
451 CVVVSCTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYPFPTTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

```

a311-1/m311-1 98.5% identity in 591 aa overlap

```

          10      20      30      40      50      60
a311-1.pep  MTVLKPSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR
              |||
m311-1      MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR
          10      20      30      40      50      60

          70      80      90      100     110     120
a311-1.pep  LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              |||
m311-1      LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
          70      80      90      100     110     120

```

a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGECIMFSGWVFD	RPQYELGSLSPVAACRRALSRLGLTKQIKWPN				
m311-1	GRGRQGRKWSHRLGECIMFSGWVFD	RPQYELGSLSPVAACRRALSRLGLDVQIKWPN				
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILITVRTGGKTAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
m311-1	DLVVGRDKLGGILITVRTGGKTAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVVDG					
m311-1	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVVDG					
a311-1.pep	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAVVNGTF					
m311-1	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAVVNGTF					
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPGAEWAKEVDGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL					
m311-1	ATVGSAPYRDLSPGAEWAKEVDGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL					
a311-1.pep	430	440	450	460	470	480
	GIRNHYRHPEEHGSDRWFNALGSRFRSNAACVVVSCGTAVTVDALTDGHLGGTIMPGF					
m311-1	GIRNHYRHPEEHGSDRWFNALGSRFRSNAACVVVSCGTAVTVDALTDGHLGGTIMPGF					
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
m311-1	HLMKESLAVRTANLNRHAGKRYFPPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
a311-1.pep	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHTX					
m311-1	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNMIIEGREYEHIX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```
1 atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51 ccggaATttt gAtgtccgCA CCATTAccat cggcaTTgaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggctcg gcaaagactT GGTGGCAacg Gcgaaacacc tTTccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgcAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAGGTA TGTCGCCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG
551 CAAAATCGT CGTGTCTGCG AACGCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGTCCA GGCGTGGTCA AAGCCGCGCT GGAAAATTCG GACGCGGTCA
701 GCCTGACCGA GGTCGCCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTGTG CGCTGGCACC GACCCCGGCC GTCGGCGACT
851 CCGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CCGTACGCAC
```

```

901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCGTC TGCTCCGTTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATTCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTTCGTCAA CCGGGGCGGC AGGATTCCCC CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1 MSIQSGEILE TVKMWADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51 TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGC AKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCETH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1 ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51 CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAACT
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAGGGA TGTCGCcTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCWG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACcGTC AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGTGCGG
551 CTAAATTTGT CGTGTCTGTC AACGCGGTGG AAGACAACCC GTTTWTGGCG
601 GGCGCGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTCG GCGTATCCGG
651 CCCAGGTGTC GTAAAGCCG CGTTGGAAAA TTCAGATGCA ACACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAAATG CTTTCAAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCGCGCA AGCcTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTGCGCGA CCCC GCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGCGG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCGGTTTG TTCGGTCGGC TTGGATATGA TTGCGGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAT GATCAACAGC AAAACCACTG CCGTGCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CACGGTCGAG TTCGGCGGCT TGTTGGgCTA
1251 CGCGCCTGTG ATGCCGGTCA AAGAAGGTTG GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1 MSIQSGEILE TVKMWADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
51 TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCX SIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGC AKIVVFC NAVEDNPFXA
201 GAFHGSGDV INVGVSGPV VKAALENSDA TTLTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCETHGTTA
301 ALALLNDAVK KGGMMASAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLGYAPV MPVKEGSCEV FVNRGGRI PA PVQSMKN*

```

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

	10	20	30	40	50	60
m312.pep	MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKIITTVGKDLVTT					
	:	:	:	:	:	:
g312	MSIQSGEILETVKMVADRNFVDVRTITIGIDLHDCISTDIDVLNQNIYNKIITTVGKDLVAT					
	:	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m312.pep	AKYLSAKYGVPIVNQRISVTPPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSA					
	:	:	:	:	:	:
g312	AKHLSAKYGVPIVNQRISVTPPIAQIAAATKADSYVSVAQTLDKAAKAIGVSFIGGFSA					
	:	:	:	:	:	:
	70	80	90	100	110	120
	130	140	150	160	170	180
m312.pep	QKGMSPSDEVLRISIPAMKTTDIVCXSNIGSTRAGINMDAVKLAGETVKRTAEITPEG					
	:	:	:	:	:	:
g312	QKGMSPSDEVLRISVPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGETIKRTAEITPEG					
	:	:	:	:	:	:
	130	140	150	160	170	180
	190	200	210	220	230	
m312.pep	FGCAKIVVFCNAVEDNPFXXAGAFHGS--DAVINVGVS					
	:	:	:	:	:	:
g312	FGCAKIVVFCNAVEDNPFMAGAFHGS					
	:	:	:	:	:	:
	190	200	210	220	230	240
	240	250	260	270	280	290
m312.pep	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDS					
	:	:	:	:	:	:
g312	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDS					
	:	:	:	:	:	:
	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDVAVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
	:	:	:	:	:	:
g312	GTTAALALLNDVAVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	:	:	:	:	:	:
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMI					
	:	:	:	:	:	:
g312	CSVGLDMI					
	:	:	:	:	:	:
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSC					
	:	:	:	:	:	:
g312	YAPVMPVKEGSC					
	:	:	:	:	:	:
	430	440	450			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

1	ATGAGTATCC	AATCCGCGCA	AATTTTAGAA	ACCGTCAAAA	TGGTTGCCGA
51	CCAGAATTC	GATGTCGCA	CCATTACCAT	CGGCATTGAT	TTGCACGACT
101	GCATCAGCAC	CGACATCGAC	GTGTTGAACC	AAATATTTA	CAACAAAATT
151	ACCACGGTCG	GCAAGAGACTT	GTGGGCACAC	GCAAAATATC	TGTCTGCCAA
201	ATACGCGGTG	CCGATTGTGA	ATGACGCGAT	TTCTGTACG	CCGATTGCC
251	AAATCGCGGC	GGCCACCCAT	GCTGATTCTT	ACGTACGCGT	GGCGCAAACT

```

301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATTG GCGGCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGCGCGCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CCAAATCGT CGTGTCTGTC AACGCGGTGG AAGACAACCC GTTTATGGCG
601 GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCCGCGT
651 ATCCGCGCCG GGTGTCGTAA AAGCCGCGTT GGAAATTCG GATGCAACGA
701 CATTGACCGA AGTTGCCGAA GTTGTGAAGA AAACCGCCTT CAAAATACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGGCGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGTT TGAGCGTCTG CGGTACGCAC
901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGCGCG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAAGCAGG CGTGTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTCCGGTCG GCTTGGATAT
1101 GATTGCCGTT CCCGCGCACA CACCGCGCA CACCATTTC GGCATCATTG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATCCCG TAACCGGTAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 CCTGTTGGGC TACGCGCCTG TAATGCCGTT AAAAGAAGGC TCATCGGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

```

a312.pep
1  MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51  TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GPVVKAALENS DATTLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

m312/a312 96.7% identity in 451 aa overlap

```

          10      20      30      40      50      60
m312.pep  MSIQSGEILETVKMVADQNF DVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
          |||
a312      MSIQSGEILETVKMVADQNF DVRTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT
          10      20      30      40      50      60

          70      80      90      100     110     120
m312.pep  AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSALV
          |||
a312      AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSALV
          70      80      90      100     110     120

          130     140     150     160     170     180
m312.pep  QKGMSPSDEV LIRSIPEAMKTTDIVCX SINIGSTRAGINMDAVKLAGETVKRTAEITPEG
          |||
a312      QKGMSPSDEV LIRSIPEAMKTTDIVCSSINIGSTRAGINMDAVRLAGETIKRTAEITLEG
          130     140     150     160     170     180

          190     200     210     220     230
m312.pep  FGCAKIVVFCNAVEDNPF XAGAFHGS G--DAVINVGVS GPGVVKAALENS DATTLTEVAE
          |||
a312      FGCAKIVVFCNAVEDNPF MAGAFHGS GEADAVINVGVS GPGVVKAALENS DATTLTEVAE
          190     200     210     220     230     240

          240     250     260     270     280     290
m312.pep  VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH
          |||
a312      VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCGTH

```

720

	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDAVKKGGMMASAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDAVKKGGMMASAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRRGGRIPAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRRGGRIPAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

```

g313.seq
1  atggacgacc cgcgcaccta cggatcgggc aatcccggcg cgaccaatgt
51  tttagcgagc ggcaaaaaaa aggcggccgc gctgacgctc ttgggcatg
101 ccgccaaagg tttggttgcc gttttgcttg cagcggtgct tcaagaaccg
151 ctcggtttat ccgacagcgc aatcgccgcc gtcgcactcg ccgcgctggt
201 cgggcatatg tggccggtgt ttttcggatt taaggcgccg aaaggcggtg
251 caacggcatt gggcggtgct ctggcactct ctctgcaac tgccttggtc
301 tgcgcgttga tttggcttgt gatggcatte ggcttcaaag tatectccct
351 tgccgcgctg gtcgccacaa ccgcgcgccc ccttgccgca ctgtttttta
401 tgccgcacat ttcttggtat ttcgcaaccc tcgcaatcgc catattggtg
451 ttgctccgcc ataagagcaa catcctcaac ctgattaaag gcaaagaaag
501 caaatcggc gaaaaacgct ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

```

g313.pep
1  MDDPRTYSG NPGATNVLRs GKkKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL VATTAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNIILN LIKGKESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

```

m313.seq
1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTAGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCGCAAC TGCCTTGCTC
301 TGCGCGTTGA TTTGGCTTGT TATGGCATTC GGCTTCAAGG TGCTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTCGCCGCA TCCTTCTTTA
401 TGCCGCACGT CTCGTGGGTT TGGCGGACCG TCGCCATTGC TTTGCTGGTG
451 TTGTTCCGCC ACAAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
501 CAAATCGGC GGCAGCCGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

```

m313.pep
1  MDDPRTYSG NPGATNVLRs GKkKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL TATIAAPVAA SFFMPHVSWS WATVAIALLV
151 LFRHKSNIIVK LLEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:



Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRS GKKKAAALTLLGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
g313	MDDPRTYGSNPGATNVLRS GKKKAAALTLLGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVS VWVATVAIALLV LFRHKS NIVKLLEGRESKIGGSRX					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILV L LRHKS N I L N L I K G K E S K I G E K R X					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

a313.seq

1	ATGGACGACC	CGCGCACCTA	CGGATCGGGC	AATCCGGGGG	CAACCAATGT
51	TTTACGCAGC	GGCAAAAAAA	AGGCGGCCGC	GCTGACGCTC	TTGGGCGATG
101	CCGCCAAAGG	TTTGGTTGCC	GTTTGCTTG	CACGCGTGCT	TCAAGAACCG
151	CTCGGTTTAT	CCGACAGCGC	AATCGCGGCC	GTGCACTCG	CCGCGCTGGT
201	CGGGCATATG	TGGCCGGTGT	TTTTCGGATT	TAAAGGCGGC	AAAGGCGTGG
251	CAACGGCATT	GGGCGTGCTT	CTGGCACTCT	CTCCACAAC	TGCCTTGTC
301	TGCGCGTTGA	TTTGGCTTGT	GATGGCATTC	GGCTTCAAGG	TGTCTCCCT
351	TGCCGCATTA	ACCGCCACAA	TCGCCGCCCC	CCTTGCCGCA	CTGTTTTTTA
401	TGCCGCATAC	TTCTTGATT	TTCGCAACCC	TCGCAATCGC	CATATTGGTG
451	TTGCTCCGCC	ATAAGAGCAA	CATCCTCAAC	CTGATTAAAG	GCAAAGAAAG
501	CAAAATCGGC	GAAAAACGCT	GA		

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

a313.pep

1	MDDPRTYGS	NPGATNVLRS	GKKKAAALT	LGDAAKGLVA	VLLARVLQEP
51	LGLSDSAIAA	VALAALVGHM	WPVFFGFKGG	KGVATALGV	LALSPPTALV
101	CALIWLVMF	GFKVSSLAAL	TATIAAPLAA	LFMPHTSWI	FATLAIAILV
151	LLRHKSNI	LNLIKESKIG	EKR*		

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRS GKKKAAALTLLGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
a313	MDDPRTYGSNPGATNVLRS GKKKAAALTLLGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPPTALVCALIWLVMF GFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVS VWVATVAIALLV LFRHKS NIVKLLEGRESKIGGSRX					
a313	TATIAAPLAALFFMPHTSWIFATLAIAILV L LRHKS N I L N L I K G K E S K I G E K R X					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```

g401.seq
1   atgaaattac aacaattggc tgaagaaaaa atcggcggttc tgattgtgtt
51  cacgctgctt gtagtcagtg tcggtctgtt gattgaagtt gtgcccttgg
101 cctttaccaa ggcggcaaca cagccggcgc cgggctgaa gccttacaat
151 gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttaca
201 ctgccactct caaatgattc gtccgttccg tgcggaaacc gagcggtacg
251 gtcattactc tgttgccgga ggtcgggtt acgaccatcc gttccaatgg
301 gggtccaaac gtaccgggcc tgatttggca cgtgtgggcg gccgctattc
351 cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401 agtccaatat gccggcattc ccgtggcttg cacgcaataa agtcgatgtc
451 gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501 cagtgatgag gaaattgcga aagcgctga ggctttggca aacaaatccg
551 agctggatgc tgtagtcgcc tatctgcaag gattgggtct ggctttgaaa
601 aacgtaaggt aa

```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```

g401.pep
1   MKLQQLAEEK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVAVA YLQGLGLALK
201 NVR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```

m401.seq
1   ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GCGGCAACA CAGCCGGCGC CGGGCTGAA GCCTTACAAT
151 GCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTG GTCCGTTCGG TCGGAAACC GAGCGTTACG
251 GTCATTACTC TGTTGCCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTG CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```

m401.pep
1   MKLQQLAEEK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVAVA YLQGLGLALK
201 NVR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

m401/g401

```

          10      20      30      40      50      60
m401.pep  MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||||
g401       MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          10      20      30      40      50      60

          70      80      90     100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW

```

723

```

g401      |||||
          IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVPESNMPAFWRLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
g401      HRIHLLNPRDVPESNMPAFWRLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
g401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1  ATGAAATTAC AACAAATGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GCGCGCAACA CAGCCGGCGT CGGGCGTGAA GCCTTACAA
151 GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCCG TCGGGAACCC GAGCGTTACG
251 GTCATTACTC TGTTGCCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATT CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAACA GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
1  MKLQQLAEEK IGVLVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGGRYSDEW HRIHLLNPRD VPESNMPAF WRLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

          10      20      30      40      50      60
m401.pep  MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||
a401      MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
          10      20      30      40      50      60

          70      80      90      100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          |||||
a401      IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVPESNMPAFWRLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
a401      HRIHLLNPRDVPESNMPAFWRLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
a401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1  ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  tttccttacc ggatTATTGA GCTTGGGTat agaagtCtTg tGGGTAAGGA
101 TGttttcgTT CGCagcAcag tccgtgcctc aggCATTTTC atttattcctt
151 gcctGttttc tgACCGgtat cgccgtcggc gCgTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCcctT TATCGGGCAG TgcttcttgT
251 GGGCGGGTAT TgccaTttt ttgatTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 CGtcGTCAGG GGGTTGATT TCCCACTTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATttgtt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTtCT GCTGctgtcc
551 cTTTGTttTg tacaCTGtTC CAAAAAGTC TCCGACTGAA TGCAGTGTGCG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTcCTAC TGCCGGATTc
651 TGCTTTTCAA AATATTGCTG GCCGTCCGGA TAGGTTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTttTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGAcg agccgcAAAT CGCACCGCTT TTGcAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTTCGACCT GATTTTGATG AATTGCACTT GGTACTGGCG
1101 TGCCTATTCC ACTAACCTGT TGAGTGCgGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCCG
1201 CATgetTTTg CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCcct AATAAAGAAC
1301 TGCTCaagca aCGCCTTTcc cgTTGATTG GCGCGGAAAG CGGCAGgcac
1351 gtATTTGACA GCAGACCGT GGATGCTGCA GCACAAAAGG TTGctctcCG
1401 TATGCTGATT CGGATGACGG AAcctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

```

1  MDMVNTKPNL SVINMLSFLT GLLSLGIEVL WRMFSFAAQ SVPQAFSFL
51  ACFLTGIAGV AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IPITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFIL MFLLPDSVFQ NIAGRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGYANT DIFNSVNGIE RAYLLPSLKS GIRRI FVVGL STGSWARVLS
301 AIPMQSMIV AEINPAYRSL IADPQIAPL LQDKRVEIVL DDGRKWLRRL
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AOKVVSRLI RMTEPSAGAE VITDDNMIVE YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

```

1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT ATATGChTTC
51  TTTCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACCCTT
151 GCCTGTTTTc TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAaA sGGTTGATT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAmCGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TwTGATTtCT GCTGCTGTCC
551 CTTTGTttTg TACACTGTTC CAAAAAGTC TCCGACTGAA TGCAGTGTGCG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTcYtAC TGCCGGATTc

```

```

651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CCGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAACTCT GGCATACGCC
851 GCATTTTCGT CGTTGGACTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCGGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAAT CGCCCCGCTT TGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG aAcCTTCGGC TGGGGCGGAA GTTATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>:

m402.pep

```

1 MDIVNTKPNT SLIYMXSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL
51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAWLLT
101 GFSGFVHHAG IFITLSAVVX XLIFPLVHHV GTDGNKSGRQ VSNVYFAXVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICXIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAynt DVFNSVNGIE RAYLLPSLKS GIRRIFFVVL STGSWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYARYRGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/g402

m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPOAFSFTLACFLTGI	10	20	30	40	50	60
g402	MDMVNTKPNTSVINMLSFLTGLLSLGIEVLWVRMFSFAAQSVPOAFSFTLACFLTGI	10	20	30	40	50	60
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAWLLTGFSGFVHHAGIFITLSAVVX	70	80	90	100	110	120
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAWLLTGFSGFVHHAGIFITLSAVVR	70	80	90	100	110	120
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQIYLLICXIS	130	140	150	160	170	180
g402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDLLSTQIYLLICLIS	130	140	150	160	170	180
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY	190	200	210	220	230	240
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIAGRDRPDRLIENKHGIVAVY	190	200	210	220	230	240
m402.pep	HRDGDKVYGANVYDGAyntDVFNSVNGIERAYLLPSLKS GIRRIFFVVLSTGSWARVLS	250	260	270	280	290	300

```

g402      HRDGDQKVYVGANVYDGYAYNTDIFNSVNGIERAYLLPSLKS GIRRI FVVGLSTGSWARVLS
          250      260      270      280      290      300

          310      320      330      340      350      360
m402.pep  AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLIILM
          310      320      330      340      350      360

          370      380      390      400      410      420
m402.pep  NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGI VMFNTTTHSPHAFATAVHSIPYAYRYGHMV
          370      380      390      400      410      420

          430      440      450      460      470      480
m402.pep  VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSTVDAAAQKVVSRLIQMTEPSAGAE
          430      440      450      460      470      480

          490
m402.pep  VITDDNMIVEYKYGRGIX
          490

g402      VITDDNMIVEYKYGRGI
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402.seq
1 ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT ATATGCTTTC
51 TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGCTCTG TGGGTAAAGGA
101 TGTTCCTCGT GCGACAGTCA TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTT TGACCCGGTAT CGCCGTCGGC GCGTATTTTG GCAAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGCACTT TTAGTTTGTG GTGCTGCGTG GTTGTTGTACG
301 GGTTTTCCG GTCTCGTCCA CCACGCCGGT ATCTTTCATTA CCGCTGTCTGC
351 CGTCGTCAGA GGGTTGATTT TCCCCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCACTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TTTGATTTCT GCTGCTGTCC
551 CTTTGTTTTG TACTCTGTT CAAAAAAGTC TCCGACTGAA TGCAGTGTGC
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTCTAC TGCCGGATTG
651 TGTCCTTCAA AATATTGCTG ACCGTCGGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACAGCGGCGC ATACATAACC GATGATTCCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCCT CCGTAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAA TCGCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATACGGGTA GCGAATGGCT CGCTGCCCAT
1051 CCTGATGAAA AATTGCACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCATTATC ACCAACCTGT TGAAGTCGGA ATTTTAAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGTT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CATAGCCCGT ACACGATATT CCGTATGCAT ACCGTTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAAG CGGCAGGCAC
1351 GTATTTGACA CGAGCACCGT GGATGCTGCA GCACAAAAGG TTGCTCTCTG
1401 TATGCTGATT GCATGACCGG AACCTTCGGC TGGTCGGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

1 MDIVNTKPNT SLIYMLSFLS GLLSLGIEVL WVRMFSAQAQ SVPQAFSFTL

51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT  
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA  
151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLECTLF OKSLRLNAVS  
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG  
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSGWARVLS  
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRHH  
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP  
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLQORLS RLIWPESGRH  
451 VFDSSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI\*

## m402/a402 99.0% identity in 497 aa overlap

m402.pep	10	20	30	40	50	60
	MDIVNTKPNSTLIYMXSFLSGLLSLGIEVLWVRMFSAFAQSVPAQAFSFTLACFLTGIAVG					
a402	MDIVNTKPNSTLIYMLSFLSGLLSLGIEVLWVRMFSAFAQSVPAQAFSFTLACFLTGIAVG					
	10	20	30	40	50	60
m402.pep	70	80	90	100	110	120
	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
a402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
m402.pep	130	140	150	160	170	180
	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICKIS					
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQQIYLLICLIS					
	130	140	150	160	170	180
m402.pep	190	200	210	220	230	240
	AAVPLECTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
a402	AAVPLECTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
m402.pep	250	260	270	280	290	300
	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSGWARVLS					
a402	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSGWARVLS					
	250	260	270	280	290	300
m402.pep	310	320	330	340	350	360
	AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHPDEKFDLILM					
a402	AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHPDEKFDLILM					
	310	320	330	340	350	360
m402.pep	370	380	390	400	410	420
	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMNTTHSPHAFATAVHSIPYAYRYGHMV					
a402	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMNTTHSPHAFATAVHSIPYAYRYGHMV					
	370	380	390	400	410	420
m402.pep	430	440	450	460	470	480
	VGSATPVVFPNKELLQORLSRLIWPESGRHVFDSSSTVDAAAQKVSRMLIQMTEPSAGAE					
a402	VGSATPVVFPNKELLQORLSRLIWPESGRHVFDSSSTVDAAAQKVSRMLIQMTEPSAGAE					
	430	440	450	460	470	480
m402.pep	490					
	VITDDNMIVEYKYGRGIX					
a402	VITDDNMIVEYKYGRGIX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGCGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTCTCTC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC AACATAGACA
951 AGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAANK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFF DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTGCAACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACGGAAG GATTAATGGT CGATTCTCTC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAANK

```



```

51 DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRIYETT AETTSGLTGT LTTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSKEIK PTEGLMVDFF DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGPX *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406 . pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFQVEQLVAASARAQVMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQVEQLVAASARAQVMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406 . pep	KVALYIATMGDQSGSLTGGGRYSIDALIRGEYINSPAVRTDYTPRIYETTAETTSGLTGT					
	:					
m406	KVALYIATMGDQSGSLTGGGRYSIDALIRGEYINSPAVRTDYTPRIYETTAETTSGLTGT					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406 . pep	LTTSLSTLNAPALSRQSDGSGSRSSLGLNIGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	:					
m406	LTTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406 . pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	:					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406 . pep	IKPKTNAFEAAAYKENYALWMGPYKVSKEIKPTEGLMVDFFSDIQPYGNHTGNSAPSVEADN					
	:					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSKEIKPTEGLMVDFFSDIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406 . pep	SHEGYGYSDEAVRQHRQGPX					
	:					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```

```

501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCGAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
1  MQARLLIPIIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAANK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTGG LTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSCKGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
301 SHEGYGYSDE AVRRHRQGPX *

m406/a406 98.8% identity in 320 aa overlap

m406.pep      10      20      30      40      50      60
MQARLLIPIILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAANKDMDLQALHGR
|||||
a406          10      20      30      40      50      60
MQARLLIPIILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAANKDMDLQALHGR

m406.pep      70      80      90      100     110     120
KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGG
|||||
a406          70      80      90      100     110     120
KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGG

m406.pep     130     140     150     160     170     180
LTSLSTLNAAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF
|||||
a406         130     140     150     160     170     180
LTSLSTLNAAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF

m406.pep     190     200     210     220     230     240
FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
|||||
a406         190     200     210     220     230     240
FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL

m406.pep     250     260     270     280     290     300
IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTTEGLMVDFS DIRPYGNHTGNSAPSVEADN
|||||
a406         250     260     270     280     290     300
IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTTEGLMVDFS DIQPYGNHMGNSAPSVEADN

m406.pep     310     320
SHEGYGYSDEVVRHRQGPX
|||||
a406         310     320
SHEGYGYSDEAVRRHRQGPX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
1  atgggtcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
51  ggcagggcggg gatggcaaga tgcagcatca ctttgacggc agggttgcgt

```

```

101 tcgtcaaacg attcggacac caagccgctg tctcggctcga ggccgagggg
151 cagctgggtc atgtcggttc agccgatgga gaagccgctc aagtattgca
201 ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301 aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 cgacgttggc cagacccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcatt cggttcgtat acgtgcccgc
501 cgaccagggt ggcgtattcg ttggatttga agtcggacat acggacgatg
551 gttttacgcy gataaacgga tgcggcaagc gttgccacgc cttcggcgat
601 tttatcgacy tagaagtcga caggggatgc gtaaccggcg atgcggcgga
651 taatttccgc tttcagttcg tcgtcttgtt tgtcaaatc caacaaggct
701 ttcgggtgga tgcgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801 tttccgacgt catcatgact ttgacgggtg cttttggcat attgtccaag
851 gcgacatcgg taatttgtac gtccagcagg ccggcataga taaagccggt
901 atcgcttcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951 cggtcgcatt gccgcagccg acgacggcag gaataccag ttcgcgcgcg
1001 atgatggcgg cgtggcaggt gcgtccgcgc cggttgggtca cgatggcgga
1051 agcacgttcc atcacgggtt cccaatccgg atcggtcgat tcggtaacca
1101 gtacgtcgcc ggcttcgacy gaatccatct cggaaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgcacaa
1201 gacgggtttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttggga tttgacggtt tcggggcggg cttgcaggat gttaggtttg
1301 ccgtccagcg cgtcgcgctc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgctg agtgtgcaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgcgg tcttcttcgg ggaacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgttcga
1501 acccatggtc ttgcgcagga tggcggttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLTLADT DIFVLLAAGG DGKMQHHFDG RFAFVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAADQV GVFGVFEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVVKF QQGFRVDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDGDFGCFWH IVQGDIGNLY VQQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHGDDG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHLLALTD FLTDGTTFAQ
401 DGEFFAVDQVA AQVAAAFLLG FDGFGAGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQRVVQC LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGFEBI KFVRVDRALY DVFAQTVRGG NKDDLTVVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atggtcggac sggccttgac cgcagatgcc gacatatttg tctgcttgc
51  ggcaggcggg gatggcaagg tgcagcatca ctttgacggc agggttgcgt
101 tcgtcaaacg attcggatac caagccgctg tcgcggctcga gaccgagggg
151 cagttgggtc atgtcggttc agccgatgga gaagccgctc aagtattgca
201 ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtctt
301 gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 caacggttgy caacccatt tcattcgcgga cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcatt cggttcgtat acgttgcgcg
501 cgaccagggt ggcgtattcg ttggatttga agtcggacat acggacgatg
551 gttttacgcy gataaacgga tgcggccaat gtcgccacgc cttcggcgat
601 tttatcgacy tagaagtcga caggggacgc gtaaccggcg atacggcggg
651 taatttccgc ttttaattcg tcgtcttgtt tgtcaaatc caacaargct

```

```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca ggttggcgaa gctgaatgag agttcgggat
801 tgccgacgtt catcatgact tttacagggt ctttaggcat attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgcccttg gcacaggata cggttaactt ttgaccgttt ttcagcaatt
951 cggttgcatg gccgcagcgg acaacggcag gaatgcccaa ttcacgcgag
1001 atgatggcgg cgtggcagggt acggccgccc cggttggtta cgatggcaga
1051 agcacgtttc atcacgggtt cccaatccgg atcgggtcat tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc ttaatacagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgcggc cttcgcataa
1201 tacggttttg tcgccgttga tggcgaagcg gcgcaggttg cggttgccct
1251 cttcttgagg ttttacggtt tcgggacggg cttgcaggat gtagagtttg
1301 cgtccaagc cgctcgctcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgccaa ctcagtaatt tcttcgctcg
1401 taatggagaa gcggttcggt tcttcctcgg ggacatcgac gttggttacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtggtttga
1501 acccatggtt ttacgcagga tggcgggctt gcccggtttg agcgtgggtt
1551 tgaacacatr aaattcgctc gggttgaccg caccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

m501.pep

```

1  MVGXALTADA DIFVLLAAGG DGKVQHFDG RFAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFVGFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QXFGVDTDL AVDDKFHTRQ
251 ADAFAQQVGE AECEFGIADV HHDFYRCFRH IVXGDIENLY VQQTGIDKAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAAVGNDGR
351 STFHHGFPIR IGHVGNFYVA GFDGIHLGSI FNQAHLLALD FLTDGAFAFX
401 YGFVAVDGEA AQVAVALFLG FYGFGTGLQD VEFVAVAVAS PFDIHRAAVV
451 FFDGQCVMRQ LSNFFVGNGE AVAVFLGDDI VGYGFTGFCF VGKNHFDVFX
501 THGFTQDGLL ARFERGFEXH KFVRVDRTLY DVFAQTVRGG NKDDLIVXGF
551 GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

m501/g501

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFDGRFAFVKRFGYQAAVAVETEGQLGHVVRADG					
g501	MVGRTLTADTDIFVLLAAGGDGKMQHFDGRFAFVKRFGHQAASVEAEGQLGHVVRADG					
	10	20	30	40	50	60
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
g501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQCLNHCFCGFAQSADERNHDFDVG					
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
g501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQCLNHCFCGFAQSADERNHDFDVG					
	70	80	90	100	110	120
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFEVGH					
g501	QTHFVTNAFQGFQGETVFEALGNITRRTTEAQHRVFFMRVYVAADQVGVFVGFEVGH					
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFEVGH					
g501	QTHFVTNAFQGFQGETVFEALGNITRRTTEAQHRVFFMRVYVAADQVGVFVGFEVGH					
	130	140	150	160	170	180
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXFGVDTDL					
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXFGVDTDL					

g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAAADNFRFQFVVLVVKFQQGFRVDADL
	190 200 210 220 230 240
m501.pep	250 260 270 280 290 300
	AVDDKFHTRQADAFAGQVGEAECEFGIADVHDFYRCFRHIVXGDIIGNLYVQQTGIDKAG
g501	AVDDKFHTRQADAFAGQIGEAECFEGIADVHDFDGCFWHIVQGDIGNLYVQAGIDKAG
	250 260 270 280 290 300
m501.pep	310 320 330 340 350 360
	IAFGTGYGNFLTTFVQQFGCIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPPIR
g501	IAFGTGYGNFLTTFVQEFGRIAAADNGRNTQFARDDGGVAGASAAVGHGDSSTFHHGFPPIR
	310 320 330 340 350 360
m501.pep	370 380 390 400 410 420
	IGHVGNQYVAGFDGIHLGSI FNQAH LALTDFLT DGA AFAXYGFVAVDGEAAQVAVALFLG
g501	IGHVGNQYVAGFDGIHLGSI FNQAH LALTDFLT DGT TFAQDGF FAVDGVAAQVAAFFLG
	370 380 390 400 410 420
m501.pep	430 440 450 460 470 480
	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDGGCVMRQLSNFFVGNGEAVAVFLGDID
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDGGQVVQCGLDFFVGNGEAVAVFFGDFD
	430 440 450 460 470 480
m501.pep	490 500 510 520 530 540
	VGYGFTGFCFVGKNHFDVFXTHGFTQDGLARFERGFEXKFFVRVDRDLYDVFAQTVRGG
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGFEXIKFFVRVDRALYDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	550
	NKDDLIVXGFGVGEHHT
g501	NKDDLIVVAGFGVGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq (partial)

1	ATGGTTCGAC	GGGCCTTGAC	CGCAGATGCC	GACATATTTG	TTCTGCTTGC
51	GGCAGCGCGA	GATGGCAAGG	TGCAGCATCA	CTTTGACGGC	AGGGTTGCGT
101	TCGTCAAACG	ATTTCGGATAC	CAAGCCGCTG	TCGCGGTCTGA	GACCGAGGGT
151	CAGTTGGGTC	ATGTCGTTTCG	AGCCGATGGA	GAAGCCGCTG	AAGTATTGCA
201	GGAATTGTTC	CGCCAATACC	GCGTTGCTCG	GCAGCTCGCA	CATCATAATC
251	AGGCGCAGGC	CGTTTTTGCC	GCGTTCCAAG	CCGTTTTCTT	TCAGGGCTTT
301	GACAACGGCT	TCGGCTTCGC	CCAAAGTGCG	GACGAACGGA	ATCATGATTT
351	CAACGTGGT	CAACCCCAT	TCATCGCGGA	CGCGTTTCAA	GGCTTTGCAT
401	TCCAAGCGA	AACAGTCTT	GAAGTTGTCG	GCGACATAAC	GCGCCGCACC
451	ACGGAAGCCC	AACATCGGGT	TTTCTTCATG	CGGTTCGTAT	ACGTTGCCGC
501	CGACCAGGTT	GGCGTATTCG	TTGGATTGTA	AGTCGGACAT	ACGGACGATG
551	GTTTTACGCG	GATAAACCAG	TGCGGCCAAT	GTCGCCACGC	CTTCGGCGAT
601	TTTATCGACG	TAGAAGTCGA	CAGGGGACGC	GTAACCGCGC	ATACGGCGGG
651	TAATTTCCGC	TTTTAATTCG	TCGTCTTGTT	TGTCAAATTC	CAACAAGGCT
701	TTGGGGTGGA	TACCGATTG	GCGGTTGATG	ATAAATTCCA	TACGCGCCAA
751	GCCGATGCCT	TCGCTGGGCA	GGTTGGCGAA	GCTGAATGCG	AGTTCGGGAT
801	TGCCGACGTT	CATCATGACT	TTTACAGGTG	CTTTAGGCAT	GTTGTCCAAA
851	GCAACATCGG	TAATTTGTAC	GTCCAGCAGG	CCGGAGTAGA	TGAAGCCGGT
901	ATCGCCTTCG	GCACAGGATA	CGGTAACCTC	TTGACCGTTT	TTCAGCAATT
951	CGGTTGCATT	GCCGCAGCCG	ACAACGGCAG	GAATACCCAG	TTCCGCGCGC

```

1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGGT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTCGCACAA
1201 GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CGGCTGCCTT
1251 CTTCTGCGGA TTTGACGGTT TCGGGACGGG CTTCGAGGAT GTAGAGTTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTTCGATG TCCATCGGGC GGCCGTAGTG
1351 TTTTTCGATG GTCAGTGCGT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGGTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGATC GACGTTTTTC
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGTCGT AACCAGATTG
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

**a501.pep**

```

1 MVGRALTADA DIFVLLAAGG DGKVQHFFDG RFAFVKRFGY QAAVAVETEG
51 QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFVGFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR F*FVVLVFKF QQGFVVDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH VVQSNIGNLY VQAGVDEAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHDDG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAAFAQ
401 DGFFAVDRKA AQVAAFFLG FDGFGTGLQD VEFVAVAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVNGE AVAVFFGDID VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVFAQTVG*S DKDDLVTVTG
551 GIEGEHH

```

**m501/a501 90.3% identity in 557 aa overlap**

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
a501	MVGRALTADADIFVLLAAGGDGKVQHFFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFNGFGFAQSADERNHDFNVG					
a501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFNGFGFAQSADERNHDFNVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQGETVFVVGDI TRRTTEAQHRVFFMRVYVAADQVGVFVGFEVGH					
a501	QPHFIADAFQGFQGETVFVVGDI TRRTTEAQHRVFFMRVYVAADQVGVFVGFEVGH					
	130	140	150	160	170	180
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVFKFQQXFGVDL					
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVFKFQQXFGVDL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVXGDIIGNLYVQQTGIDKAG					
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVQSNIGNLYVQAGVDEAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m501.pep	IAFGTGYGNFLTTFVQQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGRSTFHHGFPIR					
a501	IAFGTGYGNFLTTFVQQFGCIAAADNGRNTQFARDDGGVAGTSAPVGHDDGSAFHHRFPIW					
	310	320	330	340	350	360

735

	370	380	390	400	410	420
m501.pep	IGHVGN EYVAGFDGIHLGSI FNQAH LALTDFLT DGAA FAXYGFVA VDGEAAQVA VALFLG					
a501	VGHVGNQYVAGFDGIHLGSI FNQAYLALTDFLT DGAAFAQDGF FAVDRKAAQVA AAFVLG					
	370	380	390	400	410	420
m501.pep	430	440	450	460	470	480
	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGGQCVMRQLSNFFVGNGEAVAVFLGDID					
a501	FDGFGTGLQDVEFAVQAVASPFDVHRAAVVFFDGGQCVMRQLGDDFFVGNGEAVAVFFGDID					
	430	440	450	460	470	480
m501.pep	490	500	510	520	530	540
	VGYGFTGFCFVGKNHFDVFXTHGFTQDGLARFERGFEXXKFVRVDRTLYDVFAQTVRGG					
a501	VGYRFAGFCFVGKNHFDVFXAHGFAQDGRFACFQRGFIEFVGIDCALYDVFAQTVGXS					
	490	500	510	520	530	540
m501.pep	550	559				
	NKDDLIVXGFGVEGEHHTX					
a501	DKDDLVTGFGIEGEHH					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

g502.seq

```

1 atgatgaaac cgcacaacct gttccaattc ctgcgcgttt gtcacctgac
51 cgtcgccgtc gcttccgcac aggcgggcgc ggtggacgcg ctcaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca aaccgtccaa
151 agcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgccc
201 gggcctcttc aaatgggaat acactttgcc ctacagacag actattgtcg
251 gcgacggtca aaccgtttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcgggcgc agccccgcgc ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcaacg cccaaacgca acaacgccgc
451 ctaccaatac atccgcacgc gcttcaaagg cggcaacctc gccgccatgc
501 agcttaa
```

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

g502.pep

```

1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51 SKKKTQTAHG TFKILRPGLF KWEYTLRYRQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RNAQTQRRR
151 LPIHPHRLQR RQPRRHAA*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

m502.seq

```

1 atgatgaaac cgcacaacct gttccaattc ctgcgcgttt gtcacctgac
51 cgtcgccgtc gcttccgcac aggcgggcgc ggtagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca amccgtccaa
151 wgcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgacc
201 gggccttttc aaatgggaat acaccaaact t.acaggcaa accatcgteg
251 gcgacggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc cataggcgsc agccccgcgc ccatcctgtc
351 gaacaaarcc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgccggcta
451 ccaatacatc cgcacggct tcaaaggcgc caacctcgcc gccatgcagc
501 tyaa
```

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

m502.pep

```

1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51 XXXKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGX SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQRRRL
151 PIHPHRLQRR QPRRHAA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLPLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYV-GNAQTQRRLLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQRRLLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502.seq

1	ATGATGAAAC	CGCACAACT	GTTCCAATTC	CTCGCCGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTCTG
251	GCGACGGTCA	AACCGTTTGG	CTCTACGATG	TCGATTGGC	ACAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCCG	CCATCCTGTC
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCCC	AAACGCAACA	ACGCCGGCTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502.pep

1	MMKPHNLFQF	LAVCSLT	SVS	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKKTQTAHG	TFKILRPGLF	KWEYTS	SPYKQ	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQRRLL	
151	PIHPHRLQRR	QPRRHAA*				

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSYKQTVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYVGNAQTQRRLLPIHPHRLQRRQPRRHAA					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQRRLLPIHPHRLQRRQPRRHAA					
	130	140	150	160		



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

## g502-1.seq

```

1  ATGatGAAAc  cgcaCaacct  gttccaaATtc  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGGCG  GGTGGACGCG  CTCAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGCCC
201 GGGCCTCTTC  AAATGGGAAT  ACACTTTGCC  CTACAGACAG  ACTATTGTCT
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATCGGCGGC  AGCCCCGCGC  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGTTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CGGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GCGGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAAA
601 GCGGTGGACG  TGTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

## g502-1.pep

```

1  MMKPHNLFQF  LAVCSLTVAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTVO
51  SKKKTQTAHG  TFKILRPGLF  KWEYTLPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIGG  SPAAILSNKT  ALESSYTLKE  DGSSNGIDYV  RATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSISF  GGLNTNPQLS  RGAFKFTPPK
201 GVDVLSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

## m502-1.seq

```

1  ATGATGAAAC  CGCACAACTT  GTTCCAATTC  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGGCG  GGTAGACGCG  CTTAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGACC
201 GGGCCTTTTC  AAATGGGAAT  ACACCAAACC  TTACAGGCAA  ACCATCGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATCTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATAGCGCGC  AGCCCCGCGC  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CTGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GCGGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAAA
601 GCGGTGGACG  TGTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

## m502-1.pep

```

1  MMKPHNLFQF  LAVCSLTVAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTVO
51  SKKKTQTAHG  TFKILRPGLF  KWEYTKPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIGG  SPAAILSNKT  ALESSYTLKE  DGSSNGIDYV  LATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSISF  GGLNTNPQLS  RGAFKFTPPK
201 GVDVLSN*

```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVOQSKKKTQTAHG					
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVOQSKKKTQTAHG					
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
g502-1	TFKILRPGLFKWEYTLPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
g502-1	TFKILRPGLFKWEYTLPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGLAAMQLKDSFGNQTSISF					
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAGYQYIRIGFKGGLAAMQLKDSFGNQTSISF					
	130	140	150	160	170	180
m502-1.pep	ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGLAAMQLKDSFGNQTSISF					
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAGYQYIRIGFKGGLAAMQLKDSFGNQTSISF					
	130	140	150	160	170	180

738

```

                190      200
m502-1.pep      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||
g502-1          GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACT GTTCCAATC CTCGCCGTTT GTCCTCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGCGGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCTCTTTT AAATGGGAAT AACTTCGCC TTACAAACAG ACTATTGTCTG
251 GCGACGGTCA AACCCTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCTG
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGCG
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GCGCGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCGCCCCAAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51 SKKKTQTAHG TFKILRPLGF KWEYTSPLYQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTISIF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep      MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG
                |||
m502-1          MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep      TFKILRPLGFKWEYTSPLYQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
                |||
m502-1          TFKILRPLGFKWEYTKPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep      ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
                |||
m502-1          ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
                130     140     150     160     170     180

                190     200
a502-1.pep      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||
m502-1          GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgctcgcatc ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaagggcgt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaaatgcy ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSSTNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:



m503.pep  
1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF  
51 ASAAEMRSLR PLCARNAR\*

### Homology with a predicted ORF from *N. gonorrhoeae*

m503/g503

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

m503/a503 100.0% identity in 68 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

g503-1.seq

```
1  ATGGCGCGGT  CGTTGTACAG  GGAGGCGAAA  ACGTGGCGCA  TCGCTTTTTT
51  AACGTTATCC  AAGCCATGTA  TATTCAGGAA  CGTTCCTGT  TGGCGGGCAA
101 ATGATGCGTC  GGGCAGGTCT  TCGCGCGTTG  CGGAAGACGC  TACGGCAACG
151 GAAATGTCGC  CGCCGTCGGC  ATCGGTAATC  ATTTTGTGCC  ATGCGCGTTC
201 GATTTCCGCA  TCGAGCTGTT  CGGGGAAGGG  CGTGCTCAAA  ATCCATTGCG
251 GGATTCTTTT  GCCGACGCGT  GCCAGTTCGG  AAACGTCCTC  GACATCCAAT
301 TTTGCCAGAG  CGGCGGAAAT  GCGTTCGTTC  AGACCGTGTG  GTGCGAGAAA
351 TCGCGCGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

g503-1.pep  
 1 MARSLYREAK TWRI AFLTSL KPLIFRKVSC WPANDASGRS SAVAERTAT  
 51 EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSSTN  
 101 FARAAEMRSF RPLCARNAR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

m503-1.seq  
 1 ATGGCACGGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT  
 51 AACGTTATCC AAGCCGTTGA TGTCAAGAA GGTTTCCTGT TGTCCAGCGA  
 101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG  
 151 GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC  
 201 GATTTCCGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC  
 251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT  
 301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA  
 351 TGCGCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

m503-1.pep  
 1 MARSLYREAN TWCIASTLS KPLMFKKVSC CPANDASGRS SAVAERTAT  
 51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSSTN  
 101 FASAAEMRSL RPLCARNAR\*

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRI	AFLTSLKPLIFRKVSCWPANDASGRSSAVAERTATE	MSAPSASVI			
m503-1	MARSLYREANTWCI	ASLTLSKPLMFKKVS	CCPANDASGRSSAVAERTATE	MSAPPASAT		
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSSTNFARAAEMRSR	RPLCARNARX				
m503-1	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSSTNFASAAEMRSL	RPLCARNARX				
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

a503-1.seq  
 1 ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT  
 51 AACGTTTTC AAGCCGTTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA  
 101 ATGATGCGTC GGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG  
 151 GAAATGTCCG CGCCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC  
 201 GATTTCCGCA TCGAGCTGTT CGGGGAAAGG CGTGTCCAAA ATCCATTGGC  
 251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT  
 301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA  
 351 TGCGCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

a503-1.pep  
 1 MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAERTAT  
 51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSSTN  
 101 FASAAEMRSL RPLCARNAR\*

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRI	ASLTFSKPLIFRKVSCWPANDASGRSSAVAERTATE	MSAPPASAT			
m503-1	MARSLYREANTWCI	ASLTLSKPLMFKKVS	CCPANDASGRSSAVAERTATE	MSAPPASAT		
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSSTNFASAAEMRSL	RPLCARNARX				
m503-1	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSSTNFASAAEMRSL	RPLCARNARX				
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

g504.seq

```

1   atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgaccat ccgctgaac
151 catcctttga ccttgacgag catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttgga
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccatcgtgta ccgcatccgt gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattattttt
551 ggctgaccgg cacgcgcagc ggcttgagc agcaataacc ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaag gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatcgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgaccggtt cgcggggtgc gcttttggtc tatctcggct cggatttggt
1101 ggttttggtt acagtattta tgttttatgt gcccaaaaaa cgggcgtggg
1151 tattgttttc aaacdcaaaa atccggtttg ctatgtcttc ggcccgcagc
1201 gaacgggatt tgcagaagga atttcaaaaa cagtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

g504.pep

```

1   MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLR DASREPVVLK ATSIHQPPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKQYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMLAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLHS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPPK RAWVLSNKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

m504.seq..

```

1   atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgatttttac aatacgggta tgccgcgcga tttcgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgaccat ccgctgaac
151 catcctttga ccttgacgag catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttgga
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtagcgt gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccggtttt gcaggaaacag gattattttt
551 ggattaccgg cacgcgcagc ggcttgagc agcaataacc ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaag gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatcgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgtc gggtttgag

```

1051 atgacccgtt ccccggtgc gcttttggtc tatctcggct cgggtctgtt  
 1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg  
 1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgacagc  
 1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg  
 1251 gctcggcaag gacttgaatc atga

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

m504.pep..  
 1 ILVQDLPFEEV KLKFFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN  
 51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE  
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN  
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR  
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN  
 251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR  
 301 RYGLPEWQQD EARNRFLHLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ  
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS  
 401 ERDLQKEFPK HVESLQRLGK DLNHD\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae*:

m504/g504

	10	20	30	40	50	60
m504.pep	ILVQDLPFEEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
	:     :     :     :     :     :					
g504	MLVQDLPFEEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m504.pep	YQASFADGGSDLTFKAWNLGDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	:     :     :     :     :					
g504	YQASFADGGSDLTFKAWNLRDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
	:     :     :     :     :					
g504	MSEGAREKSLKSTLNDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPILQDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m504.pep	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI					
	:     :     :     :     :					
g504	DYFWLTGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKDAPAEI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m504.pep	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR					
	:     :     :     :     :					
g504	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKGQQDKMQGYFYEMLYGVMNAALDETIR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m504.pep	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV					
	:     :     :     :     :					
g504	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m504.pep	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK					
	:     :     :     :     :					

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g504 YLGSVLLVLGTVFMFYVPPKKRAWVLSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK  
 370 380 390 400 410

m504.pep DLNHD  
 |||||  
 g504 DLNHD  
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq  
 1 ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAAGTAAAAA AATTCCATAT  
 51 CGATTTTAC AATACGGGTA TGCCGCGCGA TTTTGCCAGT GATATTGAAG  
 101 TAACGGATAA GGCAACCGGT GAGAACTCG AGCGCACCAT CCGCGTGAAC  
 151 CATCCTTTGA CCTTGCACGG CATCACGATT TATCAGGCGA GTTTTGCCGA  
 201 CGGCGGTTTC GATTGACAT TCAAGGCGTG GAATTGGGT GATGCTTCGC  
 251 GCGAGCCTGT CGTGTGAAG GCAACATCCA TACACCAGTT TCCGTGGAA  
 301 ATTGGCAAAC ACAATATCG TCTTGAGTTC GATCAGTTTA CTTCTATGAA  
 351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAAAAGC CTGAAATCCA  
 401 CGCTGAACGA TGTCCGCGCC GTTACTCAGG AAGGTAAAAA ATACACCAAT  
 451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GGCAGGCGGT  
 501 CGAATATAAA AACTATATGC TGCCGTTTTT GCAGGAACAG GATTATTTTT  
 551 GGATTACCGG CACGCGCAGC GGCTTGCAGC AGCAATACCG CTGGCTGCGT  
 601 ATCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCGTGA  
 651 GTTTTGAAGA GATGGGGAAG GCGCGAAACG TCTGGTTGCC GACGCAACCA  
 701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGCTGGC TGCGGAAAAAC  
 751 ACGTGGAACA TCTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT  
 801 TACGTCCAAT ATCCCGAAAG AGCAGCAGGA TAAGATGCAG GGCTATTTCT  
 851 ACGAAATGCT TTACGGCGTG ATGAACGCTG CTTTGGATGA AACCATACGC  
 901 CCGTACGGCT TGCCCGAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCCT  
 951 GCTGCACAGT ATGGATGCGT ACACGGGTTT GACCGAATAT CCCGCGCCTA  
 1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TGCGTTCGTC GGGTTTGCAG  
 1051 ATGACCCGTT CCCCGGGTGC GCTTTTGGTC TATCTCGGCT CCGTGCTGTT  
 1101 GGTATTGGGT ACGGTATTGA TGTTTTATGT GCGCGAAAAA CCGGCGTGGG  
 1151 TATTGTTTTT AGACGGCAA ATCCGTTTTG CCATGTCTTC GGCCGCGAGC  
 1201 GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG  
 1251 GCTCGGCAAG GACTTGAATC ATGACTGA

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep  
 1 ILVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN  
 51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE  
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKRS LKSTLNDVRA VTQEGKKYTN  
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQYRWLR  
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN  
 251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR  
 301 RYGLPEWQQD EARNRFLLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ  
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS  
 401 ERDLQKEFPK HVESLQRLGK DLNHD\*

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPEFV KLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLEIRTVNHPLTLHGITI					
a504	ILVQDLPEFV KLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLEIRTVNHPLTLHGITI					
	10	20	30	40	50	60
m504.pep	YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE IGKHKYRLEF DQFTSMNVED					
a504	YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE IGKHKYRLEF DQFTSMNVED					
	70	80	90	100	110	120
m504.pep	MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYK NYMLPVLQEQ					
a504	MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYK NYMLPVLQEQ					
	130	140	150	160	170	180

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|||||
a504 MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKKNYMLPVLQEQ
      130      140      150      160      170      180
      190      200      210      220      230      240
m504.ppep DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
|||||
a504 DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
      190      200      210      220      230      240
      250      260      270      280      290      300
m504.ppep REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
|||||
a504 REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
      250      260      270      280      290      300
      310      320      330      340      350      360
m504.ppep RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
|||||
a504 RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
      310      320      330      340      350      360
      370      380      390      400      410      420
m504.ppep YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
|||||
a504 YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
      370      380      390      400      410      420

m504.ppep DLNHDX
          |||||
a504      DLNHDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

```

g505.seq
1 atgtttcgtt tacaattcag gctgtttccc cctttgcgaa ccgccatgca
51 catcctgttg accgcccgtc tcaaatgcct ctccctgctg tcgctttcct
101 gtctgcacac gctgggaaac cggctcggac atctggcggt ttacctttta
151 aaggaagacc gcgcgcgcat cgtcgccaat atgcggcagg cgggtttgaa
201 ccccgacacg cagacgggtca aagccgtttt tgcggaaaac gcaaaatgcg
251 gtttggaact tgcccccgcg tttttcaaaa aaccggaaga catcgaaaac
301 atgttcaaag cgttacacgg ctgggaacac gtgcagcagg ctttggaaca
351 gggcgaaggg ctgctgttca tcacgccgca catcggcagg tacgatttgg
401 gcggacgcta catcagccag cagcttcctg tccacctgac cgccatgtac
451 aagccgcca aaatcaaacg gatagacaaa atcatgcagg cgggcagggt
501 gcgcggcaaa ggcaaaaccg cggccaccgg catacaaggg gtcaaacaaa
551 tcatcaaggc cctgcgcgcg ggcgaggcaa ccatcatcct gcccgaaccac
601 gtcccttctc cgcaggaagg cggcggcggt tgggcggatt ttttcggcaa
651 acctgcatac accatgacac tggcggcaaa attggcacac gtcaaaggcg
701 tgaaaaccct gtttttctgc tgcgaacgcc tgcccagcgg acaaggcttc
751 gtgttgacac tccgccccgt ccaaggggaa ttgaacggca acaaagccca
801 cgatgccgcc gtgttcaacc gcaataccga atattggata cgccgttttc
851 cgacgcagta tctgtttatg tacaaccgct ataaaacgcc gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

```

g505.pep
1 MFRLQFRLFP PLRTAMHILL TALLKCLSL SLSCLHTLGN RLGHAFYLL
51 KEDRARIIVAN MRQAGLNPD TQVKAVFAET AKCGLELAPA FFKKPEDIET
101 MFKAHVHGEH VQALDKGEG LLFITPHIGS YDLGGYISQ QLPFHLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTGIQG VKQIIKALRA GEATIILPDH
201 VPSPQEGGGV WADFFGKPAY TMTLAAKLAH VKGVKTLFFC CERLPDQGQF
251 VLHIRPVQGE LNGNKAHDAA VFNRNTEYWI RRFPTQYLFM YNRYKTP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:



m505.seq (partial)

```

1 GGCATGTTTC GTTACAATT CAGGCTGTTT CCCCCTTTC GAACCGCCAT
51 GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACC GGCTCG GACATCTGGC GTTTTACCTT
151 TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCGAC CCAAAACGG TCAAAGCCGT TTTTGGCGAA ACGGCAAAAG
251 GCGGTTTGA ACTTGCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTTGA
351 CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGCTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
451 TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTCGCGGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
601 ACGTCCCCTC CCCTCAAGAA GGCGGGGAAG GCGTATGGGT GGATTTCTTC
651 GGCAAACCTG CCTATACCAT GACGCTGGCG GCAATATTGG CACACGTCAA
701 AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GGCGGACAAAG
751 GTTTCGATT GCACATCCGC CCCGTCCAAG GGAATTGAA CGGCGACAAA
801 GCCCATGATG CCGCGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
851 TTTTCCGACG CatATC...

```

This corresponds to the amino acid sequence &lt;SEQ ID 1370; ORF 505&gt;:

m505.pep (partial)

```

1 MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSC LHTLGN RLGH LAFYLL
51 KEDRARIVAN MRQAGLN PDP KTVKAVFAET AKGGL ELAPA FFRK PED IET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGG RYISQ QLPF PLTAMY
151 KPPKIKAI DKIMQAGRV RGK GKTAPT SIQG VKQI IKA LRS GEATI VLPDH
201 VPSPQEGG EG VWVDFG KPA YTM TLAA XLA HVKG VKTLFF CCERLP GGQG
251 FDLHIRPV QG ELNGDKA HDA AVFN RNAEY W IRRFP THI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLSLSCLHTLGNRLGH LAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLN PDP KTVKAVFAETAKGGL ELAPAFFRKPEDIETMFKAVHGW EHVQQALDKHEG					
g505	MRQAGLN PDP KTVKAVFAETAKGGL ELAPAFFRKPEDIETMFKAVHGW EHVQQALDKGEG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGG RYISQQLPFPPLTAM YKPPKIKAI DKIMQAGRV RGKGTAPT SIQG					
g505	LLFITPHIGSYDLGG RYISQQLPFPPLTAM YKPPKIKAI DKIMQAGRV RGKGTAPT GIQG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m505.pep	VKQI IKA LRS GEATI VLPDHVPSPQEGG EVWVDFG KPAYTMTLAA XLAHVKG VKTLFF					
g505	VKQI IKA LRAGEATI ILPDHVPSPQEGG -GVWADFFG KPAYTMTLAA KLAHVKG VKTLFF					
	190	200	210	220	230	
	250	260	270	280	289	
m505.pep	CCERLP GGQGF DLHIRPVQ GELNGDKA HDA AVFN RNAEY W IRRFP THI					
g505	CCERLP DGQGF VDLHIRPVQ GELNGKA HDA AVFN RTEY W IRRFP TQYLFMYNRYKTP					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

## a505.seq

```

1 ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51 CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAAGGCG
251 GTTTGGAAGT TGCCCCGCG TTTTTCAGAA AACCAGGAAGA CATAGAAACA
301 ATGTTCAAAG CCGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGA AAAACCG CGCCTACCAG CATAACAAGG GTCAAAACAA
551 TCATCAAAGC CCTGCGTTCG GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGA AAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTGC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

## a505.pep

```

1 MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSC LHTLGN RLGH LAFYLL
51 KEDRARI VAN MRQAGMNPDP KTVKAVFAET AKGGL ELAPA FFRKPEDIET
101 MFKA VHGWEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPK IKAIDK IMQAGRVRGK GKTAPTSIQG VKQI IKA LRS GEATIVLPDH
201 VPSPQEGGEG VWVDFFGKPA YMTLA AKLA HVKG VKT LFF CCERLPGGQG
251 FDLH I RVPVQG ELNGDKAHDA AVFN RNAEYW IRRFPTQYLF MYNRYKMP*

```

m505/a505 99.0% identity in 287 aa overlap

m505.pep	10	20	30	40	50	60
	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSC LHTLGNRLGH LAFYLLKEDRARI VAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSC LHTLGNRLGH LAFYLLKEDRARI VAN					
	10	20	30	40	50	60
m505.pep	70	80	90	100	110	120
	MRQAGLNPD PKTVKAVFAETAKGGL ELAPFAFFRKPEDIETMFKA VHGWEHVQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGL ELAPFAFFRKPEDIETMFKA VHGWEHVQALDKHEG					
	70	80	90	100	110	120
m505.pep	130	140	150	160	170	180
	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPK IKAIDKIMQAGRVRGKGKTAPTSIQG					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPK IKAIDKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	190	200	210	220	230	240
	VKQI IKA LRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAXLAHVKG VKT LFF					
a505	VKQI IKA LRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAXLAHVKG VKT LFF					
	190	200	210	220	230	240
m505.pep	250	260	270	280		
	CCERLPGGQGF DLH I RVPVQGE LNGDKAHDA AVFN RNAEYWIRRFPTHI					
a505	CCERLPGGQGF DLH I RVPVQGE LNGDKAHDA AVFN RNAEYWIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

## m505-1.seq

```
1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CTTTGGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCACCCC AAAACGGTCA AAGCCGTTTT TCGGAAACG GCAAAAGGCG
251 GTTTGGAACT TGCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGCG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGGTGAC CGCCATGTAC
451 AAACGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAACAAACG CGCCTACCAG CATAAAGGG GTCAAACAAA
551 TCATCAAAGC CTGCGTTTCG GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCTCTCCC CTCAAGAAGG CCGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAGAC CCTGTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGCG ACATCCGCC CGTCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCGGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAT GCCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

## m505-1.pep

```
1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGLNPD PKTVKAVFAET AKGGLLELAPA FFRKPEDIE
101 MFKAVHGW EHVQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAI DKIMQAGRVRGK GKTAPTSIOG VKQIIKALRS GEATIVLPDH
201 VPSPQEGG EGWVDFFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQ GELNGDKAHD AAVFNRAEYW IRRFPTQYLF MYNRYKMP*
```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTL	GNRLGHAFYLL	KEDRARIVAN
g505	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTL	GNRLGHAFYLL	KEDRARIVAN
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPD	PKTVKAVFAET	AKGGLLELAPA	FFRKPEDIE	TMFKAVHGW	EHVQALDKHEG
g505	MRQAGLNPD	TKTVKAVFAET	AKGGLLELAPA	FFRKPEDIE	TMFKAVHGW	EHVQALDKHEG
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAI	DKIMQAGRVR	GKGTAPTSIOG
g505	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAI	DKIMQAGRVR	GKGTAPTSIOG
	130	140	150	160	170	180
m505-1.pep	VKQIIKALRS	GEATIVLPDH	VPSPQEGG	WVDFFGKPA	YMTLAAKLA	HVKGVKTLFF
g505	VKQIIKALRS	GEATIVLPDH	VPSPQEGG	WVDFFGKPA	YMTLAAKLA	HVKGVKTLFF
	190	200	210	220	230	240
m505-1.pep	CCERLPGGQ	GFDLHIRPV	QGELNGDKA	HDAAVFNRA	EYWIRRFPT	QYLFMYNRYKMPX
g505	CCERLPGGQ	GFDLHIRPV	QGELNGDKA	HDAAVFNRA	EYWIRRFPT	QYLFMYNRYKTPX
	250	260	270	280	290	299
m505-1.pep	CCERLPGGQ	GFDLHIRPV	QGELNGDKA	HDAAVFNRA	EYWIRRFPT	QYLFMYNRYKMPX
g505	CCERLPGGQ	GFDLHIRPV	QGELNGDKA	HDAAVFNRA	EYWIRRFPT	QYLFMYNRYKTPX
	240	250	260	270	280	290

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTL	GNRLGHAFYLL	KEDRARIVAN
a505	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTL	GNRLGHAFYLL	KEDRARIVAN
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m505-1.pep  MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMFKAVHGWEHVQQALDKHEG
a505          MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMFKAVHGWEHVQQALDKHEG
              70      80      90      100     110     120

m505-1.pep  LLFITPHIGSYDLGGYISQQLPPLTAMYKPPKIKAIQAGRVRGKGTAPTSTIQG
a505          LLFITPHIGSYDLGGYISQQLPPLTAMYKPPKIKAIQAGRVRGKGTAPTSTIQG
              130     140     150     160     170     180

m505-1.pep  VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
a505          VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
              190     200     210     220     230     240

m505-1.pep  CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRFPQYLFMYNRYKMPX
a505          CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRFPQYLFMYNRYKMPX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

```

g506.seq
1  ATGGCGGTAT TTGATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
51  TGTCAAACAA AGCCTGTTTC TGC CGCTCGT TCATCAGGTT GAACAAGGCG
101 CGCGGTTGGC TGAAGTAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCGC TTGATTTTCA AAGGCGGTTT GCGGAAGTCG GGTGTGTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGCGCG GGCCTTGTCG GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGATTG ACGGGGATTT GCGGAAGTT CACACCCAAG CGGTAACGTT
351 GCGCGTCGGC GTAATTGAAC AACCGGGCTT GCAACATTTT ATCCGGGCTC
401 GCGCCGATAC CGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTTCG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATAAGGCA CTTTTCGCGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTC GGGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTGCGGCT
651 GATGGCTTTC GCGGTCGTCG GCGATGATTT TTGCAGCTTC TTCGTTGGTC
701 AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGGAAATTCA CCAAAAACG
751 TTCGCCCCTC TCCTTCCAGA AGCTGTAGGT ATGCGAACC GAGCCGTGCA
801 TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGACGGG CTTGCGGCGC CAGCGTCCAG AAGTCCAGT TGTGTTGGC
901 GGAACGCATA TTGGTGCGCG GATCGCGTTT GACGGCTTTG TTCAGGTCGG
951 GGAATTTGCG CGGTCGCGC AGGAAGAACA CCGGCGTGTT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTTC GGTATAGAAT TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAAAT TTTGGCGCGG
1151 GTGTATTGTT TGATGTCGTG TGTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACGGCGCGCG CGTTGTTTAT
1351 GGTCAGATGG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTTGTTCTCT
1401 TTCTCAGGTT GGTCAAATGG GGGGCAAACG GCTTACAGTA CGATTGCGG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTGAATCG
1501 ACATTTTATT TTCCTTTTGC AAAAATATG GATGCGATTA TACGCCAAGA
1551 TTTTCGTTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

```

g506.pep
1  MAVFDEVGRI AHGCGGVVKQ SLFLRVVHVQ EQGARLAEVV VIVLAVVPVC
51  RVAVDFORRF GEVGLLLPLA EAVGFVVVQA AVVAVGAALS VALVAVNRAT
101 RTIDGDLAEV HTQAVTLRVG VIEQTGLQHF IRARADTONE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFG IGFRHDLVDH

```

201 RPFRELAALD GFVQVALMAF AVVGDDFCSF FVGQVFNPLL AAEMEFHPKT  
 251 FARFVPEAVG MRTEAVHMAV AGGNTAVAHH DGNLVQGFQ QRPEVPVVCG  
 301 GTHIGARIAF DGFVQVGEFA RVAQEEHGRV VADHIPVAFF GIEFQRKTAD  
 351 VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR  
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGGQAVL IVGNGRAVVH  
 451 GQMGYGAFFG SHRSCSFSQV GQMGKKRLTV RFGGKRIRNR FLDCNKFLES  
 501 TFYFPFAKTM DAIIRQDFRY \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

m506.seq

1 ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT  
 51 TGCCGAACAA TGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAGGGCG  
 101 CGCGGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC  
 151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GGCGAAATCG GGTGTGTGCT  
 201 GCCATTGGCC GAAGCTGTyG GGTTCGTAGT GCGGCAGGCT GCCGyAGTTG  
 251 CCGTCGGCGC GGCCTTGCCC GTyGCGsTgr TTgCTGTgAA CAsGGCAACG  
 301 CGGACGATTG ACGGGAATTT GCGGAAGTT TACGCCCCAA CGGTAGCGTT  
 351 GTGCGTCGGC GTAATTGAAC AAACGCGCTT GCAGCATTTT ATCTsGGCTG  
 401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATGTGTCAC  
 451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CTCAAACGGA TGATAAGGTA  
 501 CTTTTTCGCG GTCTGCTTCA GGCATGACTT GGATGTACAT CGTCCATTTC  
 551 GGAAACTCGC CGCGTTCGAT GGCTTCsTAT AAGTCGCGCT GATGGCTTTC  
 601 CGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC AGGTTTTTAA  
 651 TGCCTTGTG GGTGCGGAAA TGGAATTTCA CCAAAAACG CTCGCCTGCT  
 701 TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA TATGGCGGTA  
 751 GCCGCGCGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT TGGTGCACTG  
 801 CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTGTTGGC AGAGCGCATA  
 851 TTGGTGCGCG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG GGAACCTACG  
 901 CGGGTCGCGC AGGAAGAACA CGGGCGTGT GTTGCCGACC ACATCCCAGT  
 951 TGCCTTCTTC GGTATAAAAT TTCAAGGCAA AACCGCGGAT GTCGCGTTCT  
 1001 GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC GGGCGAACAT  
 1051 CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TCCTTTGGCG TGCATACGGC  
 1101 GTTCGGGGAT GACTTCGCGC ACGAAGTCGG CGAGTTTTTC AGTCATCGCT  
 1151 CTTGTTCTCT TTCTCAGGTT GGTCAAATGG GGGTAAACGG CTTACAGTAC  
 1201 GATTTGGCGG AAAGCGTATT CGTAACCGGT TTCTTGATTG CAATAAATTT  
 1251 CTTGAATCGA CATTTTATTT CCCTTTTGTA AAAACTATGG ATGCGACTAT  
 1301 ACGCCAAGAT TTTCGCTATT AA

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

m506.pep

1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHGV EQGARLAEIV VIVLAVVPVC  
 51 RVAVDFQRRF GESGLLLPLA EAVGFVVRQA AXVAVGAALP VAXXAVNXAT  
 101 RTIDGNLAEV YAQTVALCVG VIEQTRLQHF IXAGADTGENE VARCEGLLPH  
 151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRYFFR VCFRHDLDVH  
 201 RPFRKLAAFD GFXXVALMAF AVVGDDFGGF FVGQVFNALL GAEMEFHPKT  
 251 LACFVPEAVG MRTEAVHMAV AGGDAAVAHH DGNLVQCFQ QRPEVPVVCG  
 301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIKFQKGTAD  
 351 VAFICIGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGKRTERAR  
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQOR AARTGGQAVL IVGNRRRAVVH  
 451 GQMGYRAFFG SHRSCSFSQV GQMGKKRLTV RFGGKRIRNR FLDCNKFLES  
 501 TFYFPFVKTM DATIRQDFRY \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/g506

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHGV EQGARLAEIVVIVLAVVPVCRAVDFQRRF					
	:     :       :       :       :       :       :       :					
g506	MAVFDEVGRVIAHCGGGVVKQSLFLRVVHGV EQGARLAEVVIVLAVVPVCRAVDFQRRF					
	10	20	30	40	50	60

750

	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
g506	GEVGLLLPLAEAVGFVVRQAAXVAVGAALSVALVAVNRATRTIDGDLAEVHTQAVTLRVG					
	70	80	90	100	110	120
m506.pep	130	140	150	160	170	180
	VIEQTRLQHFIXAGADTGNVARCEGGLFHHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTGLQHFIRARADTGNVARCEGGLFHHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
m506.pep	190	200	210	220	230	240
	VKRMIRYFFRVCFRDLVDVHRPFRKLAADFDFXVALMAFAVVGDDFGGFFVVGQVFNALL					
g506	VKRMIRHFFGIGFRDLVDVHRPFRELAALDFVQVALMAFAVVGDDFCSFFVVGQVFNPLL					
	190	200	210	220	230	240
m506.pep	250	260	270	280	290	300
	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
g506	AAEMEFHPKTFARFVPEAVGMRTEAVHMAVAGGNTAVAHHDGNLVQCFGQQRPEVPVVCG					
	250	260	270	280	290	300
m506.pep	310	320	330	340	350	360
	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIKFQKTADVAFICGCAAF					
g506	GTHIGARIAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIEFQKTADVAFRIGCAAL					
	310	320	330	340	350	360
m506.pep	370	380	390	400	410	420
	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERTFGVHTAFGDDFAHEVGEFF					
g506	ACHGGETGEHLGFFADFAENFGAGVFGDVVRYGKRTERTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
m506.pep	430	440	450	460	470	480
	IQPQILRQQAARTGGQAVLIVGNRRVAVHGMGYRAFGGSHRSCSFSQVGQMGKRLTV					
g506	IQPQILRQQAARTGGQAVLIVGNRRVAVHGMGYRAFGGSHRSCSFSQVGQMGKRLTV					
	430	440	450	460	470	480
m506.pep	490	500	510	520		
	RFGGKRIRNRFLDCNKFLESTFYFPFKTMDATIRQDFRY					
g506	RFGGKRIRNRFLDCNKFLESTFYFPFAKTMDAIRQDFRY					
	490	500	510	520		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1379>:

a506.seq

```

1  ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCATTGCG GCGGCGGTGT
51  TGCCGAACAA TGCCTGTTTC TCGCGTCGT TCATCAGGTT GAACAGGGCG
101 CGCGGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGC GC
151 CGCGTCGCCG TTGATTTC AAGGCGGTTT GCGGAAGTCG GGCTGCTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGCGCG GTCCTTGTC GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGGTTG ACAGGGATT GCGGGAAGTT CACGCCCAAG CGGTAGCGTT
351 GCGGTCGGC GTAATTGAAC AAACGCGCCT GCAACATTTT ATCTGGGCTG
401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCCG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATACGGCA CTTTTCCGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTC GGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTTCGCGT

```

```

651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTGGGTC
701 AGGTTTTTAA TGCCTTGTTC GGTGCGGAAA TGGAAATTTCA CCCAAAAACG
751 CTCGCCTGCT TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCACTG CTTGCGGCAG CAGCGTCCAG AAGTCCAGT TGTGTGGGC
901 AGAGCGCATA TTGGTGCAGC GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CCGGTCGCGC AGGAAGAACA CCGGCGGTGT GTTGCCGACC
1001 ACATCCCACT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGTTTTTT TTGCGGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCCCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCCTGCG CCAGCAGAGG GCCCGGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTTGTTCAT
1351 GGTGAGATGG GTTACAGGGC ATTGGGAGGT ANTCATCGCT CTTGTTCCTT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAAACG GCTTACAGTA CGATTGGCGC
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHVQ EQGARLAEIV VIVLAVVPVR
51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGNV VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRHDLVDH
201 RPFRLAALD GEVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHHD DGNLVQCFGQ QRPEVPVVCG
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRKTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRAVVH
451 GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQEQGARLAEIVVIVLAVVPVCRVAVDFQRRF					
a506	MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQEQGARLAEIVVIVLAVVPVRRVAVDFQRRF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
	:     :     :     :     :     :     :     :     :     :					
a506	GEVGLLLPLAEAVGFVVRQAAXVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVALRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIWAGADTGNVVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
a506	VIEQTRLQHFIWAGADTGNVVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRHLVDVHRPFRKLAALDGFXXVALMAFAVVGDDFGGFFVGQVFNALL					
	:     :     :     :     :     :     :     :     :					
a506	VKRMIRHFFRIGFRHLVDVHRPFRKLAALDGFVQVALMAFTVVGDDFGGFFVGQVFNALL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
a506	GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIKFGGKTADVAFICIGCAAF					
a506	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIKFGGKTADVAFICIGCAAF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEGHLGFFADFAEDFGAGVFGDVVRYGKRTERTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEGHLGFFADFAEDFGAGVFGDVVRYGKRTERTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQORAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFSQVQMGKKRLTV					
a506	IQPQILRQORAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFSQVQMGKKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKMTDATIRQDFRYX					
a506	RFGGKRIRNRFLDCNKFLESTFYFPFVKMTDATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTCCTCTG CTTCAGACGG
101 CCTTTGCGCT CTTCTGCTT GGCAACGGTT TGTTCCGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGACTTCTTC CAATTGGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAATTCCGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTC CTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC CTGCCGGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTGA TGCGTTGGTG CAGGTTTTCG CCGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTTC CTCAATTCTG
501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNLFGMGKL
51  LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
101 LLFFDLQLVF LKLHADLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTTAAGGCTT GGTTCCTCTG TTTCAGACGA
101 CCTTTGCGCT CTTCTGCTT GGCAATCGTT TGTTCCGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTGGGGC
251 AGACGCTCCT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAGCTCGGT
301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC TTGATGAATG CGTTGTAATC GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTGA TGCGTTGGTG CAGGTTTTCG TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTTC CTCAATTCAT
501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTLLQGG CFLRGGGFGF VGQVXGLVFL FQTTAFALFVL GNRLFGMGKL

```



51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLVFG NLHRPFRQLG  
101 LFFFDLQLVF FKLHADLLLL LMNALXLRLR CLLVAFDALV QVLLMADLFF  
151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng) from *N. gonorrhoeae*:

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQGGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLFIMGKLLLLLQRQFAAD					
	:	:	:	:	:	:
g507	MLLPALQGGGFLSGGGFGLVGQVQGLVFLQTAFALFVLGNLFGMGKLLLLLQRQFAAD					
	10	20	30	40	50	60

```

              70          80          90          100          110          120
m507.pep      AVCLVLLGLEGGVERGLGFFQFGQTLLVFGNLHRPFRQGLGFFFDLQLVFFKLHADLLLL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g507          AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLLFFDLQLVFLKLHADLLLL
              70          80          90          100          110          120

```

```

              130      140      150      160      170      180
m507.pep      LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRFLGSLQG
               | :|| ||||| ||||| : ||||| ||||| : ||||| : |||||
g507           LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLAQHAAFVAQFVYCLLLRFLGSLQG
              130      140      150      160      170      180

```

m507.pep	VYFVV
	:
q507	VYFVI

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

```

a507.seq
  1  ATGCTCTTGC  TGGCTTTGCA  ACAAGGCGGC  AGCTTCCTGC  GCGGCGGCGG
51  TTTCCGGCTTC  GTCAGGCAGA  TTCAGGGGCT  GGTTTTCCTG  TTTTCAGACGA
101 CTTTTCGGCT  CTTCCGTGCT  GGCACCGGTT  TGTTCGGCAT  GGGCAAGCTG
151 CTGCTGCTTC  AACGCCAGTT  CGCGGCGGAT  GCGGTTTGCC  TCGTCTCTGT
201 GGGTTTGGAA  GCGCGCATTG  AGTGTGGCTT  GGGTTTCTTC  CAATTCCGGC
251 AGACGCTCTT  CGTGTTTCGC  AACCTGCATC  GCCATTCCG  CCAATTCGGT
301 TTGCTTTTCT  TCCGCCTGCA  ACTCGTTTTC  TTCAAGCTGC  ACGCGGATTT
351 GCTGCTGCTC  CTGATGGATG  CGCTGCAATC  GCGGCTGCGC  GCGCTGCTTG
401 TCGCGTTCGA  TCGGTTGGTG  CAGGTTTTCG  TGATGGCGGA  TTTGTTCTTC
451 CAAACGGGCA  ATCTGTTTCG  GCAACACGCC  GCGTTTGTTC  CCCAATTCGT
501 GCACCGCCTG  CTGCTGCGAC  TGTTCGGCAG  TCTGCAAGCG  GTGTACTTCG
551 TCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1386: ORF 507.a>:

a507.pep

1	MLLLALQQGG	SFLRGGGFGF	VRQIQGLVFL	<u>FQTTFALFVL</u>	GNGLFGMGKL
51	LLLRQFAAD	AFCLVLLGLE	GGIECGLGFF	QFGQTLFVFG	NLHRPFRQFG
101	LLFFRLQLVF	FKLHADLLLL	LM DALHLRLR	RLLVAFDALV	QVLLMADLFF
151	QTGNLFAQHA	AFVAQFVHRL	LLRLFGSLOG	VYFV**	

**m507/a507 89.7% identity in 185 aa overlap**

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGQVXGLVFLFQTTFFALFVLGNRLFIMGKLLLLLQRQFAAD					
	:     :     :     :     :     :     :     :     :     :					
a507	MLLLALQQGGSFLRGGGFGFVVRQIQGLVFLFQTTFFALFVLGNLFGMGKLLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m507.pep      AVCLVLLGLEGGVERGLGFFQFGQTLTVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL
                |||||:| |||||:| |||||:|:| |||||
a507          AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQFGLFFRLQLVFFKLHADLLLL
                70      80      90      100     110     120

                130     140     150     160     170     180
m507.pep      LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
                ||:| |||||:| |||||:| |||||:|:| |||||
a507          LMDALHLRLRRLLVAFDALVQVLLMADLFFQTGNLFAQHAAFVAQFVHRLLLRLFGSLQG
                130     140     150     160     170     180

m507.pep      VYFVVX
                |||||
a507          VYFVVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:  
q508.seq

g508.seq

1	ATGGTAGCGT	TTGCGGTTGA	TCAGGGCCTC	CTGCTGCTGC	AACAGGGCGG
51	TTTGGGTGGC	GGCCTGAAGC	TGCGGCAGCT	TGGTTTGCAG	GGTTTGTACG
101	CGGGCGTATT	GCTCCCTGCC	CTGTTCTCTGA	ATCTGCGCAG	GTTTTTCTCTG
151	CACGGCGATG	TATTTCTCGT	CCACGCGTGT	TACGGTTTCG	GTCAACTCGT
201	CGAGCTTGAT	GTGCTGCTCG	TCGTTTGGGA	ACTCGGTTTC	ATAGCGCAGG
251	GCAAGCTCTT	GCCGGCGTTC	CTGCCAGTCC	AGGGTTTGCT	GTTCGAGCCG
301	GGCGATTTCG	TGCCGGTAGT	TTTGTTTTTG	CGGGTTGAGT	TTGTGGACGG
351	CGACTTCGGC	AAGCCCGTAT	TGGCGGTGGG	CTTCCAACAG	GGCAAGCTGC
401	GCCTGTTTCA	GACGGCCTTG	CTGCTCTTGG	CGGCTGTGCG	CGGTGGTTTG
451	CTGCTGGTGT	TCGAGTTTCG	CGGCGGCTTC	CTGCAAAGTA	GCGATGTCGT
501	CTGA				

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

g508.pep

1	MVAFGVDQGL	LLLQQGGLGG	<u>GLKLRQLGLQ</u>	<u>GLYAGVLLPA</u>	LFLNLREFFL
51	HGDVFFVQRV	YGFGQLVELD	<u>VLLVVLELGF</u>	IGEGKLLPAF	LPVQGLLFEP
101	GDLLPVVLLF	RVEFVDGDFG	KPVLAVGFQQ	<u>GKLRLFQTAL</u>	LLLAARVGG
151	LLVFEFGGGL	LOSSDVV			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

m508.seq

```
1 ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAAAGGCGG
51 TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGACAG GGTTTGCACT
101 TTAGCGTATT GTCCTCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTCTCTTG
151 CACAACAATA TATTCTTCGT CCAAGGCTCTG TACGGCTTCG CTTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTGGGA ACTCGGTTTC ATAGCGGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCG AGGGTTTGCT GTTCAAGCTG
301 GCGGATTTGC TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAGGTA ACGATGTCGT
501 CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

m508.pep

1	MVAFGVDQGF	LLLQQGGLGG	GLKLRQLGLQ	GLHFSVLLPA	LFLNLREFLL
51	HNNIFVQGL	YGFAFFKDL	VLLVVLGLGF	IGEGKLLAF	LPVEGLLFKL
101	GDLLPVVFL	LVEFVDGDF	KPVLAVGFQQ	GKLRLFQAL	LLLAAVRGG
151	LLVFEFGGF	LOGNDVV*			

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

755

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLLQQGGGLGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
g508	MVAFGVDQGLLLLQQGGGLGGLKLRQLGLQGLYAGVLLPALFLNLREFLLHGDVFFVQVRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVLELGFIGEGKLLLAFLPVEGLLFLKGLDLPVVLFLLVFVDGDFG					
g508	YGFQQLVELDVLLVLELGFIGEGKLLPAFLPVQGLLFEFGDLPVVLFLRVEFVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQ QG KLR L FQTALL LLA A VRG LLL VFEFGG GFLQ GNDVV					
g508	KPVLA VG FQ QG KLR L FQTALL LLA A VRG LLL VFEFGG GFLQ S SDVV					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```

a508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGGCGCAGCT TGGTTGCAG GGTGTGTACG
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTCTCCTG
151 TACGACAATA TATTCTTCGT CCAAACCTCG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGG ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTTGT GTTCAAGCTG
301 GGCAATTTGC TGTGGTAGT TTTGTTTTTG CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAATG GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```

a508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLYAGVLFPT LLLNLREFLL
51  YDNIFFVQTL YGFAQLFELD VLLVLELGF IGEGKLLLAFL LPIEGLLFKL
101 GNLLLVLVLEL LVELVDGDFG KPVLA VG FQ QG KLR L FQTLL LLLAAVRGGL
151 LLVFEFGGGL LQNGDVV*

```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLLQQGGGLGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
a508	MVAFGVDQGFLLLQQGGGLGGLKLRQLGLQGLYAGVLFPTLLNLREFLLYDNIFFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVLELGFIGEGKLLLAFLPVEGLLFLKGLDLPVVLFLLVFVDGDFG					
a508	YGFAQLFELDVLVLELGFIGEGKLLLAFLPIEGLLFLKGLNLLLVLVLELVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQ QG KLR L FQTALL LLA A VRG LLL VFEFGG GFLQ GNDVVX					
a508	KPVLA VG FQ QG KLR L FQTLL LLA A VRG LLL VFEFGG GFLQ NGD VVX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509.seq

756

```

1  atggtcgctg tatgtgatga acgggctgta cagcggacgt tggtagccca
51  attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgtgttag
101 tcttccaagc ctgctgtgtg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgcaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgtcga taagggaacg ttgcaatttt ttcaaatcat cgagaaattt
301 ttgggccgaa gcataaggct cgagaaagcc gaatttgcag cccatgcccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgcataat gtaggcaatg
401 gcgcggcggg aagggtcttc ggtgcggcgc atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac tttagcgcgg cggatggaaa
501 gcggcagttc gcggtaaaagt ttgtcgagtt cgtcgggta aaaacggaac
551 acggcatcgg cgtggcggcg gaaggcaaa cgcagggttt cgccagaaac
601 aaacggattg ccgtcgcggt cgcgcggcat ccagcggcgg attttaagga
651 tattcggaac gcggacatcg gtagaggcgg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg ggaagatgga
751 cagcgcgttg ttgatttcgt cgttgacgct gaggttgttg cggcgcgttt
801 cgtggtctcg ccacaagccc agaagcacgg tgtcgatttc gcggcgcagc
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgctgttcg gcagcagcgc
901 gcggatgcgg cggttgaaat tcaaaacggt ttggcgttgc acttcggtcg
951 ggtgcgcggg caaaacggcg gtaacggacg tattgtccaa ctgcgcgtgc
1001 accgatttgc cgtcggcttt ccccgctttg agcctgcgga cggtttccgt
1051 caggctgcct tctgctgcgt tgtggccggc atcttctgtg atttggcggc
1101 ggcgttcgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgtgtcgtc ggaagtggac aagagtttga
1251 ccgttttcga aaccaacggc gaggtctctt cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtccgcggcc aaagccgct ccttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctcatgtccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcca aaccgttcac actttaacca
1451 ctcatgtccc gaaatgccgt ctgaagtga acgcgcggcg acggcggcgt
1501 tacaatcgcc cgcaactgtt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctctgctgc ggtacagccg ccacatcttc
1601 ttgggacgaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
1651 tttggtcgtc ggctgcggcg gattgggcgc cgcgcgccct gccctatctc
1701 gccgcctcgg ggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1  MVAVCDERAV QRTLVAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAVAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAAFALRQQR
301 ADAAVEIQNG LALHFGRVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVAG I FVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRADV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLRI
451 VQDMQLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVPKCR LKLNAARRRR
501 YNRPQLFFSE HHHRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
551 FGRRLRRIGR RRPCISPPIR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1  ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTTTTGTCT CTTCGTTTCA GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTGT GAAAAGCTCG GCAACCACAT CGGCGTGTTT
151 GCCTGCGTGT TGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGACGGCTG
251 CCGTTGTGTA TAAGGGAACG TTGCAATTTT TTCAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGGCGGT AGGGTTCTTC GCGCGGGCGG ATTTCTTCGT CGGGCGATTT
451 GTCGGACAAC GCCGTTACAT CGCCGTTGAC TTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGTT CGCCGCGATA GAAGCGGAAC

```

m509.pgp

m509/g509

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGHNHIGVFACVLAQVERH					
g509	MVAVCDERAVQRTLVAQFAQQGGLFLLFVQAVVVFQACVLEKLGHNHIGVFACVLAQVERH					
	10	20	30	40	50	60
m509.pep	HVKAEHGYGTDEVCGQTAFGKQTAADVVDKGTLOFFQIIQKLLCRSIRLEKAEFAAHTQTER					
g509	HVEAEHGHGTDEVCGQTAFGKQAAAVVDKGTLOFFQIIIEKFLGRSIRLEKAEFAAHAQTER					
	70	80	90	100	110	120
m509.pep	ARFAHSARHNVGDGAAVGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVFEAAI					
g509	ARFAHSARHNVGGAAVRFFGAGDFFVRRREGCQCHYVVVDFDAADGKRQFAVKFVFEAAV					
	130	140	150	160	170	180

	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGFGRNKRIVAVAAADPAADFEDVRNADAGIGRLKVVFHFLAVELGQ					
g509	KTEHGIGVAAEGKAQGFARNKRIVAVAAADPAADFKDIRNADIGIGRLKVVFHFLAVEFGQ					
	190	200	210	220	230	240
m509.pep	GFPEKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQDQSVDFAAQPCQRVGIGAAAFALRQQC					
g509	GFKKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQKHGVDFAAQPCQRVGIGAAAFALRQQR					
	250	260	270	280	290	300
m509.pep	ADA AVEAXDGLALHFGRVGRQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFRAAASG					
g509	ADA AVEIQNGLALHFGRVGRQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFCVVAG					
	310	320	330	340	350	360
m509.pep	FFVDLAAAFVHVFGDVQNLGEQAAGQGXIVGLLFVQLRQYFFNQCRVVGSGQEFDCFD					
g509	IFVDLAAAFVHVFGDIQNLGEQPAKQKQIVGLPFVQLRQYFFNQCRVVGSGQEFDRFD					
	370	380	390	400	410	420
m509.pep	NQRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNIVNVPQMPHPCQTV					
g509	NQRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQDMQLHDFPLI-AVNTVNVNVPQMPHPCQTV					
	430	440	450	460	470	480
m509.pep	HTLTARVPKCRLKLNAARRQRYNRPQLFFSEHHHDHRTQRRCIPAAVQPPHPLGRNRH					
g509	HTLTTHVPKCRLKLNAARRRRYNRPQLFFSEHHHDDRTRQRRRTPAAVQPPHPLGRNRH					
	480	490	500	510	520	530
m509.pep	RRAAETFRRAYFGRRLRRFGCRRTCPTLPLRV SAR					
g509	RRAAEAFRRAYFGRRLRRIGRRRRCPI SPPRGSAR					
	540	550	560	570		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1397>:

```

a509.seq
1  ATGGTCGCTG TATGTGATGA ACGGACTGTA CAGTGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGCGGCT TGTTTTGCT CTCGTTGAG GCTGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTGTT
151 GCCTGCGTGT TGGCGCAGGT CGAGCGGCAT CATGTGGAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGGCGGCTG
251 CCGTTGTGCA TAAGGGAATG TTGCAATTTT TTCAAATCAT CGAGAAATTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTGTCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCAATG
401 GCGCGACGGT AGGGTTCTTC GCGCGGGCG GTTCTTCGT CGGGCGATTG
451 GTCGACAAC GCCATCACAT CGCCGTTGAC TTTGACGCGG CGGATGAGAG
501 GCGGCAAGTC GCGGTAGAGT TTGTGAGTT CGCCACGGTA AAAACGGAAC
551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAA CGCAAGGTTT CGGCAGAAAC
601 GAACGGATTG CCGTCGCGGT CGCCGCGAT CCAGCCGCGG ATTTTGAGGA
651 TGTCCGGAAC GCGGACATCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCAAAA AAGCTCATCG GAAAGATGGA
751 CACGCCGTTG TTGATTTGCT CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTTC GCGGCGCAGC
851 CGTGCCAGCG CGTCGCATT GGTACAGCGT TCGCGTTGCG GCAGCAGCGC

```

```

901 GCGGATGCGG CGGTTGAAAT TCAAGACGGT CTGGCGTTGC ACTTCGGTGC
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTCG CGTCGGCTTT CCCCGCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTGGCGGC
1101 GCGCTTCGTG GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTCGTCCA ATTGCGGCAA
1201 TACTTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CCGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATCCGC GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCATTGCCG TAAATACTGT
1401 AAATGTACCT CAAATGCCGC ATCCGTGCCA AACCGTTCAC ACTTTAACCG
1451 CCCGTGTCCC GAAATGCCGT CTGAAGTTGA ACGCCGCCCG ACGGCAGCGT
1501 TACAATCGCC CACAACGTT TTT.TCCGAA CATCATCATG ACCACGACCG
1551 AACACGACAA CGACGATGCA TTCCTGCTGC GGTACAGCCG CCACATCCTC
1601 TTGGACGAAA TTGGCATCGA AGGGCAGCAG AAACTTTCCG CCGCGCATAT
1651 TTTGGTCGTC GGCTGCGGCG GTTTGGGTGC CGCCG.CCCT GCCTATCTC
1701 GCCGCTTCCG GCATCGGCAC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

```

a509.pep
1  MVAVCDERTV QWTLMAQFAQ QGGLFLLFVE AVVVFAQCVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGYGT DEVCQTAFGK QAAAVVDKGM LQFFQIIEKF
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VNGATVGFF GAGGFFVGRF
151 VGQRHHIAVD FDAADGERQF AVEFVEFATV KTEHGIGVAA EGKTQGFGRN
201 ERIAVAVAAD PAADFEDVRN ADIGIGRLKV VFHLAVELGQ GFKAHRKDG
251 HAVVDFVUDA EFVAARFAGL PQAQQDSVDF AAQPCQRVGI GTAFALRQQR
301 ADAAVEIQDG LALHFGRVRG QNGGNRIVQ LPLHRAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQG*I VGLLFVQLRQ
401 YFFNQCRADV GSGQEFDRFD NORRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LIAVNTVNPV QMPHPCQTVH TLTARVPKCR LKLNAAARRQR
501 YNRPQLFXSE HHHDHDRTRQ RRCIPAAVQP PHPLGRNWHR RAAETFRRAY
551 FGRRLLRRFGC RXPCPISPLP ASAR*

```

m509/a509 93.0% identity in 575 aa overlap

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFAQCVLEKLGNHIGVFACVLAQVERH					
a509	MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVFAQCVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
m509.pep	70	80	90	100	110	120
	HVKAHEHGYGTDEVCQTAFGKQTAADVVDKGTLLQFFQIIQKLLCRSIRLEKA EFAAHTQTER					
a509	HVEAEHGYGTDEVCQTAFGKQAAAVVDKGM LQFFQIIEKF LCRSIRLEKA EFAAHTQTER					
	70	80	90	100	110	120
m509.pep	130	140	150	160	170	180
	ARFAHSARHNVDGGAAGVFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
a509	ARFAHSARHNVDGATVGFFGAGGFFVGRFVGQRHHIAVDFDAADGERQFAVEFVEFATV					
	130	140	150	160	170	180
m509.pep	190	200	210	220	230	240
	EAEHGIGVAAEGKAQGFGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
a509	KTEHGIGVAAEGKTQGFGRNERIAVAVAADPAADFEDVRNADIGIGRLKVVFHLAVELGQ					
	190	200	210	220	230	240
m509.pep	250	260	270	280	290	300
	GFKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGTAFALRQQC					
a509	GFKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGTAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360

760

```

m509.pep  ADAAVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFRFEPADGFRQAAFRAAASG
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      ADAAVEIQDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFRFEPADGFRQAAFRAAASG
          310      320      330      340      350      360

          370      380      390      400      410      420
m509.pep  FFVDLAAAFVHVFGDVQNLGEQAAGQGXIIVGLLFVQLRQYFFNQCRVAVGSGQEFDCFD
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      FFVDLAAAFVHVFGDVQNLGEQAAGQGXIIVGLLFVQLRQYFFNQCRVAVGSGQEFDRFD
          370      380      390      400      410      420

          430      440      450      460      470      480
m509.pep  NQRRGFFVQVEVEQGLFQKFRVRQRSLVWIVQNMQLHDFSLSSAVNIVNVQMPHPCQTV
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      NQRRGFFVQVEVEQGLFQKFRVRQRSLVWIVQNMQLHDFSLI-AVNTVNVVQMPHPCQTV
          430      440      450      460      470

          490      500      510      520      530      540
m509.pep  HTLTARVPKCRLKLNAARRQRYNRPQLFFSEHHHDHRTQRRCIPAAVQPPHPLGRNRH
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      HTLTARVPKCRLKLNAARRQRYNRPQLFXSEHHHDHRTQRRCIPAAVQPPHPLGRNWH
          480      490      500      510      520      530

          550      560      570
m509.pep  RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRV SARX
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      RRAAETFRRAYFGRRLRRFGCRXPCPISPLPASARX
          540      550      560      570

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1  atgccttcgc ggacaccgca gggaaaaagg ggttattcct gccccaaagcg
51  ggatagtgcc ttttggcagg cgttgtccat atcggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggaggtttt caataggtcg
151 tggacgacgt tgagcgcggc cataatgacg attttttcgc tgtccgcgac
201 gcggccgcct tcgcggatgg cttcggcttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcgtgcatg acttcgatgt agacttggtc gatgttcac ctttaatcct
351 tattgctgcg tttcctgccg ttgggggagg cgcgctgcca gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1  MPSRTPQGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTISR
101 GVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTTCCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGC TGTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTCAGCCGG
301 GGCGTGCAWg ACTTCSatGT GGACTTGTTT GATGTTTCAT CTTTAATCCT
351 TATTGCTGCG TTTCTGCCA TTGGGGGAGG CCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTISR
101 GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:



Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

```

      10      20      30      40      50      60
m510.pep  MPSRTPQGKRGYSCAKRDSA FQWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT
          |||:|||||
g510      MPSRTPQGKRGYSCPKRDSA FQWQALSISVILRAKSPIAKSPPFREVFNRSWTTLSAAIMT
          10      20      30      40      50      60

      70      80      90     100     110     120
m510.pep  IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILILIAA
          |||:|||||
g510      IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVHDFDVLFDVHPLILILIAA
          70      80      90     100     110     120

      130
m510.pep  FPAIGGGALPVRX
          |||:|||||
g510      FPAVGGGALPVRX
          130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

```

1  ATGCCTTCGC GGACACCGCA GGGAAAAAGG GGTATTCTCT GCGCCAAGCG
51 GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGCG TGTCGCCGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC  GGTCAGCCGG
301 G.CGTGCATG ACTTCGATGT GGACTTGTTT GATGTTTCATC CTTTAATCCT
351 TATTGCTGCG TTTCTGCCG TTGGGGGAGG CGCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

```

1  MPSRTPQGKR GYSCAKRDSA FQWQALSISAI LRAKSPIAKS PPFREVFNRS
51 WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 XVHDFDVLDF DVHPLILILIAA FPAVGGGALP VR*

```

m510/a510 97.0% identity in 132 aa overlap

```

      10      20      30      40      50      60
m510.pep  MPSRTPQGKRGYSCAKRDSA FQWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT
          |||:|||||
a510      MPSRTPQGKRGYSCAKRDSA FQWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT
          10      20      30      40      50      60

      70      80      90     100     110     120
m510.pep  IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILILIAA
          |||:|||||
a510      IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRXVHDFDVLFDVHPLILILIAA
          70      80      90     100     110     120

      130
m510.pep  FPAIGGGALPVRX
          |||:|||||
a510      FPAVGGGALPVRX
          130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

```

1  atgaaagtgc ttgttttagg tgcgggtggt gccggcgat cctccgtgtg

```

g512.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1407>:

m512.seq (partial)

```

1      . . GTTTGGAAAC GCTACGGCGT GCCGTACCGC CGTCTGAAAC CCGAAGAATG
51     TGCAGAATTT GAGCCTGCGC TGGCACGCGT TACCGCCAAA ATTGCCGGCG
101    GCCTGCACCT GCCTGCAGAT GCGACCGGCG ACTggCGCCT CTTCACTGAA
151    AACCTATACA AATTGTGTCA GGAAGAGGGC GTACGGTTTC ATTTCAACCA
201    AAACATCAGC CGCATCGACC ACAACGGGCT GCGCATCAA ACCGTTGAAA
251    CCAACAGGG CGTTTGAAG CAGATGCCGT TGTCTGCGCG CTCGGTTGCT
301    TCAGCAGGAG GGTTTGGCG CAGTTGGATC TCAATCTGCC CATTATATCC
351    GTCAGAGGCT ATTCCTTGA

```

m512.pep (partial)

```

1  ..VLERYGVYPYR RLKPEECAEF EPALARVTAK IAGGLHLPAD ATGDWRLFTE
51  NLYKLCQKEG VRHFHNQNIS RIDHNGLRIK TVETKQGGLK QMPLSARSVA
101 SAGRFWRSWI SICPFIPSKA IP*

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 512 shows 93.4% identity over a 122 aa overlap with a predicted ORF (ORF 512.ng) from *N. gonorrhoeae*:

m512/g512

[illegible]

250 260 270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
1  ATGAAAGTGC TTGTTTTAGG TGCTGGTGTT GCCGGCGTAT CTTCCGCGTG
51  GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAAACCAGT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GCGTGCCGT ACCGCCGTCT
501 GAAGCCCGAA GAATGCGCAG AATTCGAGCC TGCCTGGCA CGCGTTACCG
551 CCAAAATTGC CGGCGGCCTG CACCTGCCCC CAGACGCGAC CGGCGACTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAGGAAA AGGGCGTACG
651 GTTTCATTTC AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAAACCGT TGAAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAAGT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
1  MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
51  YTPPWAAPGI PTKALKWLFK SHPPLFRPD GSLYQIEWLW QMLQHCTAAR
101 YQINKERMVR MSEYSREMFR RFEAQTMNF EGRKKGLQI FRQTKVEEAA
151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK QGGLKQMPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVYPYRRLKPEECAEFEPALARVTAK
a512                                |||||
TGMNFEGRKKGTLQIFRQTKVEEAAKQDIAVLERYGVYPYRRLKPEECAEFEPALARVTAK
130      140      150      160      170      180

                                40      50      60      70      80      90
m512.pep    IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGRLRIKTVETKQGGLK
a512    IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQNISRIDHNGRLRIKTVETKQGGLK
190      200      210      220      230      240

                                100      110      120
m512.pep    QMPLSARSVASAGRFWRWSWISICPFIPSKAIPX
a512    QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
250      260      270
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
1  ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
51  TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151 GATTTGAGCG GTGCGGCGCT GAcgCAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGCG GCGGGTTTCC TCGCCGTGAT CCGTTTATG TTTGCCTTTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301 AAAAGCCATT GGCTGATTAC CGCCGTTTTC CGTATGCTGG TTTTGGCGTG
351 GGTCTATTTT GCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

501 AATGGGCAAA GACCCCGAGT TCAAACTTTc cgAACATCCG GGCCTGAAAC  
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG  
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI  
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL  
 151 LSPLAFMLLR DYTAKLMGK DPEFKLSEHP GLKRRIKSDV W\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq

1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT  
 51 TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTTGTGAT ACCATCATCG  
 101 TTTGTTCTTG CACCGCTTC ATCATCTGA TTTACCAACA GCCTTATGGC  
 151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG  
 201 GCAATGGGGC GCGGGTTTC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT  
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC  
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG  
 351 GGTCTATTTT GCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG  
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG  
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA  
 501 AATGGGCAAA GACCCCGAGT TCAAACTTTc cgAACATCCG GGCCTGAAAC  
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG  
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI  
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL  
 151 LSPLAFMLLR DYTAKLMGK DPEFKLSEHP GLKRRIKSDV W\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

m513.pep	10	20	30	40	50	60
	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
	10	20	30	40	50	60
m513.pep	70	80	90	100	110	120
	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
m513.pep	130	140	150	160	170	180
	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMMLRDYTAKLMGKDPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMMLRDYTAKLMGKDPEFKLSEHP					
	130	140	150	160	170	180
m513.pep	190					
	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

```
1  ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51  CGATCCGATG TGGTCATACT TGGTTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACCACGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTTC TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTTGGA TGTGGGTAAAC CGCCTTAATC GGTATGAGT CCGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCAGGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTGTTTCGC CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTGGGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CCGAAATCGT
651 CGTCCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCAATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTCAGAT TTTTTCGGGC
751 GCGTTCAAAT TCACGCGGCG AGCAGGCGGC TTAATCGGCG GTCTGATTTT
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CCTGTATTCC AACGAGGCGG
851 GTATGGGTTC CGCGCCGAAC GCCGCCGCCG CCGCCGAAGT GAAACACCCT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTGC ATACCATCAT
951 CGTTTGTCTT TGCACCGCCT TCATCATCTT GATTACCAA CAGCCTTACG
1001 GCGATTGAG CGGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCCGTC ATCCTGTTTA TGTTCGCCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CCTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```
a513.pep
1  MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLEFTVTTG FVQFRLFGRS
51  IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGGPGA
101 VFWMWVTALI GMSSAFVESS LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFALSL IFCFGFVFEA VQNTNIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNIPI PDVFGQIFSG
251 AFKFDAAAGG LLGGLISQTM MMGIKRGlys NEAGMGSAPN AAAAAEVKHP
301 VSQGMQMLG VFVDTIIVCS CTAFIILIYQ QPYGDLGAA LTQAAIVSQV
351 GQWGAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYTAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*
```

m513/a513 100.0% identity in 191 aa overlap

```
m513.pep                                     10      20      30
                                         MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
a513                                     260      270      280      290      300      310
DAAAGLLGLISQTM MMGIKRGlys NEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

          40      50      60      70      80      90
m513.pep  TIIVCSCTAFIILIYQ QPYGDLGAA LTQAAIVSQV GQWGAGFLAV ILFMFAFSTVIGNY
          320      330      340      350      360      370
a513  TIIVCSCTAFIILIYQ QPYGDLGAA LTQAAIVSQV GQWGAGFLAV ILFMFAFSTVIGNY

          100      110      120      130      140      150
m513.pep  AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANV PLVWDMADMA MGIMAWINLVAILL
          380      390      400      410      420      430
a513  AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANV PLVWDMADMA MGIMAWINLVAILL

          160      170      180      190
m513.pep  LSPLAFMLLRDYTAKL KMGKDPEFKL SEHPGLKRRI KSDVW
          110      120      130      140      150
```

a513 LSPLAFMLLRDYTA KLKMGKDPEFKLSEHPGLKRRIKSDVWX  
440 450 460 470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq  
1 atggttcaaa tacaggttgt gcgcgcgcgc gccgttgccc gtggtctgca  
51 ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttcgacaatg  
101 ccgttttgaa tcacgaagcg cggcgcgcgc gcaacacctt ccgcatcaaa  
151 atagctgctg cggaaagagc gggggatgtg cgttctctcg cgcaggttga  
201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt  
251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag  
301 cccgccccaa acggtgggtat cgaagaggac ggggtagctg cctgtcggga  
351 tgctgcggct gccgagtcgg cgcgaagtgc ggcgggcggc ggtttgaccg  
401 atggtttcgg ggctgtccat atccggatgg cggcagcgcg aatcgtacca  
451 gtactgcgcg tgcattccgt tttcgtcggc ggcgacgacg ctgcaggaaa  
501 tgctgtggtg cgtgctttgc cgtgtgcgg caaaaccgtg ggtgttgccg  
551 taaacgtatt ggtactgtcc ggtttgcacc gccgcgcctt cggagttttc  
601 gatgcggctg tccgtgtcca acgctgcctg ttcgattgt tttgccaagc  
651 cgacggcgcg ttccgtatcc aaatccatt cgtggtaaa gtcggggctg  
701 ccgattgtgt gcgccatcaa ctccgggtcg gcaagtccgg cgcaaccgtc  
751 ttcggcggcg tggcgggcga tgcggcgcg ggcgcggcgc gtgtcgcgca  
801 gggcttgctc ggagaagtgc gcggtgccgc cgcggccttt gcgtttgccg  
851 acgtaaacgg taatgtccag cgatttgtcc tgctggaact cgatttgttc  
901 gatttcgccc aagcgcacgc tgacgctttg tccgagcgat tcgctgaagt  
951 cggcttcggc ggcggtcgcg ccgctgtctt ttgccaagtc gacggtgcgg  
1001 cggcagaggt cgaggagtcc ggaagcggcg tggttgaaca gcataacaat  
1051 ctttcttggg ggagcgttgt ggcattttta

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep  
1 MVQIQVVRAA GVARGLHSEF ARAVTAEEIA FDNAVLNHEA RRGNTFRIK  
51 IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADDEVSDQ  
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP  
151 VVALHSVFVG GDDAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF  
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV  
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLELDLF  
301 DFAQAHADAL SERFAEVGFG GGRARCFQCV ERAAAEEVEF GSGVVEQHNN  
351 LSWWSVFAF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)  
1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA  
51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC  
101 GCGCCGCCCG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCCGAAAC  
151 GGTGGTATCG AAGAGGACGG GGTAGCTGCC TGTCGGGATG CTGCGGCTGC  
201 CGAGTCGGCG CAAAGTGCGG CGGCGGGCGG TTTGACCGAT GGTTCGGGG  
251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG  
301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG  
351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTGCGCGTA AACGTATTGG  
401 TAATGGCCCG TTTGCACCGC CGCGCTTCG GAGTTTTCGA TGCGCTCATC  
451 CTCGTTTCAAG GCGGCTTGTG CGCATTTGTT TGCCAAGCCG ACGGCGGCTk  
501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CCGGGTCGCC GATGTGTTTT  
551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CGGCGGTGTG  
601 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTTGCAGG GCTTTTTCGG  
651 AGAAGTCGGC AGTACTGGCG CGGCCTTTGC GTTTGCCGAC GTAAACGGTA  
701 ATGTCCAGCG ACTTGTCTCG CTGGAACGCG ATTTGTTsGA TTTsGCCCCAG  
751 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG  
801 CGGTGCGGCC CGTCGCTTTT GCCAAGTCGA GCGTGCAGCG GCAGAGGTCTG  
851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA  
901 TGCTTTGCGG CATTTTAA

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

767

```

1  ..GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51  GGIEEDGVAA  CRDAAAESA QSAAGGGLTD  GFGAVHIRMA AGGIVPVVAL
101 HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151 LVQGGFLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201 AGDVDGGFDG VLQGFPGEVG STGAFAFAD VNGNVQRLVL LELDLXDXAQ
251 PHADALSQXF AEIGFGGGCA RRFCQVERAA AEVEEFGSGV VEQHRNLSXX
301 CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

m515/g515

m515.pep				10	20	30
				GKSGGCAFFA	QVEEIGQDFS	ADAVDQETALA
				::		
g515	AEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDVRFFA	QVEEIGQDFF	ADAVDQETALA			
	30	40	50	60	70	80
m515.pep		40	50	60	70	80
		VERAAGECADEVSDKTARNGGIEEDGVAA	CRDAAAESAQSAAGGGLTDGFGAVHIRMAA			
g515	VERAAGECADEVSDQPARNGGIEEDGVAA	CRDAAAESAQSAAGGGLTDGFGAVHIRMAA				
	90	100	110	120	130	140
m515.pep		100	110	120	130	140
		GGIVPVVALHAVFVGGNDAAGNAVVRALP	VCGKTVGVAVNVLVMAGLHRR	AFGVFDALIL		
g515	GGIVPVVALHSVFVGGDDAAGNAVVRALP	VCGKTVGVAVNVLVLSGLHRR	AFGVFDAAVR			
	150	160	170	180	190	200
m515.pep		160	170	180	190	200
		VQGGFLFALFCQADGGXRIQIPFVVKVG	ADVCHQTGIGKSGATVFGGVAGD	VDGGFDGV		
g515	VQRCLFALFCQADGGFRIQIPFVVKVG	ADVLRHQLGVGKSGATVFGGVAGD	VGGGADGV			
	210	220	230	240	250	260
m515.pep		220	230	240	250	260
		LQGFPGEVGSTGAFAFADVNGNVQRLVL	LELDLXDXAQPHADALSQXFAEIGF	GGGCAR		
g515	AQGLFGEVGGAGAAFAFADVNGNVQRF	VLLLELDLFDFAQAHADALSERFAE	VFGGGRAR			
	270	280	290	300	310	320
m515.pep		280	290	300		
		RFCQVERAAAEVEEFGSGVVEQHRNLSXX	CFAAF			
g515	CFCQVERAAAEVEEFGSGVVEQHNNLS	SWSVVAF				
	330	340	350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

a515.seq

```

1  ATGTTTCAAA TAAAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTGTGA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGATGTG CGGTTCTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGCGCGCG GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTTGCCG

```

```
a515.pep
  1  MVQIKVVRAA  GVARGLHSEF  ARAVTAEIEA  FDNAVLNHEA  RCGGNAFRIK
51  IAAAEAGADV  RFFAQVEEIG  QDFFDADAVD  ETALAVERSA  GECADVSDK
101  TARNGGTIED  GVVACRDAAA  AESAQSAAGG  GLTDGFGAVH  IRMAAGGIVP
151  VVALHAVFVG  GNDAAAGNAV  RALPVCCKTV  GVAVNVLVMA  GLHRRAFGVF
201  DALILVQGGL  FALFCQADGG  FRIQIPFVVK  VGVADVLRHQ  LGVGKSGATV
251  FGGVAGDVXX  GADGVAQGLF  GEIGAGAAAF  AFADVNGNVQ  RLVLKLDLF
301  DFAQPHADAL  SQ*FAEIGFG  GGCARRFCQV  ERAAAEVEEF  GSGVVEQHRN
351  LS**CFAAF*
```

[illegible]

g515-1.seq  
1 ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GGC GTTGCCC GTGGTCTGCA



```

51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101  CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151  ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201  GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251  TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301  CCCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351  TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGGGGGCGGC GGTGTGACCG
401  ATGTTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451  GTAGTCGCGC TGCATTCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501  TAGTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGG
551  TAAACGTATT GGTAGTGTCC GGTGTGACG CCGCGCCTT CGGAGTTTTT
601  GATGCGCGCTG TCCGTGTCCA ACGTGCCTG TTCCGATTGT TTTGCCAAGC
651  CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701  CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751  TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GGCAGGACG GTGTGCGCA
801  GGGCTTTGTT GGAGAAGTCG GCGGTGCCGG CGCGGCCTT GCGTTGCGG
851  ACGTAAACGG TAATGTCCAG CGATTGTGTC TGCTGGAACG CGATTGTGTC
901  GATTTCGCCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCGTGAAGT
951  CGGCTTCGGC GCGGTGCGG CCCGCTGCTT TTGCCAAGTC GAGCGTGGG
1001 CCGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTTCTTGGT GGAGCGTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEEIA FDNVNLNHEA RRGNTFRK
51  IAAERAGDV RFFAQVEEIG QDFADAVDQ ETALAVERAA GECADEVSDQ
101  PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151  VVALHVSFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201  DAAVRVQRCL FALFCQADGG FRIQIPFVK VGVADVLRHQ LGVKGSGATV
251  FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RVLLELDLF
301  DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAVEVEF GSGVVEQHNN
351  LSWWSVVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCG GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101  CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCTT CCGCATCAAA
151  ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201  GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251  TGGCGGTAGA GCGCGCCGCC GGAGAGTGGC CCGACGAGGT GTCCGATAAG
301  ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351  TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGGGGGCGGC GGTGTGACCG
401  ATGTTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451  GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501  TGCTGTGGTG CGTGCTTTCG CGGTGTGCGG CAAAACCGTG GGTGTGCGG
551  TAAACGTATT GGTAAATGGC GGTGTGACG CCGCGCCTT CGGAGTTTTT
601  GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCCGATTGT TTTGCCAAGC
651  CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701  CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751  TTCGGCGGTG TGGCGGGCGA TGTCGATGGC GGCTTTGACG GTGCTTGCA
801  GGGCTTTTTC GGAGAAGTCG GCAGTACTGG CCGCGCCTT GCGTTTGCCG
851  ACGTAAACGG TAATGTCCAG CGACTTGTC TGCTGGAACG CGATTGTGTC
901  GATTTCGCC AGCCGCACGC TGACGCTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEEIA FDNVNLNHEA RCGNFRK
51  IAAERAGDV RFFAQVEEIG QDFADAVDQ ETALAVERAA GECADEVSDK
101  TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151  VVALHVSFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201  DALILVQGLL FALFCQADGG FRIQIPFVK VGVADVCHQ TGIGKSGATV
251  FGGVAGDVGG GFDGVLQGFF GEVGSTGAAF AFADVNGNVQ RVLLELDLF
301  DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

```

          10      20      30      40      50      60
g515-1.pep  MVQIQVVRAAGVARGLHSEFARAVTAEEIAFDNAVNLNHEARRGNTFRIKIAAERAGDV
          |||
m515-1      MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVNLNHEARCGNFRIKIAAERAGDV
          10      20      30      40      50      60

```

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	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAFVGGNDAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
	190	200	210	220	230	240
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGADVLRHQ					
m515-1	GVAVNVLVVSGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGADVLFCHQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
g515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAAFADVNGNVQRFVLELDLF					
m515-1	TGIGKSGATVFGGVAGDVGGFDGVLQGGFGEVGGSTGAAAFADVNGNVQRFVLELDLF					
	250	260	270	280	290	300
	310	320	330	340	350	360
g515-1.pep	DFAQAHADALSERFAEVGFGGGRARCFQVERAAAEVEEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GCGTTCGCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAATAGCC TTCGACAATG
101 CCGTTTGTAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAATCAGGG CAGGACTTTT TTCCGATGTC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCCGGA
351 TGTCGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTTCGCG
551 TAAACGTATT GGTAATGGCC GGTTCGCACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GGCGCGGACG GTGTCGCGCA
801 GGGCTTTGTT GGAGAAATCG GCGGTGCCGG CGCGGCCCTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTCG TGCTGAAACT CGATTGTGTC
901 GATTTCGCCC AGCCGCACGC TGACGCTTTC TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNVNLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADDEVSDK
101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAFVVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGGF FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNGGIEEDGVVACRDAAA					

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```

m515-1      RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
              70      80      90      100      110      120

              130      140      150      160      170      180
a515-1.pep  AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              |||
m515-1      AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              130      140      150      160      170      180

              190      200      210      220      230      240
a515-1.pep  GVAVNVLVMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVLRHQ
              |||
m515-1      GVAVNVLVMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVLRHQ
              190      200      210      220      230      240

              250      260      270      280      290      300
a515-1.pep  LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
              |||
m515-1      LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
              250      260      270      280      290      300

              310
a515-1.pep  DFAQPHADALSQX
              |||
m515-1      DFAQPHADALSQX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

```

g516.seq
1  atgttggtcc gtaaaacgac cgccgccgtt ttggcggcaa ccttgatact
51  gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacgtt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgccca attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgccg tcaatcccga agattcggcg aagctgacgg
251 gccttttgaa ggccgggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccc gtcaaattcg aagcgcccgg
351 cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcgggtcaaa
451 ctcgacaatc ggaccattta cagcgctgct gtatccgcca aaggcaaata
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaagtg
551 tgcccgcgca tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctgtttg gaaatatctt atatacgccc cccttggtga tattggatgc
651 ggccggccgc gtgctggtct tgccatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

```

g516.pep
1  MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGYYAT PQKLNADYHF EQSVADIYY TVTEKHTDKS
201 KLFGNILYTP PLLILDAAA VLVLPALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

```

m516.seq
1  ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGCgc CTTCCGTTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGAAAAG GGCAGCCTGG TGATGATGGG
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCCGCG AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

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501 CTACGCCACA CCGCAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG  
 551 TGCCTGCCGA TATTATTAC ACGTTACTG AAGAACATAC CGACAAATCC  
 601 AAGCTGTTTG CAAATATCTT ATATACGCC CCCTTTTGA TACTGGATGC  
 651 GCGGGCGCG GTACTGGCCT TGCCTGCGC GGCTCTGGT GCGGTCGTGG  
 701 ATGCCGCCG CAAATGA

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

m516.pep  
 1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV  
 51 VAEDNAQLEK GSLVMMGGKY WFVVPEDSA KLTGILKAGL DKPFQIVEDT  
 101 PSYARHQALP VKLESPGSQN FSTEGCLRLY DTDKPADIAT LKQLGFPAVK  
 151 LDNRTIYTRC VSAKGKYYAT POKLNADYHF EQSVPADIYY TVTEHTDKS  
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

m516/g516

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMWGMNPNVSETITRKHVDKQIRAFGVVAEDNAQLEK					
g516	MLFRKTTAAVLAATLILNGCTMLRGMNPNVSTITRKHVDKQIRAFGVVAEDNAQLEK					
	10	20	30	40	50	60
m516.pep	GSLVMMGGKYWFVVPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN					
g516	GSLVMMGGKYWFAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSQN					
	70	80	90	100	110	120
m516.pep	FSTEGCLRLYDTDKPADIATLKQLGFPAVKLDNRTIYTRCVSAKGKYYATPOKLNADYHF					
g516	FSTGGLCLRYDTGRPDDIAKLEKQLEFKAVKLDNRTIYTRCVSAKGKYYATPOKLNADYHF					
	130	140	150	160	170	180
m516.pep	EQSVPADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
g516	EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLILDAAGAVLALPAAALGAVVDAARK					
	190	200	210	220	230	239
m516.pep	EQSVPADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
g516	EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLILDAAGAVLALPAAALGAVVDAARK					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

a516.seq  
 1 ATGTTGTTC GTAAACGAC CGCGCCGTT TTGGCGGCAA CCTTGATGTT  
 51 GAACGGCTGT ACGGTAATGA TGTGGGTAT GAACAGCCCG TTCAGCGAAA  
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTCGGTGTG  
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAGG GGCAGCCTGG TGATGATGGG  
 201 CGGGAATAC TGGTTCGTG TCAATCCTGA AGATTCGGCG AAGCTGACGG  
 251 GCATTTTGAA GGCCGGGTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC  
 301 CCGCGCTTG CCTACCAAGC CCTGCCGTC AACTCGAAT CGCCCGCCAG  
 351 CCAGAATTTC AGTACCGAAG GCCTTTGCCT GCGCTACGAT ACCGACAGAC  
 401 CTGCCGACAT CGCCAAGCTG AAACAGCTT AGTTTGAAG GGTGGAATCT  
 451 GACAATCGGA CCATTTACAC GCGCTGCGTC TCGCCAAAG GCAATACTA  
 501 CGCCACACCG CAAAACTGA ACGCCGATTA TCATTTTGAG CAAAGTGTGC  
 551 CTGCCGATAT TTATTACAG GTTACGAAA AACATACCGA CAAATCCAAG  
 601 TTGTTTGAAT ATATTGCATA TACGCCACC ACGTTGATAC TGGATGCGGT  
 651 GGGCGCGGTG CTGGCCTTG CTGTCGCGC GTTGATTGCA GCCACGAATT  
 701 CCTCAGACAA ATGA

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

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```

1  MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFFVNPEDSA KLTGILKAGL DKQFQMVPEPN
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIAKL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVADIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDVAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

m516.pep      10      20      30      40      50      60
MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVVDKDQIRAFGVVAEDNAQLEK
|||||
a516          10      20      30      40      50      60
MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVVDKDQIRAFGVVAEDNAQLEK
|||||

m516.pep      70      80      90      100     110     120
GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN
|||||
a516          70      80      90      100     110
GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKQFQMVPEPNPRFA-YQALPVKLESPASQN
|||||

m516.pep     130     140     150     160     170     180
FSTEGLCLRYDTPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
|||||
a516         120     130     140     150     160     170
FSTEGLCLRYDTPADIAKLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
|||||

m516.pep     190     200     210     220     230     239
EQSVADIYYTVTEHTDKSKLFANILYTPFFLILDAAGAVLALPAAALGAVVDAARKX
|||||
a516         180     190     200     210     220     230
EQSVADIYYTVTKKHTDKSKLFENIAYTPTTLILDVAVGAVLALPVAALIAATNSSDKX
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1  atgcatcggg tttcagacgg cattggagtg tcagtcgtgt tctgccgatt
51  cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcacg
151 tgcgtctttc aatcccgatt tgatgttttt gggcaggctc atttggtcgg
201 tgtcgccggg aatgacggct ttcgcgccga agccgatgca ggtcaggaaac
251 attttcattt gttcgggctt ggtgttttgc gttcgtcga ggatgatgta
301 tgcgcgcttg agcgtcctgc cgcgcatata ggcgagcggg gcgatttcaa
351 tcaggccctt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagagggcat cataaagcgg acggaggtag gggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence &lt;SEQ ID 1436; ORF 517.ng&gt;:

```

g517.pep
1  MHRVSDGIGV SVVFCRFVGF DDFLHQMPD NVFAGEGMEI QSCHAVQFLT
51  CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGFNQAF FNQLGYTVKA HQVIBGIIKR TEVGVDFLGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1  ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51  CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGTTGTGCA GTTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCT ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAAGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCTGA GGATGATGTA
301 TCGCGCGTTG AGCGTCCTGC CGCGCATATA GGCGAGCGGG GCGATTTCAG
351 TCAGGCCCTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA  
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep

1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT  
51 RIFXSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV  
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ  
151 VSGQEAQFLA GFDGWAH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	:     :     :     :     :     :					
g517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGEGMEIQSCHAVQFLTCVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDCAVERPAAHIGERGDFNQAF					
	:     :     :     :     :     :					
g517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKR TKVGIDFLGQVSGQEAQFLAGFDGWAH					
	:     :     :     :     :					
g517	FNQLGYTVKAHQVIEGIIKRTEVGVDFLGQVSGQEAQFLTGFDGRPN					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq

1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT  
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG  
101 CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGCCGTGCA GTTCTCAGC  
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGCAGGTCG ATTGGCTGG  
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTGAGAAC  
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGA  
301 TCGCCCGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCAATCTCAA  
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTCGAAGCC CATCAGGTCA  
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG  
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA  
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep

1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT  
51 RIF\*SRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV  
101 CAVERPAAHI GERGNLQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ  
151 VTGQKTQFLA GFDGRPH\*

m517/a517 93.4% identity in 167 aa overlap

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	:     :     :     :     :     :					
a517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHAVQFLTRIFXSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDCAVERPAAHIGERGDFNQAF					
	:     :     :     :     :     :					
a517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDCAVERPAAHIGERGNLQTF					

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	70	80	90	100	110	120
m517.pep	130	140	150	160		
	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	130	140	150	160		
	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTGQKTQFLAGFDGRPHX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1  atgacgtttt cggcggcaaa gctcaacatt tcggcactga tgttggtgtct
51  ttcggcagga atgaccggtt tactttccgc ttttttactg ctccgaccgg
101 aaggcagcat cttattcaac cattttttca gcataaatat tctgaccgga
151 agagcggcat ctccacgggc aaccgtgttc agactgcata aggcggtagc
201 attccacaag atgccgaaaa ccataagcaa aatgcgtaga aactacgccg
251 tccgaatcac gccgcctect cggcgggcaa cgcttcatta taacagattg
301 ccccttaaaa aatcagacct tgcttttgtg gcggagtctg aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1  MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RLHQAVRFHK MPKTISKMRN NYAVRITPPP RAATLHYNRL
101 PLKKSDFAFV AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTGCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCa GCATAAATAT TCTGACCCGA
151 AGAGCGGCAT CTCACAGGC AACCGTGTT AGACGGCATC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCG TAGAACTAC GCCGTCCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTT TGTGGCAGAG TCTGAAATT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPOATVF RRHQARFARC RTINKRRRNY AVRITPPSXA ATRHYNRLPS
101 AAGLVRRERR RCAVILSNR KKSDPAFVAE SEI*

```

Computer analysis of this amino acid sequence gave the following results:

#### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep      MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF
g518          MTFSAAKLNISALMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
              10          20          30          40          50          60

              70          80          90          100         110
m518.pep      RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSN
g518          RLHQAVRFHKMPKTISKMRNRYAVRITPPPPRAATLHYNRLPL-----
              70          80          90          100

m518.pep      120      130
g518          GRKKSDFAFVAESEI
              |||||
g518          --KKSDPAFVAESEI
              110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCGACCCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCA GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTC AGACGGCATC AGGCGGTACG
201 ATTCCGAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCAGCC GTCTCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 .....AAAAAAT CAGACCCTGC TTTGTGGCA GAGTCTGAAA
401 TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFL LRPESILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*
```

m518/a518 79.9% identity in 134 aa overlap

	10	20	30	40	50	60
m518.pep	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF					
a518	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF					
	10	20	30	40	50	60
	70	80	90	100	110	119
m518.pep	RRHQA-RFARCTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSNG					
	:					
a518	RRHQAVRFRKMPTINKRRRNYAVRITPPSXAATRHYNRLPS-----					
	70	80	90	100		
	120	130				
m518.pep	RKKSDPAFVAESEIX					
a518	-KKSDPAFVAESEIX					
	110					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggcttcaa
51  atcctttgtc gtcaccccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatttt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcttc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcggy ggcttggggt
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccgcct tcaaaaccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggaataag cccgccaaag ttgccgaaat cgggaaccct
901 aattttcggc ggcataaaaa attttcgcca gaagcaaaaa cggccaataa
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```



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101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG  
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS  
 201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAAN  
 251 RQIAAALQTQ SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP  
 301 NFRRHEKFSP EAKTAK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

m519.seq (partial)  
 1 ..TCCGTTATCG GCGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA  
 51 AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG  
 101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCGCAAGAA  
 151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC  
 201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA  
 251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT  
 301 GCGGTCAATG CGTCAAATGC CGAGAAAAATC GCCCGCATCA ACCGCGCCAA  
 351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA  
 401 TCCGTCAAAT TGCCGCGGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC  
 451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA  
 501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTGCGGAC ATCGGCAGCC  
 551 TGATTTCGTC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

m519.pep (partial)  
 1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE  
 51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGQREAE IQQSEGEAQA  
 101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIROIAAA LQTGGGADAV  
 151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGLISAGMK IIDSSKTAK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

m519.pep				10	20	30
				SVIGRMELDKTFEERDEINSTVVAALDEAA		
g519	YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
m519.pep		40	50	60	70	80
		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGQREAE				
g519	GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLAGQREAE					
	150	160	170	180	190	200
m519.pep		100	110	120	130	140
		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANA EAIROIAAALQTGGGADAV				
g519	IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANA EANRQIAAALQTQSGADAV					
	210	220	230	240	250	260
m519.pep		160	170	180	190	200
		NLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL- ISAGMKIIDSSKTAK				
g519	NLKIAGQYVTAFKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK					
	270	280	290	300	310	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

a519.seq  
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA  
 51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG  
 101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT  
 151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT

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```

201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGTTGCCG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCGCGG GTATGAAAT TATCGACAGC AGCAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFGRKSFV VIPQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
101 SNYIMAITQL AQTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GOREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAELI
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

m519/a519 99.5% identity in 199 aa overlap

m519.pep
10 20 30
SVIGRMELDKTFEERDEINSTVVAALDEAA
a519 YFQVTDPKLASYGSSNYIMAITQLAQTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
90 100 110 120 130 140

m519.pep
40 50 60 70 80 90
GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
a519 GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
150 160 170 180 190 200

m519.pep
100 110 120 130 140 150
IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAELIRQIAAALQTQGGADAV
a519 IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAELIRQIAAALQTQGGADAV
210 220 230 240 250 260

m519.pep
160 170 180 190 200
NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSTAKX
a519 NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSTAKX
270 280 290 300 310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGT AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGGGCGG ATGCGGTCAA

```

801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG  
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG  
901 ATTTCTGCCG GCATGAAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFKSFV VIPOQEVHV ERLGRFHRAL TAGLNILIPF  
51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS  
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG  
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS  
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEL  
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL  
301 ISAGMKIIDS SKTAK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.aeq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA  
51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG  
101 GCGGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT  
151 ATCGACCGCG TCGCCTACCG CCATTGCGTG AAAGAAATCC CTTTAGACGT  
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG  
251 GCATCATCTA TTTCAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG  
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC  
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA  
401 TCAACAGTAC TGTGTGTGCG GCTTTGGACG AGCGCGCCGG GGCTTGGGGT  
451 GTGAAGGTTT TGCATTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT  
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAAGCGGAA AAACGCGCCC  
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT  
601 GGTACGCGCG AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTCAGGCTGC  
651 GGTCAATGCG TCAATGCCG AGAAAATCG CCGCATCAAC CGCGCCAAAG  
701 GTGAAGCGGA ATCCTTGCGC CTGTGTGCGG AAGCCAATGC CGAAGCCATC  
751 CGTCAAAATG CGCGCCGCTT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA  
801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG  
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG  
901 ATTTCTGCCG GTATGAAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFKSFV VIPOQEVHV ERLGRFHRAL TAGLNILIPF  
51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS  
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG  
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS  
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEL  
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL  
301 ISAGMKIIDS SKTAK\*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQQAITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMAQQAITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep						

780

```

m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

a519-1.seq

```

1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCGTCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCTC ATACGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCGCGCGG AGCTTGGGGT
451 GTGAAGGTTT TGCATTATGA GATTAAAGAC TTGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTACAGCGC AAGCCGAAAT CCAACAATCC GAAGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTGTTGCGG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCAA GCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAACCG CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

a519-1.pep.

```

1  MEFFIILLAA VVVFQKSFV VIPQEVHV VRLGRFHRAL TAGLNILIPP
51  IDRVAYRHS LKEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLSYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGR KIEQINLAS
201 GQREAEIQQS EGEAAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFQKSFVVIPQEVHVVERLGRFHRALTAGLNILIPPIDRVAYRHS
              |||||
m519-1      MEFFIILLVAVVFQKSFVVIPQEVHVVERLGRFHRALTAGLNILIPPIDRVAYRHS
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIYFQVTDPKLSYGS SNYIMAITQLAQTTLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIYFQVTDPKLSYGS SNYIMAITQLAQTTLRSVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRS MQAQITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRS MQAQITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              |||||

```

```

m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQVVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQVVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

#### Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in *E. coli* as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in *E. coli*. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1   atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctggtgcc gttaataatg ccggcgatgg
101 atttaacctt gtttgcgcgc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccc ctaactgcgc ttcaaattgg acgatgacgt ttgtttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccc tgccgcgcga caattcgacc aagacatcga cgtctttacg
351 cggaacagat tcgaacggat cttttgacaa gggcgggcga cgggcccatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgcccaa gggcggggaa atttctctcg cgttgtcccc caacacggca
501 gccgcaccgc cgccgaccgt acctaacgct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1   MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILILFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNATSL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1   ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCGGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCC CTAAGTCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GGCGAGCAGT TTTTGTGTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

```

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```

301 GCAATGCCGG TACCGCCGaa CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCACACAGT TCGAACGGAT CTTTGACAAA GGCTGc.CGG ACGGGCAGGT
401 TTGTGCGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATT
451 CGCGCCCCAA GCGACGGGAA ATTTCTCTCCG CGTTGTCCsCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
  1 MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDILILFAA KPSRRALMIG
 51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF
151 RAPSDGKFPP RCXATROPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

```

m520/g520
      10      20      30      40      50      60
m520.pep MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW
|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g520      MPALLSIRANALPFSRISERMKLLVPLIMPAMDILILFAAKPSRTALMIGIPPATAASNW
      10      20      30      40      50      60

      70      80      90     100     110     120
m520.pep TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNNTASLAMPVPPNNSTTTSTSSRATS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g520      TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNNTASLAMPVPPNNSTKTSTSLRANS
      70      80      90     100     110     120

      130     140     150     160     170     180
m520.pep SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATROPYRRRPYPNLKDR
|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g520      SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFLRCPATRQPHRRRPYLSLKDR
      130     140     150     160     170     180

      190
m520.pep CLLASLCLLVSRKCKY
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g520      CLLASLCLLVSRKCKY
      190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
  1 ATGCCTGCGC TTCTTTTCAGT ACATCGG.CA AACGCGCTGC CTTTTTCGCG
 51 CATTTTCGAG AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTAATGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTTCG TCCCGTATTC GGCGAGCAGT TTTTGTGTTG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
301 GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCACACAGT TCGAACGGAT CTTTGACAAA GGCTG.CGG ACGGGCAGGT
401 TTGTGCGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATT
451 CGCGCCCCAA GCGACGGGAA ATTTCTCTCCG CGTTGTCCCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
  1 MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDILILFAA KPSRRALMIG
 51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

```

151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY\*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCPATRQPYRRRPYPNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRLKCKYX					
a520	CLLASLCLLVSRLKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCTGTTG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTtCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGC GGGCTTTTTC
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSLLTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCTGTTG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTC GGGCTTTTTC
351 TTCACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```

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101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP  
 151 TVPKPKRPMF TGFIVSPCKP TEM\*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSLR	ATSSNGSLTKA	ADGQIWRAFSSLK	
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSSLK	
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKR	REISSALSRNTA	APPTVPKPKRPM	FTGFI	VSPCKPTEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTA	AVPPPTVPKPKR	PMFTGFI	VSPCKPTEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq

1 ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT  
 51 TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA  
 101 CTGCCGCTTC AAATTGGACG ATGACGTTT GTTTTCCGC CAGCGGAAG  
 151 ATTTCTGTTG CGTATTCGGC GAGCAGTTT TTGTTGGCGG TAACGATGTG  
 201 TTGCGCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC  
 251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACAGTGC GACCAGTTCTG  
 301 AACGGATCTT TGACAAGGC TCGGGACGGG CAGGTTTGTC GGGCTTTTTC  
 351 TTCACTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCAAGCGAC  
 401 GGGAAATTC CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG  
 451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC  
 501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep

1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTCFCSASGK  
 51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS  
 101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP  
 151 TVPKPKRPMF TGFIVSPCKP TEM\*

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSSLK	
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSSLK	
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKR	REISSALSRNTA	AVPPPTVPKPKR	PMFTGFI	VSPCKPTEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTA	AVPPPTVPKPKR	PMFTGFI	VSPCKPTEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq

1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACCTTTCCC TGATTTC AAG  
 51 CCCATTGGGT GCGAATGCGG CCAAATCTA TACCTGCACA ATCAACGGAG  
 101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTG



151	CCCCCAATCG	GCAACTACAG	CAGCGAACGC	TATATCCTGC	CCCAAACGCC
201	CGAACCGCGCA	CCATCACCCTG	CAAAACGGCGG	ACAGCGCTGTC	AAATATAAAG
251	CCCCGGTCAA	AACAGTATCC	AAGCCGGCAA	AAATCCAATGC	GCCGCCTCAA
301	CAGCAGCTCTG	TAAATTAACAG	CAGACGCTCC	ATTTCgaag	caGaattaag
351	cAatgaacgc	aaagccctGa	ctGaAGCCCCA	AAAAATGTTA	TCACAagca
401	gtCtGGCAAA	AGGCGcaAC	AtcaaCCatc	aaaAaatcaa	cgcattgtaa
451	AGCAATGTTt	tggacAGACA	GCAAAATaTc	Caagcactgc	aaaGagAATt
501	GGGACGTATG	TAA			

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>:

q521n.pep

1 MKSKPLILI NLSLISSPLG ANAAKIYTC T INGETVYTTK PSKSCHSTDL  
51 PFIGNYSSR YILPQTPEPA PSPSGGQAV KYKAPVKTVS KPAKSNTPPQ  
101 QAPVNNRRS ILEAELSNER KALTEAQKML SQARLAKGNN INHQKINAL\*  
151 SNVLDRONI QALORELGRM \*

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1473>:

m521.seq

1	ATGAAATCAA	AACCTCTCTT	AATCCTAATC	AACTTTTCCC	TGATTTCAAG
51	CCCATTGGGT	GCGAATGCGG	CCAAAATCTA	sACCTGCACA	ATCAACGGAG
101	AAACCGTTTA	CACCA <sub>s</sub> CAAG	CCGTCCAAAA	GCTGCCACTC	AACCGATTTG
151	CCCCCAATCG	GCAACTACGC	CAGCGAAGCG	TATATCCCGC	CCCCAACGCC
201	CGAACCGGTA	TCATCATCGT	CAACCGCGCG	ACwGGTTGTG	ACCATATAAG
251	CCCCGGTCAA	AACAGTATCC	AAACCGGC <sub>AA</sub>	AATCCAATAC	CGCGCGCGCG
301	CAACAAGCAC	CCTCAAACAA	CAGCAGACGC	TCCATTCTCG	AAACAGAATT
351	GAGCAACGAA	CGCAAAGCAT	TGTTTGAAGC	CCAAAAATG	TTATCACAAG
401	CACGTCTGGC	AAAGGGCGGC	AACATCAACC	ATCAAGAAAT	AAATGATTA
451	CAAAGCAATG	TATTGGACAG	GCAGCAAAAT	ATTCAAGCCC	TGCAAAGGGA
501	ACTGGGCGGT	ATGTAA			

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

m521.pep

1 MKSKLLLLILI NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTD  
51 PPIGNYSSER YIPPQTPEPV SSPSNGGXV KYKAPVKTVS KPAKSXTPPP  
101 QQAPSNNRRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL  
151 QSNVLDROON IOALORELGR M\*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

m521/q521

```

      10      20      30      40      50      60
m521.pep  MKSKLLILINFLISPLGANAAKIXTCTINGETVYTXKPSKSchSTDLPPIgNYSSER
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g521      MKSKLPILILINLSLISPLGANAAKIYTCTINGETVYTTKPSKSchSTDLPPIgNYSSER
          10      20      30      40      50      60

      70      80      90      100     110     120
m521.pep  YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQApsNNsRRSILEtELSNE
          ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g521      YILPQTPEPAPSPSNGGQAVVKYKAPVKTVSKPAKSNTPP-QQAPVNNSRRSILEAEELSNE
          70      80      90      100     110

      130     140     150     160     170
m521.pep  RKALVEAQKMLSQARLAKGgNINHqEINALQSNVLDROQNIQALQRELGRMX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g521      RKALTEAQKMLSQARLAKGgNINHqKINALXSNVLDROQNIQALQRELGRMX
      120     130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1475>:

a521.seq

1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTCAAG

```

51 CCCATTGGGT GCGAATGCGG CCAAAATCTA CACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCCAAAA GCTGCCTCTC AACCGATTTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACATC
201 CGAACCGACA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AACAGAAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CAGTCTGGC AAAAGGCGGC AACATCAACC ATCAAGAAAT CAACGCATTG
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATCCAAGCAC TGCAAAGAGA
501 ATTGGGACGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI NFSLISSPLG ANAAKIYCT INGETVYTTK PSKSLSTDL
51  PPIGNYSSER YIPPQTSEPT PPSNGGQAV KYKAPVKTVS KPAKSNTPPP
101 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSVLDRQON IQALQRELGR M*

```

m521/a521 94.2% identity in 171 aa overlap

	10	20	30	40	50	60
m521.pep	MKSLLLLILINFLISSPLGANAAKIXTCTINGETVYTXKPSKXSCHSTDLPPIGNYSSER					
a521	MKSKLPLILINFLISSPLGANAAKIYCTINGETVYTTKPSKSLSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQAPSNNRRSILETELSNE					
	:       :					
a521	YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQAPSNNRRSILETELSNE					
	70	80	90	100	110	120
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc cgaaacacga aacgccgacg gaagagcagg ttgccgcgcg
51  caaaaaagca aaagccaaaa tccgcaccat ccgcatttgg gcgtgggtca
101 ttttggcggt gctcgcttca accgccctgc tctcccaatg cgcgatgtcc
151 aaaccgcagg caaaacagaa aattgtcgag tcttgcataa aaaatattcc
201 gtttgcgtga aaatggcaga acgatttgaa agcgcgcggc ttggatgcgg
251 acaatacccg tctcgccgtc gactactgca aatgtatgtg ggagcagcct
301 ttggacggat tgagcgagaa acagatcagc tccttcggca aactcgggtg
351 acaagaacag cttgacctgc tcggcggcgc aaacgcgttt gaaactcgag
401 acaacaatg tgtcgcggtt ttgaaagccg attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
51  KPQAKQKIVE SCMKNIPFAE KWQNDLKARG LDADNTRLAV DYCKMWEQP
101 LDGLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
51  CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTGGT GCGTGGGTCA
101 TTTTGGCGTT GCTCGCTTTA ACCGCCCTGC TCTCCAATG CCGCATGTCC
151 AAACCGCAGG CAAAACAGAA AATTGTGCGAG TCTTGCGTGA AGAATATTCC
201 GTTTGCCGAA AAATGGCAAA ACGATTTCGG GGCCCGCGGT TTAGATTCAA
251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

```

m522.ppt

```

1  MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMs
51 KPOAQKQIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKCMWEQP
101 LDRLSEKQIR SFGKLGAEQ LDLLGGANAF EARDKQCVAD LKSE*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m522/q522

[illegible]

a522.seq

1	ATGACTGAGC	CGAAACACGA	AATGCCGACG	GAAGAGCAGG	TTGCCGCGCG
51	CAAAAAAGCA	AAAGCCAAAA	TCCGCACCAT	CCGCATTGG	GCATGGGTCA
101	TTTTGGCGTT	GCTCGCTTCA	ACCGCCCTCG	TC7CCCAATG	CGCGATGTCC
151	AAACCCGAGG	CAAAACAGAA	AATGTCTGAG	CTTTCGCTGA	AGAATATTCC
201	GTTTGCCGAA	AAATGGCAAA	ACGTTTTCGG	GGCCCGCGGT	TTAGATTCAA
251	ACAATACCCG	CCTTACCGTC	GACTACTGCA	AATGTATGTG	GGAGCAGCCT
301	TTGGACAGAT	TGAGCAGGTA	ACGAGTATCT	TCCTTCGCGA	AACTCGGCGC
351	ACAAGAACAG	CTTGACCTGC	TCGCGCGAGT	AAATGCTTTT	GAAACGCGAG
401	ACAAGCAGTG	TGTTGCCGAT	TTGAATCAG	ATAAA	

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMs  
51 KPOAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKCMWEQP  
101 LDRLSEKQIS SFGKLGAEQ LDLLGGANAF ETRDKOCVAD LKSE\*

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWA <del>V</del> VILALLALTALLSQCAMSKPQAKQKIVE					
a522	MTEPKHEMPTEEQVAARKKAKAKIRTIRIWA <del>V</del> VILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLD <del>S</del> NNTRLAVDYCKCMWEQPLDRLSEKQIRSF <del>G</del> KLGAQEQ					
a522	SCVKNIPFAEKWQNDLRARGLD <del>S</del> NNTRLTVDYCKCMWEQPLDRLSEKQISS <del>F</del> KLGAQEQ					
	70	80	90	100	110	120

788

```

                130      140
m522.pep      LDLLGGANAFEARDKQCVADLKSEX
                |||||:|||||
a522          LDLLGGANAFETRDKQCVADLKSEX
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

```

g523.seq
  1  atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
51  gacgggaacg gtttatcttt tggtgtcag cgcggtttg gcgggttcgg
101 gcattgccta cgggctgact ggcagcacgc ctgccgccgt cttgaccgcc
151 gcaactgcttt ccgcgctggg catttggttc gtacatgcca aaaccgccgt
201 gggaaaagtt gaaacggatt catatcagga tttggatacc ggaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt tttttatcgc
301 ggtacgcact ggcaggcgca aaatacgggg caggaagtgt ttgaaccggg
351 aacgcgcgcc ctcctcgccc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

```

g523.pep
  1  MTVWFVAAVA VLIIELLTGT VYLLVVSAA AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKAEILRYT GGNRYEVFYR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

```

m523.seq (partial)
  1  ..GCCGTCTTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGGT CGGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCTGCCGC CGTCTTGACC GncGCTCTGC TTTCCGCGCT GGGTATTTnG
151 TTCGTACACG CCAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTTGGAT GCCGGACAAT ATGTCGAAAT CCTCCGACAC ACAGCGGGCA
251 ACCGTTACGA AGTTTTtTAT CGCGGTACGc ACTGGCAGGC TCAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACTCGC GCCCTCATTG TCCGCAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

```

m523.pep (partial)
  1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDLG AGQYVEILRH TGGNRYEVFY RgTHWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng) from *N. gonorrhoeae*:

m523/g523

```

                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTXALLSALGIXF
                |||||:|||||
g523          MTVWFVAAVAVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTAALLSALGIWF
                10      20      30      40      50      60

                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDLGAGQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g523          VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEVFEPGTRA
                70      80      90      100     110     120

                120
m523.pep      LIVRKEGNLLIITHP
                |||||:|

```

g523 LIVRKEGNLLIIANPX  
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

a523.seq  
1 ATGACTGTAT GGTTTGTTGC CGCTGTTGCC GTCTTAATCA TCGAATTATT  
51 GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG  
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC  
151 GCTCTGCTTT CCGCGCTGGG TATTTGGTTC GTACACGCCA AAACCGCGGT  
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG  
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC  
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG  
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA  
401 AACCTTAA

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

a523.pep  
1 MTVWFVAAVA VLIIELLTGT VYLLVVSAAAL AGSGIAYGLT GSTPAAVLTA  
51 ALLSALGIWF VHAKTAVGKV ETDYQDLDA GQYAEILRHA GGNRYEVFYR  
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP\*

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTVWFVAAVAVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIITHPX				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

g525.seq  
1 atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca  
51 agcggcggct gccgaaatgg ttcaaatcga aggcggcagc taccgcccgc  
101 tttatctgaa aaaagatacc ggcctgatta agtcaaacc gttcaaactg  
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca  
201 cccccaatgg caaaaaggca ggatcgggtc caaacaggca gaacccgctt  
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg  
301 ggcgaattga aacagccggg taccaatatt tcctgggttg ccgccaacgc  
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat  
401 ttgccggact tgcttccgcc acgcagaaaa aacggctcaa acgaacccgg  
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc  
501 tgcacgatgt cggcaaaagca ccgcccgaac tactgggggtg tttatgatat  
551 gcacgggctg a

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

g525.pep  
1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL  
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA  
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKKRLKRTR  
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

m525.seq  
 1 ATGAAGTATG TCCGGTTATT TTWCCTCGGC GCGGCACTCG cCrCACTCA  
 51 ArCGGCGGCT GcCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCrC  
 101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG  
 151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA  
 201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT  
 251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGc GCCGAAGgCG  
 301 GgCGAATTAA AACCAACCGT AACCAATGTT TCCTGGwTG CCGCCAACgC  
 351 CTAtTGC GCCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT  
 401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA A.CGGCTCAA ACGAACCCGG  
 451 CTACAACCGC ACTATTCTCG ATTGGTATGC CGACGGCGGA CGGAAAGGCC  
 501 TGCACGATGT CGGCA.AAGG CCGCCCGAAC TACTGGGGCG TTTATGATAT  
 551 GCACGGGCTG A

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

m525.pep  
 1 MKYVRLFXLG AALAXTOXAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL  
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA  
 101 GELKQPVNTV SWXANAYCA AQGKRLPTID EWEFAGLASA TQKXRLKRTR  
 151 LQPHYSRLVC RRRTERPARC RXKAARTGA FMICTG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

m525/g525

	10	20	30	40	50	60
m525.pep	MKYVRLFXLGAALAXTOXAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF					
	:					
g525	MKYVRLFFLGTALAGTQAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m525.pep	AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVNTVSWXANAYCA					
g525	AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVNTISWFAANAYCA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m525.pep	AQGKRLPTIDWEFAGLASATQKXRLKRTRLQPHYSRLVCRRTTERPARCRXKAARTTGA					
g525	AQGKRLPTIDWEFAGLASATQKRLKRTRLQPHYSRLVCRRTTERPARCQSTARTTGV					
	130	140	150	160	170	180
m525.pep	FMICTGX					
g525	FMICTGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

a525.seq  
 1 ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA  
 51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC  
 101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG  
 151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA  
 201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT  
 251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG  
 301 GGCGATTTAA AACCAACCGT AACCAATGTT TCCTGGTTCG CCGCCAACGC  
 351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT  
 401 TTGCCGGACT TGCTTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCGG  
 451 CTACAACCGC ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC  
 501 TGCACGATGT CGGCAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT  
 551 GCACGGTCTG A

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
1  MKFTRLLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

      10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
          ||::||: | |||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      MKFTRLLFLCAALAGTQAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
          10      20      30      40      50      60

      70      80      90      100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWXAAANAYCA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
          70      80      90      100     110     120

      130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQXKRLKRLRQLPHYSRLVCRRTTERPARCRXKAARTTGA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AQGKRLPTIDWEFAGLASATQXKRLKRLRQLPHYSRLVCGWRPERPARCRQXVARTTGA
          130     140     150     160     170     180

m525.pep  FMICTGX
          ||||
a525      FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
1  ATGAAGTACG TCCGGTTATT TTCTCTCGGC ACGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGCAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAGGCCT
501 GCACGATGTC GGCAAAGACC GCCCGAACTA CTGGGGTGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTCG AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAACTATG CCGCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAACT TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
1  MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKGLHDV GKDRPNYWG YDMHGLIEWE TEDFNSLLS
201 SGNANAQMFC SGASVGASDS SNYAFLRYG IRTSLQSKYV LHNLFRCAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
1  ATGAAGTATG TCCGGTTATT TTCTCTCGGC GCGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

```
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACCAACCGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCGCC ACGCAGAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```
1 MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGRSRYAPKA
101 GELKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKGRPNYWG VYDMHGLIEWE TEDFNSSLSS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLFGRCTS
251 R*
```

m525-1/g525-1 97.6% identity in 251 aa overlap

```
10 20 30 40 50 60
m525-1.pep MKYVRLFFLGAALAGTQAAAEMVQIEGGSYRPLYLKDTGLIKVKPFKLDKYPVTNAEF
g525-1 MKYVRLFFLGTALAGTQAAAEMVQIEGGSYRPLYLKDTGLIKVKPFKLDKYPVTNAEF
10 20 30 40 50 60
70 80 90 100 110 120
m525-1.pep AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGRSRYAPKAGELKQPVNTVSWFAANAYCA
g525-1 AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGRSRYAPKAGELKQPVNTISWFAANAYCA
70 80 90 100 110 120
130 140 150 160 170 180
m525-1.pep AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGKRLHDVGKGRPNYWG
g525-1 AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGKRLHDVGKDRPNYWG
130 140 150 160 170 180
190 200 210 220 230 240
m525-1.pep YDMHGLIEWETEDFNSSLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV
g525-1 YDMHGLIEWETEDFNSSLSSGNANAQMFCSGASVGSADSSNYAAFLRYGIRTSLSQSKYV
190 200 210 220 230 240
250
m525-1.pep LHNLFGRCTSRX
g525-1 LHNLFGRCSRX
250
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

a525-1.seq

```
1 ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATAACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGATTAA AACCAACCGT AACCAATGTT TCCTGGTTTC CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCGCC ACGCAGAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA CTGGTATGCG GATGGCGACC GGAAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA
```



This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKFTRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGRKDLHDV GKGRPNYWGV YDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

```

              10      20      30      40      50      60
m525-1.pep  MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
              10      20      30      40      50      60
a525-1      MKFTRLFLC AALAGTQAAA AEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
              10      20      30      40      50      60

              70      80      90      100     110     120
m525-1.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVNTVSWFAANAYCA
              70      80      90      100     110     120
a525-1      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVNTVSWFAANAYCA
              70      80      90      100     110     120

              130     140     150     160     170     180
m525-1.pep  AQGKRLPTID EWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWGV
              130     140     150     160     170     180
a525-1      AQGKRLPTID EWEFAGLASATQKNGSNEPGYNRTILDWYADGDRKDLHDVGKGRPNYWGV
              130     140     150     160     170     180

              190     200     210     220     230     240
m525-1.pep  YDMHGLIEWE TEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV
              190     200     210     220     230     240
a525-1      YDMHGLIEWE TEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV
              190     200     210     220     230     240

              250
m525-1.pep  LHNLGFRCTSRX
              250
a525-1      LHNLGFRCTSRX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atggttttac cagtctcctt ttttcagcct gtccagttgg cggcggtcgc
51  gcttggtcgg tctgccgtcg ggatgggagg aagtatgctg gctgaattgg
101 tcgagctggt tgcactcttc cctcaatgct gccgttttcg cgtctctctc
151 atacagaagc cgcgcctcgg gtgccgggag gcgttggtgg ttcaaacctt
201 taaccttgat tttatgggga aggggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tggttttact gtttttgact ttcgagccgt ttacttgaac
301 cctacccagt tcgatatgct tttgcgcaag ggaacgggtc ttgaaaaaac
351 gtgccgccca aagccatttg tccagccgca tggcggaaga atcgtgcttg
401 tctttcatac gattttgttt gaaataattg aatttgtttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLVPSFFQP VLAAVALGR SAVGMGGS DAELVELFALF PQCCRFRVFF
51  IQKPRLGCR ALVVQTFNLD FMKGIERQV DNIADVYGT VDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
51  GCTTGGTGCG TCTGCCGTGCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCCTCTTC CCTCAATGTT GCCGTTWTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCTCGG ATGCCGGGCG GCCTTGTTGG TTCAAACCTT

```

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201 TAACCKTGAT TTTATAGGGA AGGG.AATTk AgCkTCaGty GrTwATaTCG  
 251 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC  
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC  
 351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG  
 401 TCTTTCATAC GATTTTGTGTT GAAATAATTG AATTTGTTC GAGTTTAGCA  
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

m527.pep  
 1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLf  
 51 IQKPRXGCRA ALVVQTFNXd FIGKXNXASV XXIADVYGFT VFDLRAVYLN  
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA  
 151 \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRXRVLf	IQKPRXGCRA
g527	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRFRVFF	IQKPRXGCRA
	10	20	30	40	50	60
	70	80	90	100	110	120
m527.pep	ALVVQTFNXd	FIGKXNXASV	XXIADVYGFT	VFDLRAVYLN	NPTQFDVLLRK	GTGLEKTCRP
g527	ALVVQTFNLD	FMGKIERQVD	NIADVYGFT	VDFRAVYLN	NPTQFDMLLRK	GTGLEKTCRP
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGR	IVLVFHTILF	EIIEFVSSLA			
g527	KPFVQPHGGR	IVLVFHTILF	EIIEFVSSLA			
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

a527.seq  
 1 ATGGTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTGCG  
 51 GCTTGCTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG  
 101 TCGAGCTGTT TCGCTCTTTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC  
 151 ATACAGAAGC CGCGCCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT  
 201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG  
 251 CCGATGTCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC  
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC  
 351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG  
 401 TCTTTCATAC GATTTTGTGTT GAAATAATTG AATTTGTTC GAGTTTAGCA  
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

a527.pep  
 1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLf  
 51 IQKPRXGCRA ALVVQTFNLD FIGKIERQV DNIADVYGFT VFDLRAVYLN  
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA  
 151 \*

m527/a527 93.3% identity in 150 aa overlap

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRXRVLf	IQKPRXGCRA
a527	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRFRVLf	IQKPRXGCRA
	10	20	30	40	50	60

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	70	80	90	100	110	120
m527.pep	ALVVQTFNDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
a527	ALVVQTFNLDFIGKIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaaattc gggaataaaa atatacggca acggtgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcggggtg gtatgagtgt ttgtccttgt
101 ccggtctggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggcggcgaga gtccgctgtc ttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatcctt
251 actttttatag gaaaataggg aagtttgaag cctgcgggtt ggattggcgt
301 acgcgtgacg gcaaaccttt gtttgagagg ttcaaacagg aaggtttcga
351 ctgtttggaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQGGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

m528/g528	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
g528	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPLSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
g528	YEIPLSDGNSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLVERFKQGGFDCLE					
	70	80	90	100	110	120

m528.pep      K  
 |  
 g528          KQGLRRNGLSERVRW

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

a528.seq  
 1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT  
 51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT  
 101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT  
 151 GCGGCGGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA  
 201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT  
 251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT  
 301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA  
 351 TTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC  
 401 GATGGTAA

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

a528.pep  
 1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI  
 51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR  
 101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW\*

m528/a528 95.0% identity in 121 aa overlap

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
a528	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
a528	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE					
	70	80	90	100	110	120

m528.pep      K  
 |  
 a528          KQGLRRNGLSERVRW  
 130

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

g528-1.seq  
 1 ATGGAAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCAAT  
 51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTGT  
 101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT  
 151 GCGGCGGAGA GTCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA  
 201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAATCTT  
 251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT  
 301 ACGCGTGACG GCAAACCTTT GATTGAGAGG TTCAAACAGG AAGGTTTCGA  
 351 CTGTTTGAA AAGCAGGGGT TCGGCGCAA CGGCTGTCC GAGCGCGTCC  
 401 GATGGTAA

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

g528-1.pep  
 1 MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI  
 51 GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR  
 101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

m528-1.seq  
 1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT

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```

51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CCGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGA
351 CTGCTTGAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51 GGESPPSLGD YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

	10	20	30	40	50	60
g528-1.pep	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED					
	:         :     :     :     :     :     :					
m528-1	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g528-1.pep	YEIPLSDGNRSVRANEYESAOKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE					
	:     :     :     :     :     :     :					
m528-1	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE					
	70	80	90	100	110	120
	130					
g528-1.pep	KQGLRRNGLSERVRWX					
	:					
m528-1	KQGLRRNGLSERVRWX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CCGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAG AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

	10	20	30	40	50	60
a528-1.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED					
	:         :     :     :     :     :     :					
m528-1	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a528-1.pep	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE					
	:     :     :     :     :     :     :					
m528-1	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE					
	70	80	90	100	110	120
	130					
a528-1.pep	KQGLRRNGLSERVRWX					
	:					
m528-1	KQGLRRNGLSERVRWX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

```
g529.seq (partial)
  1 atgaccata tcaaaccgt cattgccg ctcgcactca tcgggcttgc
 51 cgcctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggtcgcaccg cctgatcaaa ctcgaagtcc cgcctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc ggctcgggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccagcggatg
251 ccggaagtat tgaaaagcgt caaaggcgtc cgcttcgagc ggcgacggca
301 gccaacgcct ggcttgcgt tgacggcaaa tccccgccg aaatctccgc
351 cgctttctg.
```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

```
g529.pep (partial)
  1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPN
 51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAFAF..
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

```
m529.seq
  1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
 51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTCGCACCG CCGATCAAAA CTGAAGTCC CACCTGATTT GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTTC GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCGA CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
351 CTGGAAGGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
451 CCCCAAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 CTACTCCACC GCGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCG
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GCGCACCGT GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTGCCA ACGGCTCGCG CATCGTCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

```
m529.pep
  1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPN
 51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAELVLSV KGVRLERDGS
101 QRWLVDGKS PAEIWPLLKA FWQENGFDIK SEEPAIGQME TEWAENRAKI
151 PQDSLRLRFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGKDKDTTV WQPSPSDPNL EAAFLTRFMQ YLGVDGQOAE NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRTVLAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPGLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

```
g529/m529
          10      20      30      40      50      60
g529.pep  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA
```

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```

m529      |||||
          MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPDPDLNPNPDQGNLYRLPA
          10      20      30      40      50      60

          70      80      90      100     110     120
g529.pep  GSGAVRAGDLEKRRTPAVQQPADAGSIEKRQRRLPLRAATAANAWLVVDGKSPAEISAAFX
          |||||:|||||
m529      GSGAVRASDLEKRRTPAVQQPADAENVLKS VKGVRLER-DGSQRWLVVDGKSPAEIWPLLK
          70      80      90      100     110

m529      AFWQENGFDIKSEEP AIGMETEWAENRAKIPQDSLRLRLFDKVGLGGIYSTGERDKFIVR
          120     130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1523>:

a529.seq

```
1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51 GCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTGCGACCG CCGATACAAA CTCGAAGTCC CACCTGATT T GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCGTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGGATTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATC
251 CCGAAGTATT TAAAGAGCTC AAAGGTGTCC GCCTCGAGCG CGACGCCAGC
301 CAACGCTGGC TCGTGTGCGA CGGCAAGTCT CATGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG TGCCAAAATC
451 CCCCAGACA GCTTGGCCG CCTATTGAC ACAGTCGGTT TGGGCGGCAT
501 CTACTCCACC GCGCAGCGCG ACAAATTCAT CGTCCGTATC GAAGCAGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGCGA AAGACAAGAA CCGACCGTA TGGCAGCCCT CCCCGTCCGA
651 TCCCAACCTC GAAGCCGCTT TCTGACGCG CTTTATGCAA TATTTGGGCG
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCTTCCC
751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGATACCGC AGAAATCGCG GCGCACCGC GCTCGCCCTC GACCCGATCA
851 GGCTGACCGT CGTCCGTGAA AACACCGAAG GCCACCTTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTG CTATGCCGAG CCGTGC CGCA ACGGCTCGCG CATCGTCTG
1051 CTCAACAAAG ACGGCAAGCG ATATGCCGCG AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TCGGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1524; ORF 529.a>:

a529.pep	1	MTHIKPVIAA	LALIGLAACS	GSKTEQPKLD	YQSRSHRLIK	LEVPPDLNPN
	51	DQGNLYRLPA	GSQAVRASDL	EKRRTPAVQQ	PADAEVLKSV	KGVRLERDGS
	101	QRWLVDVGKS	HAETIWPLLKA	FWQENGFDIK	SEEPAGIGME	TWEAENRAKI
	151	PQDSLRLRLFD	TVGLGGIYST	GERDKFIVRI	EQQKNGVSDI	FFAHKAMKEV
	201	YGGKDKDQTTV	WQPSPSDPNL	EAAFLTRFMQ	YLGVDGQQAE	NASAKKPTLP
	251	AAEMARIEG	KSLIVFGDYR	RNWRRTALAL	DRIGLTVVGQ	NTERHAFLVQ
	301	KAPNESNAVY	EQKPGFLFKRL	LGKGKAEPKA	EQPELIVYAE	PVANGSRIVL
	351	LNKDGSAYAG	KDASALLGKL	HSELR*		

**m529/a529 99.2% identity in 375 aa overlap**

	10	20	30	40	50	60
m529.pep	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVFPDLNPNPDQGNLYRLPA					
a529	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVFPDLNPNPDQGNLYRLPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m529.pep	GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLERDGSQRWLVDVGKSPAEIWPPLKA					
a529	GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLERDGSQRWLVDVGKSHAEIWPPLKA					
	70	80	90	100	110	120
	130	140	150	160	170	180

800

```

m529.pep  FWQENGFDIKSEEP AIGQMETEWAENRAKIPQDSLRLRLFDKVLGGIYSTGERDKFIVRI
           |||||
a529       FWQENGFDIKSEEP AIGQMETEWAENRAKIPQDSLRLRLFDTVLGGIYSTGERDKFIVRI
           130      140      150      160      170      180

           190      200      210      220      230      240
m529.pep  EQGKNGVSDIFFAHKAMKEVYGGKDKDTTVWQPSDPNLEAAFLTRFMQYLGVDGQQAE
           |||||
a529       EQGKNGVSDIFFAHKAMKEVYGGKDKDTTVWQPSDPNLEAAFLTRFMQYLGVDGQQAE
           190      200      210      220      230      240

           250      260      270      280      290      300
m529.pep  NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTVLALDRIGLTVVGQNTERHAFLVQ
           |||||
a529       NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTALALDRIGLTVVGQNTERHAFLVQ
           250      260      270      280      290      300

           310      320      330      340      350      360
m529.pep  KAPNESNAVTEQKPLFKRLLGKGAEKPAEQPELIVYAE PVANGSRIVLLNKDGSAYAG
           |||||
a529       KAPNESNAVTEQKPLFKRLLGKGAEKPAEQPELIVYAE PVANGSRIVLLNKDGSAYAG
           310      320      330      340      350      360

           370
m529.pep  KDASALLGKLHSELRX
           |||||
a529       KDASALLGKLHSELRX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga ggcgcgcaat gacgggtttg atatgggtca tcgtgtcatc
51  ctgtgtgatg gatattaaag tggttgatcat gttatgccgt ccgaacgggt
101 cagacggcat ggctatattt aaagtgtgcc tgaggctttc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgcacg
201 tgcggtccgc atccgcccaa ggcggatacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgctgtaaat cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCV M DIKVFVMLCR PNGSDGMAIF KVVLRLSGRR
51  GLLPVRLPSA ERAAGARAVR IRPRIPPIS VRRDWVRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  WTGAGTGCGA GCGCGGCAAT GACGGGTyTG ATATGGGTCA TCGTGTGATC
51  sTGTGTGATG GATATTAAAG TGtYTGTTGC GwTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGAckTTGC wTGTCGTTT yCCGTCAGCG GAACGAGCGG CAGGCGGACG
201 TGCGGTTCGC ATCTGCCCAg GGCgGATACC GCCCATTTcG GTGCGCGGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CGGTCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL IWVIVSSCV M DIKVXVAXCR PNGSDGMXIF KVVLRLSGRR
51  GLLXVRFP SA ERAAGGRAVR ICPGRIPPIS VRRGWVRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

```

m530/g530

m530.pep  XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFP SA
           |||||

```



q530	MSASAAMTGLIWVIVSSCVMDIKVFVMLCRPNNGSDGMAIFKVVLRLSGRRGLLPVRLPSA	60
	10 20 30 40 50 60	
m530.pep	ERAAGGRAVIRICPGRIPIISVRRGWVRRTWCRKSESVGR	99
	:            :	
q530	ERAAGARAVRIRPRRIPIISVRRDWRRTWCRKSESAGR	99

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1529>:

```
a530.seq
1  ATGAGTGCGA GCGCGGCAAT GACGGGTTTG ATATGGGTC TCGTGTCA TC
51  CTGTGTGATG GATATTAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTTTTCG CTGTCCGCCT TCCCTCAGCG GAACAGCGCG CAGGCGGAGT
201 TGCGGTTTCG ATCTGCCCCA GTCGGATAAC GCCCATTTCC GTGCGGCGGG
251 GCTGGGTTTC CAGAACATGG TGTCTAAAT CGGAATCAGC CGTCGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1530; ORF 530.a>:

a530.pep  
1 MSASAAMTGL IWVIVSSCVM DIKVFVALCR PNGSDGMAIF KVLRLSRR  
51 GLLPVLRLPSA ERAAGGRAVR ICPGRIPPI S VRRGWVRRTW CRKSEAGR\*

**m530/a530 93.9% identity in 98 aa overlap**

	10	20	30	40	50	60
m530.pep	XSASAAMTGLIWVIVSSCVM DIKVXVAXCRPNGSDGMXIFKVVLR LSGRRGL LXVRFP					
a530	MSASAAMTGLIWVIVSSCVM DIKVFVALCRPNGSDGM AIFKVVLR LSGRRGL LPVRLP					
	10	20	30	40	50	60
	70	80	90	100		
m530.pep	ERAAGGRAVRICPGRIPPISVRRGWVRRTWCRKSES VGRX					
a530	ERAAGGRAVRICPGRIPPISVRRGWVRRTWCRKSESAGR X					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 1531>:

g531.seq

1	ATGACCGCCC	TACTCGTCAT	CCTCGCCCTC	GCCCTGATAG	CCGTCGGCAC
51	GGCAGGCATC	GTCTATCCCG	CCCTGCCCGG	CTTGGCATTG	ATGTTTGCCG
101	GAACATGGCT	GCTTGCCTAT	GCCGGCGGCT	ATCAAATCTA	CGGCGCAGGC
151	ATCTTGTGGA	CGGTCGGACT	CATCCAGCCT	GCGGCATAC	TGGCGGACTA
201	TATGGCAGGC	ATGTTGGGGG	TAAAAATAC	TGGGGCAGG	AAACTCGCGC
251	TCCGAGGTGC	ATTGGCCGGC	AGCATCATCG	GCATATTTTT	CTCCCTTCCC
301	GGACTAATAC	TCGGCCCTTT	TATCGGCGCG	GCGGCAGGCG	AACTGATCGA
351	TCGGCCTGAT	ATGCCTTCAG	CAGGTAAAGC	GGGCTTGGGT	ACGCTGTTGG
401	GGTCTGTCT	CGGCACGGCG	TTCAAATATC	GCTGCGCCGT	ATCCATCTTG
451	TTTATCTCTG	TGGTGAATA	CATCGCATAC	CTGTTTTAA	

This corresponds to the amino acid sequence <SEQ ID 1532; ORF 531.ng>:

g531.pep

1	MTALLVILAL	ALIAVGTAGI	VYPALPGLAL	MFAGTWLLAY	AGGYQIYGAG
51	ILWTVGLISL	GGILADYMG	MLGVKYTAG	KLAVRGALAG	SIIGIFSLP
101	GLILGPFIGA	AAGELIDRRN	MLQAGKAGLG	TLLGLVVGTA	FKIGCAVSIL
151	FILLVKYIAY	LF			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1533>:

m531.seq

```
1  ATGACCGTAC TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
51  GCGGGGCATC GTTTaCCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
101 GAACATGGCT GCTTGCCCTAT GCCGGCGGCT ACCAAATCTA CGCGCGGGC
151 GTTTGTGTGA CGGTCGGACT CATCAGCCTT GCCGGCATC TGGCGGACTA
201 TGTGGCAGG ATATGGGGGA CAAAATATAC CGGAGCGGGC AAGCTCGCCG
251 TTCGCGCGC ATTGGCCGGC AGCATCATCG GCATATTTT CTCCCTTCCC
301 GGAATAATC TCGGTCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA
```

m531.pcp

1 MTVLTVILAL ALIavgTAGI VYPALPGLAL MfagTWLLAY AGGYQIYGAG  
51 VLWTVGLISL AGILADYVAG IWGTKYTGAG KLAVRGALAG SIIGIFFSLP  
101 GLILGPFIGA AAGELIERRN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL  
151 FILLVKYIAY LF\*

### Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m531/g531

	10	20	30	40	50	60
m531.pep	MTVLT	VILALALIAVGTAGI	VYPALPGLALMFAGT	TWLLAYAGGYQIYGAGV	LWTVGLISL	
	:					
g531	MTALL	VILALALIAVGTAGI	VYPALPGLALMFAGT	TWLLAYAGGYQIYGAGI	LWTVGLISL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADYVAGI	WGTYTGAGKLAVRGALAGSI	IIGIFFSLPGLILGPF	IGAAAGELIERN		
	:	: :				
g531	GGILADY	MAGMLGVKTYTGAGKLAVRGALAGSI	IIGIFFSLPGLILGPF	IGAAAGELIDRRN		
	70	80	90	100	110	120
	130	140	150	160		
m531.pep	MLQAGKAGL	GTLLGLVVGTA	FKIGCAVSILFILLVKYI	AYLF		
g531	MLQAGKAGL	GTLLGLVVGTA	FKIGCAVSILFILLVKYI	AYLF		
	130	140	150	160		

a531.seq

1	ATGACCGCCT	TGCTCGTCAT	CCTCGCCCTC	GCCCTGATAG	CGCGCGGTAC
51	GGCGGGCATC	GTTTACCCCG	CCCTGCCCGG	ATTGGCATTG	ATGTTTGCCG
101	GAACCTGGCT	GCTCGCTAC	TCCGCGCGCT	ACCAATCTA	CGCGCGGGC
151	GTTTGTGGA	CGGTCGGAT	CATCAGCCT	GCGGCGATAC	TGGCGGACTA
201	TGTGGCAGC	ATATGGGGGA	CAAAATATAC	GCGAGCGGAG	AGGCTCGCGC
251	TTCGCGGCGC	ATTGGCCGGC	AGCATCATCG	GCATATTTTT	CTCCCTTCCC
301	GGAATAAT	TCGGTCCCTT	TATCGGCGCG	GCGGCAGGCG	AACTGATCGA
351	ACGGCGCAAT	ATGCTTCAGG	CAGGTAAAGC	GGGCTGGGCT	ACGCTGTTGG
401	GGCTTATCGT	CGGTACGGCG	TTCAAAATCG	GCTGCGCGGT	ATCCATCTTG
451	TTTATCCTGT	TGGTGAATA	CATCGCCTAC	CTGTTTTAA	

a531.pep

```

1  MTALLVILAL ALIAAGTAGI VYPALPGLAL MFACTWLLAY SGGYQIYAG
51 VLWTVGLISL AGILADYVAG IWGTYGTAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGELIERN MLQAGKAGL TLLGLIVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

```

	10	20	30	40	50	60
m531.pep	MTVLT	VILALALIAVGTAGI	VYPALPGLALMFAGT	TWLLAYAGGYQIY	GAGVLWTVGLISL	
	:					
a531	MTALL	VILALALIAAGTAGI	VYPALPGLALMFAGT	TWLLAYSGGYQIY	GAGVLWTVGLISL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADY	VAGIWG	TKYTGAGK	LAVRGALAGSI	IIGIFFSLPGLIL	GPFPIGAAGELIERRR

803

```

a531      |||||
          AGILADYVAGIWGTYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN
          70      80      90      100      110      120

          130      140      150      160
m531.pep  MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          |||||:|||||
a531      MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1 atggctgaaa caatgaaaaa acaggcggat tcgcctgatt tgggtgacgg
51 tttggaagac aggccgccgt tcggtaatgc gctcttgagc gcggttaccc
101 atcttttggc gattttctgt ccgatgatta cgcccgcgct gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctgg tgtcgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggtcaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1 MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51 GALELPVEMT AYLVSAMVA SGVGYLQVN RFGSVGSGML SIQRYRHDC
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1 ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51 TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGC CGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTGCG GCACCTATTG GCAGGTCAAC CGCTTCGGGC
251 CGGTGCGGTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTCTGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTGCGGATT ACCGATTTTC GCGGCGGCTT CGGCGCGAAG GCGGACGGCA
551 CGTTCGGCTC GATGGAAAAC TTGGGGCTGG CATCGCTGGT GTTGTCTGAT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCG CTGTGCGCA TGAGCGGCAT
651 TCGGGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTAAATACG GTTTTGCTTT CGACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACGACCG ATTGAAGGCG AGGAATACAC CAAACGCCTG
901 CGCGGCGGCG TGTGGCTGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTACGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCG CGTTGTCGGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTT GATGTTCCGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACCTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1 MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51 GALELPVEMT AYLVSAMVA SGVGYLQVN RFGVPVSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```



201 VLVFNCKMNP LLRMSGIAVG LIAGYIVAlF LGKVDFSALQ NPLPLVTLPVP  
251 FKYGFAPDWH AFIVAGAlFL LSVFEAVGDL TATAMVSDQP IEGEYTKRL  
301 RGGVVLADGLV SVIATALGSL PLTTFAQNNG VIQMTGVAQR HVGKYIAVIL  
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRRREA  
401 VIATSVGLG LGVAFEPFVFNKNLPVLVFQNS ISAGGITAVL LNLVLPEDKT  
451 EAAVKPDTH LEH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from *N. gonorrhoeae*:

q532/m532

	10	20	30	40	50	60
g532.pep	MAETMKKQADSPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	:	:				
m532	MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	
g532.pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLSIQRYRHCARRGDERGRFEX					
m532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

a532.seq

```
1 ATGAGCGGTC AGTTGGGCCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51 TTTGGAGGAT AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCCGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGATGCTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT CTCGTTCTGT
301 ACCGTCATGA TTGCGCTCGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT TTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGTGTGGT GGTGATGCTG ATCGGCTTGA GTTTGGTACA
501 CGTCGGTATT ACCGATTTCG GCGGCGGCTT CGGCGCAAAG GCGGACGGCA
551 CGTTCGGCTC GATGGAAAAA TTGGGGCTGG CATCGCTGGT GCTGCTGATT
601 GTGCTGGTGT TCAATTGTCAT GAAAAACCGC CTGCTGCGGA TGACGGGCAT
651 TGCGGTCGGT CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC GGCAC TGCAA AACCTGCCGC TGTTACGCT GCCCGTACCG
751 TTTAAATATG GTTTTGCTTT TGA CTGGCAC GCATTTATTG TGGCGGGTGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTG ACGGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCTTG
901 CCGCGCGCGC TGTTGGCGGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGACA AACAACGGC GTGATTCAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGA CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGCGC CGATGGTTTT GATGTTCCGC TTGATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGCCACG GCATCCGCAG GCGCGAAGCG
1201 GTAATTGCGG CAACGTCGGT CCGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTGG TCTTGCCGA AGATAAAC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA
```

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532.pap

1	MSGQLGKGAD	APDLVYGLED	RPPFGNALLS	AVTHLLAIFV	PMITPALIVG
51	GALELPVEMT	AYLVSMAMVA	SGVGTYLQVN	RFGPVGSGML	SIQSVNFSFV

805

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALE LGKVDFSALQ NLPLVTLVPV
251 FKYGFAFDWH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
301 RGGVLADGLV SVIATALGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRL VSHGIRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

m532.pep	MSGQLGKGADAPDLVYGLED	RPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
a532	MSGQLGKGADAPDLVYGLED	RPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
m532.pep	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLS	IQSVNFSFVTVMIALGAGMKEGGLTKDAM
a532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLS	IQSVNFSFVTVMIALGAGMKEGGLTKDAM
m532.pep	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK	
a532	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK	
m532.pep	ADGTFGSMENLGLASLVLLIVLVFNCMKNP	LLRMSGIAVGLIAGYIVALFLGKVDFSALQ
a532	ADGTFGSMENLGLASLVLLIVLVFNCMKNP	LLRMSGIAVGLIAGYIVALFLGKVDFSALQ
m532.pep	NLPLVTLVPVPFKYGFADWHAFIVAGAI	FLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL
a532	NLPLVTLVPVPFKYGFADWHAFIVAGAI	FLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL
m532.pep	RGGVLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASR	HVGKYIAVILVLLGLFPVVG
a532	RGGVLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASR	HVGKYIAVILVLLGLFPVVG
m532.pep	RAFTTIPSPVLGGAMVLMFGLIAIAGVRLVSHGIRREAVIAATSVGLGLGVAFEPEVF	
a532	RAFTTIPSPVLGGAMVLMFGLIAIAGVRLVSHGIRREAVIAATSVGLGLGVAFEPEVF	
m532.pep	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX	
a532	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

```

g535.seq
1  atgccctttc ccgttttcag acaantattt gcttngtcct tgctacggtt
51  ttttgccgta ggtcggatcc tcgaatccga catttccaac agcgggtttt
101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatattaca tcgcttccaa ttctgcaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagttaga tggctcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttgcggc tgtttgaagt

```

806

```

351 catcgatgat tttgtcccgt tgtacggtgg tttggcgcgt gttgccgtag
401 ctgtcgaagg cgggtttttt gacggacagg tagtgcaata cttctggcgg
451 gatttcttcg acgaagcggg atgcgatgcc gaattgggtt tgtccgtgca
501 gcatgcgttg ctgtgccatg gtgatgtaga ggcgtttgcg ggcgcgggtg
551 atggcgacgt acatgagggc gcgttcttct tcgagggcgc cgcgctcggc
601 aaggctcatt tcgctgggga aacgcccctc ttccataacc gtgaggaaga
651 cggcgttgaa ttccaagcct ttggcggcgt ggacggtcat cagttggacg
701 gctttttcgc ctgcccctgc ttggttttcg ccggaattcga gggcggcgtt
751 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

```

g535.pep
1  MPFPVFRQXF AXSLRFFAV GRILESDISN SGFSETINAS NVFVGYEYP
51  ACISNLHRFQ FRKLGIOFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
101 DVLSDAEACV GLRLFEVIDD FVPLYGGLAR VAVAVEGGFF DGQVVQYFWR
151 DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
201 KAHFAGETPL FHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
251 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

```

m535.seq
1  aTGCCCTTtC CCGTTTTCAG ACGGCCTTTT GCTTTGTCCT TACTtACGTT
51  TTTTGCCGTA AGTCAGATTC TTGTATCCGA CATTCCAAC AGCGGTGTTT
101 CGGAAACAAT AGACCGCTCA AATGTTTTG TCGGATACGA ATATCCGACC
151 TACATTTCAA ATTTACATCT CTCCAATTG CGCAAATTG GTGTCCAAC
201 CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTCCCT
251 TTATCTGCGG CATCGATAAT CACGCCGGTG CCGAATTGCG CGTGGCGGAC
301 GTTTTGTCGG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
351 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GGCGCGTGT GCCGTAAC
401 TCGTAGGCAG GCTTTTGGAC GGACAGGTAG TGCAATACTT CGGGTGGGAT
451 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCAGCA
501 TCGTGTGTTG CGCCATGGTG ATGTAGAGGC GTTTGCGGGC GCGGGTGATG
551 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCGCCGC GTTCGGCAAG
601 GCTCATTTTC CTGGGGAAGC GGCCTTCTTC CATGCCGGTG AGGAAGACGG
651 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
701 TTTTCGCCTG CGCCTGCCTG GTTTTCACCG GATTCGAGGG CCGCATTGCT
751 TAGGAAGGCG AGAATGGGGA AGGCGGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

```

m535.pep
1  MPFPVFRPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
51  YISNLHLFQF RKLGVQLFHA LFAEIDGQSG GFAFICGIDN HAGAEFGVAD
101 VLSDETETCVG LGLFVVVDDF IFGCGGLARV AVTVVGRFLD GQVVQYFGWD
151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFFEEAAAFGK
201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
251 XEGENGEGGV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

m535/g535

```

          10      20      30      40      50      59
m535.pep  MPFPVFRPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ
          |||||: || || |||||: || |||||: |||||: |||||: ||||| ||
g535      MPFPVFRQXFAXSLRFFAVGRILESDISNSGSETINASNVFVGYEYPACISNLHRFQ
          10      20      30      40      50      60

          60      70      80      90      100     110     119
m535.pep  FRKLGVLQFHALFAEIDGQSGGFVFCGIDNHAGAEFGVADVLSDETETCVGLGLFVVDD
          |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
g535      FRKLGIOFFHALFAEVDGQSGGFVFCGIDNHAGAEFGVTDVLSDAEACVGLRLFEVIDD
          70      80      90      100     110     120

```

807

	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGR <del>L</del> FDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFA						
	:      :   :       :						
g535	FVPLYGGLARVAVAVEGGFFD <del>G</del> QVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
m535.pep	180	190	200	210	220	230	239
	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGH <del>E</del> LDGLFACAC						
	:      : :      :      :      :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGV <del>E</del> FQAFGGVDGHQLDGGFFACPC						
	190	200	210	220	230	240	
m535.pep	240	250	260				
	LVFTGFEGGIAXEGENGE <del>G</del> GVV						
	:    :      :    :						
g535	LVFAGFEGGVAQEGEDGEGGIV						
	250	260					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1547>:

```
a535.seq (partial)
1   TTCAGACGGC CTTTTCGCTT GTCCTTGCTA CAGTTTTTTG CCATAGGTCG
51  GATTCTCGAA TCCGACATTT CCAACAGCGG TTTTTCGGAA ACGATAGACG
101 CGTCAAATAT TTTTTCGGTA TACGAGTATC CAGCTTCATT TTCAAATTTA
151 CATCGCTTCC AATTTCGCAA ACTTGGTGTC CAACTGCTTC ACGCCTGTTT
201 TGCCGAAATT GATGTCAGT CGGGCGGATT CGCCTTTATC TGCGGCATCG
251 ATAATCACGC CGGTGCCGAA TTTGGCGTGG CGGACGTTTT GTCCGATACG
301 GAAACCTGCG TAGGTTTGGG GCTGTTTGTA GTCGTCGATG ATTTTGTCTT
351 TGGGCGCGCG GGTTTGGCGC GTGTGCCAT AGCGCTCGTA GCGCGGCTTT
401 TTGACGGACA GGTAGTGCAA TACTTCGGGC GGGATTTCTT CGACGAAGCG
451 GGAGACGATG CCGAATTGGG TTTTGCCTGT CAGATGCGT TGTTGCGCCA
501 TGGTGATGTA GAGCGGTTTG CGGGCGCGGG TGTATGGCGAC GTATACACAG
551 CGGCGTTCTT TTTCCGAGGC CGCGCGTTCC GCAAGGCTCA TTTCGCTGGG
601 GAAGCGGCCT TCTTCCATGC CGGTGAGGAA TACGGCGTTA AATTCCAAGC
651 CTTTGGCGCG GTCCACGGAT ATGAGTTGTA CGGCTTTTTC GCCCGGCCT
701 CTTTGGTTTT GTCCGAGATC GAGAGCAGCA TTGCTTAGGA AAGCGAGGAT
751 GGGGAAGGCG GGGTCGTCTG A
```

This corresponds to the amino acid sequence <SEQ ID 1548; ORF 535.a>:

a535.pep (partial)

1	FRRPFALSL	OFFAIGRILE	SDISNSGFSE	TIDASNIFVG	YEYPACISNL
51	HRFQFKRLGV	QLFHALFAEI	DGQSGGFAFI	CGIDNHAGAE	YFGRADVLSDT
101	ETCVGLGLFV	VVDDFVFGRG	GLARVAIAV	GGFFDGGVQV	YGVDFDFDEA
151	GDDAEIGLSV	QHALLRHGDV	EAFAGAGDGD	VHQAAFFFEA	AAFGKAHFAG
201	EAAFFHAGEE	YGVKQFAFGG	VHGHELYGFF	ARACLVFAGF	ESSIA*ESED
251	EGGGVV*				

**m535/a535** 88.7% identity in 256 aa overlap

```

      10      20      30      40      50      60
m535.pep  MPFPVFRRFALSLLTFFAVSQILVSDISNSGVSETIDASNVFVGVEYPTYISNLHLFQF
          |||:|||:|:|||:|||:|||:|||:|||:|||:|||
a535      FRRPFALSLQFFAIGRILESDISNSGFSETIDASNIFVGVEYPACISNLHRFQF
          10      20      30      40      50

      70      80      90      100     110     120
m535.pep  RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEEFGVADVLSDTETCVGLGLFVVVDDF
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a535      RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEEFGVADVLSDTETCVGLGLFVVVDDF
          60      70      80      90      100     110

      130     140     150     160     170     180
m535.pep  IFGCGGLARVAVTVVGR LFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG
          :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a535      VFGRGGLARVAIAVVGFFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG
          120     130     140     150     160     170

```

```

              190      200      210      220      230      240
m535.pep    AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACACL
              |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a535         AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKFQAFGGVHGHELYGFFARACL
              180      190      200      210      220      230

              250      260
m535.pep    VFTGFEGGIXEGENGEGGVVX
              ||:|||:|||:|||:|||:|||
a535         VFAGFESSIAXESEDGEGGVVX
              240      250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

g537.seq

```
1 atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
51 tttctacatt acccaaaacc aatccctgcc cgcgggcgaa cttgtctatc
101 cgtccgcacc gcaaatcagg gacggcgcgcg atgcgctgca ctacctcaac
151 cgcattcgca cacaaatcgg tttagcgcg cttggcacag cgccggtttt
201 ggaaaaattcc gccgcgacgc agccacgcta tctcacgctc aatcccgaa
251 acggacacgg cgaacaccat cccgacaatc cgcactacac cgcacaaaag
301 ctgaccgaac gcacacgcct tgcggggtat ctctacaacg gcgtgcatga
351 aaacatcagc acggaagagg aagccgccga atcgtcgcac agcgacatcc
401 gcacgcagca acgcgaagtg gacgctttga tgagcgcaat ctaccaccgc
451 ctttcgctgc ttgaccgcca tccagcagaa cgaggtcggt catttgttgc
501 cgaaaacggc aaaaccgtcc tctgtattca tcagggcaac ggcagcttgc
551 agcgcgcctg tgcaaaagga agcgggcagc cggaagcagg acggaatat
601 taccgtaacg cttgccacaa cgggtgcggcc gtttatgctg acgaagccat
651 gccgctaacg gaattgcttt ataccgccta tccggttggc ggcgcgcgcg
701 tgccttattt ttacgggaa cgtccgcgac cgtgcgga atatgaatc
751 acaggcaatc ctgccagcat tgatttttcc gaggcgcgag gcaaaattgc
801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgccccgtca
851 ggggttttaac cgcgcggcaac gacctaacg gcaggctgac cgcgcaccaa
901 ttcgcccatt tcccgtcca acctttggaa tacggcacgc tttatacggc
951 ggtatttcgac ttgtctcgca acggacggca cgcgcaggcg aaatggcagt
1001 ttgaaccg aaaccgcgt tacccttatt ttgaggtaaa cggcggcgag
1051 acacttgccg ttagaaaagg cgaaaaatat ttcatccact ggcgcggcag
1101 ctgggtgtctg gaagcgtgta cccgttatac ctaccggcgg cagttcggca
1151 acagcgtgtc catactccgg cacgaagcgg gccgcattgt cttcagcgtc
1201 agcggaatgt cgggaagccg catcaggctt actccgaag acagcccgga
1251 acgcggtgta accctttatt tgcaggattg a
```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

g537.pep

1	<u>MKSLFIWLLL</u>	<u>LGSAAGVFYH</u>	TQNQSLPAGE	LVYPSAPQIR	DGGDALHYLN
51	RIRTQIGLHA	LAHAVPLENS	ARRHARYLTL	NPEDGHGHEH	PDNPHYTAQK
101	LTERTRLAGY	LYNGVHENIS	TEEEAAESND	SDIRTQQRQV	DALMSAIYHR
151	LSLLDRHTDE	AGAAFVRENG	KTVLVFNQGN	GSFERACAKG	RQPEAGRKYR
201	YRNACHNGAA	VYADEAMPVT	ELLYTAYPGV	GGALPYFYGE	RDPVPPEYEI
251	TGNPASIDFS	EAAGKIAMKS	FKLYQGKNEI	RPVRVLTAGN	DPNGRLTAHQ
301	FALFPLKPLE	YGTLYTAVFD	YVRNGRHAQA	KWQFRTRKPD	YPYFENVNGE
351	TLAVRKGEKY	FIHWRGRWCL	EACTRYTYRR	QFGNSLSILR	HEAGGIVFSV
401	SMAGSRIPL	TRPDSPERGV	TLYLQD *		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

showing partial DNA sequence was identified in *N. meningitidis* (SEQ ID m537.seq (partial))

```
1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCCG CGGCAGGCGT
51 TTTCTACCAT ACCCAAAmCC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAAAATCAGG GACGGCGGGC ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTGCAACAAG CTGGCACACG CGCCGGTTTT
201 GGAAAACTCC CGCCGCAgCG ACGCAAGCTA CCTCAGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAGAAG
```



301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA  
 351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC  
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC  
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)  
 1 MKSLFIRLLL LGSAAGVFYH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN  
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDPNPHYTAQK  
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR  
 151 LSLDRHTDE SGAA...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

m537/g537

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
g537	MKSLFIWLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRITQIGLHA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHH PDPNPHYTAQKLTERTRLAGYLYNGVHENIS					
g537	LAHAPVLENSARRHARYLTLNPEDGHGEHH PDPNPHYTAQKLTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
g537	TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAVRENGKTVLVFNQGN					
	130	140	150	160	170	180
	190	200	210	220	230	240
g537	GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq  
 1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCCG CGGCCGGCGT  
 51 TTTCTATCAT ACCCAAACC AATCCCTGCC CGCGGGCGAA CTGTCTATC  
 101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC  
 151 CGCATCCGCG CCCAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTTT  
 201 GGAAAATTCG GCCCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG  
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG  
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA  
 351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC  
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC  
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGCG  
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG  
 551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT  
 601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT  
 651 GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC  
 701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC  
 751 ACGGGCAATC CTGCCAGCAT TGATTTTTCG GAGGCGGCAG GCAAAATTAC  
 801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCCGTCA  
 851 GGGTTTAAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA  
 901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC  
 951 GGTATTGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT  
 1001 TTAGAACCCG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGGCGAG  
 1051 ACACTTGCGG TTAGAAAAGG CGAAAATAT TTCATCCACT GGCGCGGACG  
 1101 CTGGTGTGTTG GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

810

1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTACAGCGTT  
 1201 GACGGAATGG CGGGCAGCCG CATCACGCTT GCACCGGAAG GAGAAACGGA  
 1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

a537.pep  
 1 MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN  
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK  
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR  
 151 LSLDRHTDE AGAAFVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY  
 201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPPEYEI  
 251 TGNPASIDFS EAAGKITMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAYQ  
 301 FALFPLKPLE YGTLTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE  
 351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPGSRLSIGR HKAGGIVFVS  
 401 DGMAGSRITL APEGETERGV TLYLQD\*

m537/a537 98.2% identity in 164 aa overlap

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
a537	MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQK LTERTRLAGYLYNGVHENIS					
a537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQK LTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
a537	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDEAGAAFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
a537	GRFERHCAQGRNQPEAGRKYRYRNACHNGAVVYTDEAMPAQELLYTAYPVGNGALPYFHGE					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

g538.seq  
 1 atgtcaggtga gaacaggacg gaacagtgcc actcaggcgc aaccggaacg  
 51 cgtcatgctg gtggcgctaa tgttgataa agatgatac ggcagcaatg  
 101 ccgcccgtct gaacggtttt cagacggcat tggcggaagc cgtcgagctg  
 151 gtcaaagcgg cggcgggcga ttccgtacgc gtggagactg ccaaaccgca  
 201 ccgcccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt  
 251 cggaaagcag tgcgcagac ggcattgatt tggctgatt caaccacgaa  
 301 cttactccca cgcaggaacg caatttgaa aaaatcctcc aatgccgcgt  
 351 attggacaga gtggggctga ttctggcgat tttcgccgc cgcgccgca  
 401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttgcg  
 451 ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggtat  
 501 cggcatgaaa gggccgggcg aaaccaaact ggaaccgac cgccgattaa  
 551 ccgcccacg gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa  
 601 cagcgcgccc tgcgcgcgaa gtcccgcgag tggggcagaa tcaaaacgtt  
 651 tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc  
 701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac  
 751 acgacggcgc ggcggctgta catcagtcgc gcacaaactg atttccgcct  
 801 cgataccgct ggattcgtca gcgatctgcc gcacaaactg atttccgcct  
 851 tttccgcac cttggaagaa accgtgcaag ccgatgtgct gctgcacgtc  
 901 gtcgatgctg ccgcccggaa cagcgggag cagattgaag acgtggaaaa  
 951 cgtactgcaa gaaatccatg cccacgatat tccgtgcac aaggtgtaca  
 1001 acaaaaccga cctgctgccg tctgaagaac aaaacacggg catatggcgc  
 1051 gacgctgcgg gaaaaattgc gcgcgtccgc atttccgttg ctgaaaaaac

This corresponds to the amino acid sequence <SEQ ID 1556; ORF 538.ng>:

g538.pep

```

1  MSGRTGRNSA TQAQPERVML VGVMLDKDDT GSNAARLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLTVFNHE
101 LTPPTQERNLE KILQCRVLDL VGLILAIFAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLTAHRINA LKKQLANLKK
201 QRALRRKSRE SGRIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
251 TTARLYISP ACSIILTDTV GFVSDLPKHL ISAFSATLEE TVQADVLLHV
301 VDAAARNSGO QIEDVENVLQ EIIAHDIPII KVINKTDLIP SEEQNTGIWR
351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

m538.seq

```

1  ATGACAGGCA GAACAGGCGG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTTGGACAA AGATGGTACG GGCAGTAGTG
101 CCGCCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCTGAGCTG
151 GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTGCGCAC GGGCAAGGCG GCGGAGCTGT
251 CAGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTCACGCCCA CGCAGGAACG CAACCTTGAA AAAGAACTsA AATGCCGCGT
351 ATTGGACAGG GTAGGGCTGA TTCTGGCGAT TTTCGCTCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CGCAATTGAG CCATTGGCGG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAACT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGATAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TCGCGCGCAA GTCnCGCGAA TCGGGCACA TCAAAACGTT
651 TGCGCTGGTC GGCTATACAA ATGTCGGAAA ATCCAGCCTG TTCAACCGGC
701 TGACAAAGTC GGGCATATAT GCAAAGGACA AGCTTAGTCC CGAATGCAGC
751 ATTATCCTGA CCGATACCGT CGGATTCTGn AGCGATCTGC CGCacAACT
801 GATTTCGCC TTTTCgCC.A CGCTGGAAGA AACCGCGCAA GCCGATGTGC
851 TGCTGCACGT CGTCGATGCC GCCGCTCCGA ACAGCGGACA GCAGATTGAA
901 GACGTGGAAC ACGTACTGCA AGAAATCCAT GCCGGCGATA TTCCGTGCAT
951 cAAGGTGTAC AACAAAACCG ACCTGCTGCC GTCTGAAGAA CAAAACACGG
1001 GCATATGGCG CGACGCTGCG GGAAAAATTG CCGCCGTCCG CATTTCCGTT
1051 GCTGAAAATA CCGGTATAGA CGCACTGCGC GAAGCcATTG CCGAGTCTTG
1101 TGCCCGCCGA CCAACACAG ACGAAACCGA AATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

m538.pep

```

1  MTGRTGGNGS TQAQPERVML VGVMLDKDGT GSSAARLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLTVFNHE
101 LTPPTQERNLE KELKCRVLDL VGLILAIFAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LIKQLANLKK
201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDKLSPECS
251 IILTDTVGFV SLDLPHKLISA FSXTLEETAQ ADVLLHVDA AAPNSGQQIE
301 DVENVLQEIH AGDIPCIKVY NKTDLLPSEE QNTGIWRDAA GKIAAVRISV
351 AENTGIDALR EAIAESCAAA PNTDETEMP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

m538/g538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
	:       :					
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAELSEAVAADGIDLTVFNHELTPTQERNLEKELKCRVLDL					
g538	VETAKRDRPHTALFVGTGKAELSEAVAADGIDLTVFNHELTPTQERNLEKILQCRVLDL					

812

	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSORGGIGMKGPGETKLETD					
g538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSORGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
g538	RRLTAHRINALKKQLANLKKQALRRKSRESGRIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDTVGFVSDLP HKLISAFSXTLEETAQADVLLHV					
g538	AKDQLFATLDTTARRLYISPACSIILTDTVGFVSDLP HKLISAFSATLEETVQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
g538	VDAAARNSGQQIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
g538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1  ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGTCT GAACGGTTT CAGACGGCAT TGGCGGAAGC TGTGAGCTG
151 GTCAAAGCGG CGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTGCGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTCGCCCCG CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGCGG AAACCAAACT GGAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TGCGCCGCAA GTCCCGCGAA TCGGGCACAA TCAAAACGTT
651 TGCCTGGTGC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC GGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCGTCA GCGATCTGCC GCACAACTG ATTTCCGCCT
851 TTTCGCGCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAATA
951 CGTACTGCAA GAAATCCATG CCGCGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGA CTGCTGCCG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCGTCCGC ATTTCCGTTG CTGAAAATAC
1101 CGGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1  MTGRTGRNGS TQAPPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLVVFNHE
101 LTPTQERNLE KILQCRVLDL VGLILAI FAR RTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKQLANLKK

```

813

201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD  
 251 TTARRLYISP ECSIILTDV GFVSDLPKLI ISAFSATLEE TAQADVLLHV  
 301 VDAAAPNSGQ QIEDVENVLQ EIHADIPCI KVYNKTDLLP SEEQNTGIWR  
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP\*

m538/a538 94.6% identity in 392 aa overlap

m538.pep	10	20	30	40	50	60
	MTGRTGGNGSTQAQPERVMLVGVMLEKDKGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
a538	MTGRTGRNGSTQAQPERVMLVGVMLEKDKGTGSSATRLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
m538.pep	70	80	90	100	110	120
	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLNVFNHELTPTQERNLEKELKCRVLDR					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLNVFNHELTPTQERNLEKILQCRVLDR					
	70	80	90	100	110	120
m538.pep	130	140	150	160	170	180
	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLSQRGGIGMKGPGETKLETD					
a538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
m538.pep	190	200	210	220	230	240
	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
a538	RRLIAHRINALKKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
m538.pep	250	260	270	280		
	AKDKL-----SPECSIILTDVGFVSDLPKLI SAFSXTLEETAQADVLLHV					
a538	AKDQLFATLDTTARRLYISPECSIILTDVGFVSDLPKLI SAFSATLEETAQADVLLHV					
	250	260	270	280	290	300
m538.pep	290	300	310	320	330	340
	VDAAAPNSGQ QIEDVENVLQEIHADIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
a538	VDAAAPNSGQ QIEDVENVLQEIHADIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
m538.pep	350	360	370	380		
	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
a538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

1	atggaggatc	tgcaggaaat	cgggttcgat	gtcgccgccg	taaaggtagg
51	tcggcagcgc	gaacatcatc	gtctgcatca	taccagatcc	ggcaacggca
101	aggcggacga	tgtattgttt	gcgttctttt	tggttgccgg	cttcgatttt
151	tgcgcgtca	taggtgccc	cgggtgtagc	tgtctgccgg	atttcaaca
201	gaatgtcggg	gaggcggatt	ttgccgtcgt	cccagacgac	gcggcagcgg
251	tgcgtgctgt	aattgaggtc	gatgcggacg	atgccgtctg	tgcgcaaaag
301	ctgctgttcg	atcagccaga	cgcaggcggc	gcaggtaatg	ccgctgagca
351	tcagcactgc	ttcgtgcgtg	ccattatggg	tttccacaaa	gtcggatttg
401	acttcgggca	ggtcgtagag	gcggatttgg	tcgaggattt	cttggggcgg
451	cagttcgggt	tttttcgcgt	cggcgggtgc	tcgtttgtaa	taactgccca
501	agccggaatc	gatgatgctt	tgtgcgactg	cctgacagcc	gacgcagcag
551	gtttcgcggg	cttcgccttc	gtacgcggac	gtcagatgca	ggttttcggg
601	aacgtccagc	ccgcagtggg	aacagggttt	tttcatggca	tttcggtttc

```

651 gtctgtgttt ggtgcgccgg cacaatactc ggcaatggct tcgcgcagtg
701 cgtctatacc ggtattttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcccatat gcccgtgttt tgttcttcag acggcagcag
801 gtcggttttg ttgtacacct tgatgcacgg aatatcgtgg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgct gttccggcg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgcacgg tttcttccaa
951 ggtgcgcgaa aaggcggaat tcagtttgtg cggcagatcg ctgacgaatc
1001 cgacggatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgcgcgtc tgcgagagt ggcgaaaagc tggcttttcg catatatgcc
1101 cgacttggtc agccggttga acaggctgga ttgcccgaac ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

g539.pep

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQQNVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGPHK VGLDFGQVVQ ADLVEDFLGR
151 QFGFFRVGGA SFVITAQAGI DDALCDCLTA DAAGFAVFAF VADGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHPVVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCPLFRA
301 AASTCSSTS ACTVSSKVAE KAEISLCGRS LTNPVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

m539.seq (partial)

```

1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCTTTT TGGTTGGCGG CTTTCGATTTT
151 TTGCGCGTCA TAGGGTGCAG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCaGCGG
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTG TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAACCACGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCTGACAG GCGGATTTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTTGCCTGT CGGCGGTGCG TTGTTTGTA TAACTGCCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaAGG
551 GTTTCGCGGT CTTCTGTTTC GTAACGGACA GTCAGGTGGA GGTGTTTCGGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTTCATGGA TTTTCGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTTT
751 CCCGCAGCGT CGCGCCATAT GCCCGTGTGT TGTTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGAGCGG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCAGCG TTTCTCCAG
951 CGTGGcG.AA AAGCGGAAA TCAGTTgTG CGGCAGATCG CTnACGAATC
1001 CGACCGTATC GGTcAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

m539.pep (partial)

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVPHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFRLRVGGA LfVITAQARV NNALCDRLTA GAQGFVAVFV VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHPVVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPLFGA
301 AASTCSSTS ACAVSSSVAX KAEISLCGRS LTNPVSVRI MLHSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

m539/g539

```

          10      20      30      40      50      60
m539.pep  MEDLQEIGFDVAAVKVGRQREHHRLHHPQPGNGEADDVLF AFFLVGGFDFLRVIGCGGVA
          |||||
g539       MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLF AFFLVGGFDFLRVIGCGGVA

```

815

	10	20	30	40	50	60
m539.pep	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	70	80	90	100	110	120
	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
m539.pep	130	140	150	160	170	180
	LARAAVGFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	130	140	150	160	170	180
	FVRAIMGFHKVGLDFGQVVQADLVEDFLGRQFGFFRVGGASFVITAQAGIDDALCDCLTA					
m539.pep	190	200	210	220	230	240
	GAQGFVAFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
g539	190	200	210	220	230	240
	DAAGFAVFAFVADGQMVFQVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
m539.pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSTFSTSSICCPLEFA					
g539	250	260	270	280	290	300
	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISWAWISCSTFSTSSICCPLEFA					
m539.pep	310	320	330	340		
	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	310	320	330	340	350	360
	AASTTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRRAVVSRAKS					
g539						
	WSFAYMPDLVSRLNRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTTCGATTTT
151 TTGCGCGTCA TAGGGTGCGG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTG TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAACACGCG CTCGCGCGTG CCGCGGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCGTACAG GCGGATTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTTGC GCGCGGTGCG TTGTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GGCGCAGCAG
551 GTTTCGCGGT CTTCTGTTTC GTAACGGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTTT TTTTCATGGCA TTTTCGGTTT
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAT TGCGGACGGC GGCAATTTTT
751 CCCGCAGCGT CGCGCCATAT GCCCGTGTTC TGTTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGC GCGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CGGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTGAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GGCAGAAAGC TGGTCTTTCG CATATATGCC
1101 CGACTTGGTC AGCCGTTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF

```

816

```

51  LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFRLVGGG LRVITAQARV NNALCDCLTT GAAGFAVVFV VTDGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHPVFV CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTTCSSTS ACAVSSSSVAE KAEISLCGRS LTNPTVSVRI MLHSGMLYSR
351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

m539/a539 97.1% identity in 345 aa overlap

```

          10      20      30      40      50      60
m539.pep  MEDLQEIGFDVAAVKVGQRQREHRLHHPQPGNGEADDVLFAFFLVGGFDFLRVIGCGGVA
          |||||
a539      MEDLQEIGFDVAAVKVGQRQREHRLHHPQPGNGEADDVLFAFFLVGGFDFLRVIGCGGVA
          10      20      30      40      50      60

          70      80      90     100     110     120
m539.pep  YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR
          |||||
a539      YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR
          70      80      90     100     110     120

          130     140     150     160     170     180
m539.pep  LARAAGVFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA
          |||||
a539      LARAAGVFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDCLTT
          130     140     150     160     170     180

          190     200     210     220     230     240
m539.pep  GAQGFVAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS
          |||||
a539      GAAGFAVVFVFTDGQMVFVFNQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS
          190     200     210     220     230     240

          250     260     270     280     290     300
m539.pep  ATEMRTAAIFPAASRHPVFVFCSSDGSRSVLLYTLMHGISPAPWISCSTFSTSSICCPFLGA
          |||||
a539      ATEMRTAAIFPAASRHPVFVFCSSDGSRSVLLYTLMHGISPAPWISCSTFSTSSICCPFLGA
          250     260     270     280     290     300

          310     320     330     340
m539.pep  AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG
          |||||
a539      AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSGMLYSRRAVVSSVAKS
          310     320     330     340     350     360

a539      WSFAYMPDLVSRLNRLDLPTLVX
          370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

```

g540.seq
1  atgccgccct ccgacgcgg caacgggggtg ttttatcaaa acggcaaaact
51  tgccaatgcg gtttcgcgtt gccgattgcc aaaccggcaa acctttcccg
101  tgccggtgcc gaaccgatg ccgtctgaac cttcagacgg catcggtgtg
151  ttatttgtcc actcggacgg gtgcaggttc gtattgtgtc gattcgtcgc
201  cgtaatacag cacgccgagt ttgacgggga tgcgtccctg cgatttgagg
251  tgggcgttgg aatcgcgcaa ggaatacggc cagccgcagt attcctgctg
301  gtagaagttt tcgcgtttgc tgatttcaat catacgcgcg ccgccgccgc
351  ctttgcgcca gttgaagtc caataggcca catcatcgt aggcgcggcg
401  gcacggtgtc cgcagtcgtt gatttgcgcc atattttcc agcgtga

```

This corresponds to the amino acid sequence &lt;SEQ ID 1568; ORF 540.ng&gt;:

```

g540.pep
1  MPPSRRGNGV FYQNGKLANA VSACRLPNRQ TFPVPVNPMP PSEPSDGIGC

```



51 LFVHSDGCRF VLRCRFVAVIQ HAEFDGDASL RFAVGVGIAQ GIRAAAVFLL  
 101 VEVFADFND HTRAAAFAP VEVPIGHIIIV RRGTVSAVV DLRHIFPA \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1569>:

m540.seq (partial)  
 1 ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTGT  
 51 CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTCTGC GCCGTAATAC  
 101 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTCG GGTGGGCATT  
 151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCCTGC TGGTAGAAGT  
 201 TTTCACGTTT GCTGATTTC AATCATGCGC CGCTGCCGCC GCCTTTGCGC  
 251 CAGTTGAAAT CCAATACAC CACATCATC TAAGCGCGG CGGCGCGGTG  
 301 TCCGAGTCG TTGATTTCG CCATATTTT CCAGCGTGA

This corresponds to the amino acid sequence <SEQ ID 1570; ORF 540>:

m540.pep (partial)  
 1 ..PNMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL\*FAVGI  
 51 GIPQGIGTTA IFLLVEVFTF ADFNHARAAA AFAPVEIPIH HIIVRRGGAV  
 101 SAVVDLRHIF PA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 540 shows 85.7% identity over a 112 aa overlap with a predicted ORF (ORF 540.ng) from *N. gonorrhoeae*:

m540/g540

m540.pep				10	20	30
				PNMPSEPSD	GIGCLFVHPD	GGRFVLCRFV
g540	GNGV	FYQNGKLANAVS	ACRLPNRQTF	VPVNPMPSEPSD	GIGCLFVHSDG	CRFVLCRFV
	10	20	30	40	50	60

  

m540.pep		40	50	60	70	80	90
		AVIQHAEFDG	DSALXFAVG	GIGIPQGI	GTTAIFLL	VEVFTFADF	NHARAAAFA
g540		AVIQHAEFDG	DASLRFVAV	GVGIAQGI	RAAVFLL	VEVFADFND	HTRAAAFAP
	70	80	90	100	110	120	

  

m540.pep		100	110
		HIIVRRGGAV	SAVVDLRHIFPAX
g540		HIIVRRGGTV	SAVVDLRHIFPAX
	130	140	

L' estremita' N-terminale di meningococco e' assente perche' interviene la fine del contig

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1571>:

a540.seq  
 1 ATGCCGTCCT CCCGACGCGG CAACGGGGTG TTTTATCAAA ACGGCAAAC  
 51 TGCCAATGCG GTTTCGATT GCAGATTGCC AAACCGGCAA ACCTTCCCG  
 101 TGCCGATGCC GAACCGATG CCGTCTGAAC CTTAGACGCG CATCGGGTGT  
 151 TTATTGTGCC ACCCGGATGG GTGCAGGTTT GTATTGTGTC GATTCTGCG  
 201 CGTAATACAG CACGCGGAGT TTGATGGGGA TTCTGCCCTG TGATTGCGG  
 251 TGGGCGTTGG AATCCCTCAG GGAATAGGCA CAACCGCAAT ATTCCTGCTG  
 301 GTAGAAGTTT TCACGTTTGC TGATTTCAT CATACGCGCG CTGCCGCCGC  
 351 CTTGCGGCCA GTTGAAATCC CAATACACCA CATCATCGTA AGGCGCGGCG  
 401 GCGCGGCGGC CGCAGTCGTT AATCTGGTTC ATGTTTTTCC A

This corresponds to the amino acid sequence <SEQ ID 1572; ORF 540.a>:

a540.pep (partial)  
 1 MPSSRRNGV FYQNGKLANA VSDCLPNRQ TFPVMPNPM PSEPSDGIGC  
 51 LFVHPDGCRF VLRCRFVAVIQ HAEFDGDASL \*FAVGVGIPQ GIGTTAIFLL  
 101 VFTFADFND HTRAAAFAP VEIPIHHIIIV RRGAAAAVV NLVHVFP

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m540/a540 92.8% identity in 111 aa overlap

				10	20	30
m540.pep				PNMPSEPSD	GIGCLFVHPD	GGRFVLCRFV
a540	GNGVFYQNG	KLNAVSDCRL	PNRQTFFV	PMNMPSEPSD	GIGCLFVHPD	GCRFVLCRFV
	10	20	30	40	50	60
		40	50	60	70	80
m540.pep	AVIQHAEFDG	SALXFAVGIGI	PQGIGTTAIF	LLVEVFTFAD	FNHARAAAAF	APVEIPIH
a540	AVIQHAEFDG	SALXFAVGIGI	PQGIGTTAIF	LLVEVFTFAD	FNHTRAAAAF	APVEIPIH
	70	80	90	100	110	120
		100	110			
m540.pep	HIIVRRGGAV	SAVVDLRHIF	PAX			
a540	HIIVRRGGAAA	AVNVLHVHVF	P			
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

g542.seq  
 1 atgccgaaat ggtcgcgcac acggcggtgc agcgctcctt cgctgatgtt  
 51 cagcgccggt gtcagccggt tgacttggtg tgcgccgcgc tcgaacgcgc  
 101 cattcaggtt gcggctgaag tcttcagacg gcatagcgtc tgcttccgcc  
 151 gtttgccccc ccgcccggct gatgccgtct gaaaccgtgt cccacaaatc  
 201 cgacagcagc cgcaacacgt ccgcctcgcg gcgcaatgtt tcgcccacaa  
 251 gcccttttgg gacggtttgc aggcaggatg ccgccaagcc gcgcaggttt  
 301 gggggcaaat cccatatact gaccggttcg cggttaa

This corresponds to the amino acid sequence &lt;SEQ ID 1574; ORF 542.ng&gt;:

g542.pep  
 1 MPKWSRIRRC SVLSLMFSAA VSRLTWCAPP SNAAFVRVLK SSDGIASASA  
 51 VCPAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF  
 101 GKGSHILTGS R\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

m542.seq  
 1 ATGCCGAAAT GGTGCGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT  
 51 CAGCGCGTCT GTCAGCCGGT TGAATTGGTG TGCGCCGTCG GCAAACGCGG  
 101 CATTTAGGGT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC  
 151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC  
 201 CGACAGCAGC CGCAACACGT CCGCCTCGCG .CGCAATGTT TCGCCCAAAT  
 251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC  
 301 GGGGGCAAAAT CCCATATCCT GACCGGTTTC CGGTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1576; ORF 542&gt;:

m542.pep  
 1 MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFVRVLK SSDGIASASA  
 51 VCPAAGSMPS ETVSHKSDSS RNTSASRAMF RPNAPLGRNV SPKCPFGTAF  
 101 RQDAAKPRRF GKGSHILTGS R\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

m542/g542

		10	20	30	40	50	60
m542.pep		MPKWSRIRRC	SVLSLMFSAS	VSRLTWCAPS	ANAAFVRVLK	SSDGIASAS	AVCPAAGPMPS
g542		MPKWSRIRRC	SVLSLMFSA	VSRLTWCAPP	SNAAFVRVLK	SSDGIASAS	AVCPAAGSMPS
		10	20	30	40	50	60
		70	80	90	100	110	
m542.pep		ETVSHKSDSS	RNTSASXRN	VSPKCPFGT	AFRQDAAKP	RRFEGKGSH	ILTGSRX

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```

|||||
g542  ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```

a542.seq
1  ATGCCGAAAT  GGTCGCGCAT  ACGGCGTTGC  AGCGTCCTTT  CGCTGATGTT
51  CAGCGTGTCT  GCCAGCCGGT  TGAATTGATG  TGCGCCGCCG  GCAAACGCGG
101 CATTCAGGAT  GCGGCTGAAG  TCTTCAGACG  GCATAGCGTC  TGCTTCGGCC
151 GTTTGCCCGC  CCGCCGGCCC  GATGCCGTCT  GAAACCGTGT  CCCACAAGTC
201 CGACAGCAGC  CGCAACACGT  CCGCCTCGCG  GCGCAATGTT  TCGCCCAAAT
251 GCCCCTTTGG  GACGGCTTTC  AGGCAGGATG  CCGCCAAGCC  GCGCAGGTTG
301 GGGGGCAAAT  CCCATATCCT  GACCGGTTTC  CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

```

a542.pep
1  MPKWSRIRRC  SVLSLMFSVS  ASRLT*CAPP  ANAAFRMLK  SSDGIASASA
51  VCPAAGPMPS  ETVSHKSDSS  RNTSASRRNV  SPKCPFGTAF  RQDAAKPRRF
101 GKGSHILTGS  R*

```

m542/a542 94.6% identity in 111 aa overlap

```

              10      20      30      40      50      60
m542.pep  MPKWSRIRRC SVLSLMFSVSASVSRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
|||||
a542      MPKWSRIRRC SVLSLMFSVSASRLTXCAPANAAFRMLKSSDGIASASAVCPAAGPMPS
              10      20      30      40      50      60

              70      80      90      100     110
m542.pep  ETVSHKSDSSRNTSASXRNVS PKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
|||||
a542      ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

g543.seq
1  atggtttgtc  ggattattgc  cgccgttttt  ggctttcaac  tcggcaatca
51  gcccgtcgat  gcctttggct  ttgatgattt  cgccgaattg  gttgcggtac
101 acggtaacca  ggctcgtgcc  ttcgatggcg  acgttgtagg  tacggtattt
151 gccgcgctt  tggtaggtgg  taaagtccat  attgacgggc  ttctgaccgg
201 ggatgccgac  ttcggcacgg  acgacgattt  ccttgccgcc  cttattgacg
251 atgggattgt  ctttgacgtt  gacggtcgcg  tttttgaatt  tcagcatcgt
301 gccggaatag  gtgcggatca  gcagggtttg  aaattctttg  gccaacgcct
351 gtttttgcg  gtcggacgcg  gtacgccaag  ggttgccgac  cgccaatgcg
401 gtcatacggt  ggaaatcgaa  atagggaacc  gcataggctt  cggttttgg
451 gcgtgcagaa  gccgcgtcgc  cgcttttgag  gatggtcaaa  acctgtgtgg
501 cgttttggcg  gatttgtccc  actgcgtcgg  ccggggaggc  aaatgccatg
551 ccgatgctca  aaataccgat  gcccaatgcg  ctgatgaagg  aggatttttt
601 cacgatgtct  ttccctgaaa  tggatgtgta  tgttattctt  gcggcttttt
651 ccgcattgcc  gccctcagcg  tttttctcgg  cgaagctggt  catgaattta
701 ccgatcaggt  tttccagaac  cattgcagaa  ctggttacgg  agatggtgtc
751 gccggcagca  aggttttcgg  tatcgccgcc  ctgctgcagc  ccgatgtact
801 gttcgcccaa  aagtcgccaa  gtcaggattt  gcgcggaac  gtcactgctg
851 aactgatact  tgccgtccaa  atcaaggcgc  accctcgctt  gataggattt
901 cgggtcaagc  ccgatagcgc  cgacgcgccc  gaccaatacg  cctgcggatt
951 tgacgggggc  attgaccttc  aaaccgcca  tgtcgccgaa  atcggcataa
1001 acggcgtaag  ttttgtccga  accgcggaac  gccgcgcgc  ccgccacgcg
1051 gaaagcgaga  aaggcaaccg  ccgccgcgcc  gatcaagacg  aacagtccga
1101 cccaaaattc  caatatgttc  tttttcatta  a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

```

g543.pep
1  MVCRLFAAVF  GFQLGNQPV  AFGFDDFAEL  VAVHGNQARA  FDGDVVGTVF

```

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```

51 AAALVGGKVH IDGLLTGDAD FGTDDDFLAA LIDDGIVFDV DGRVFEFQHR
101 AGIGADQQGL KFFGQRLFLR VGRGTPRVAD RQCGHTLEIE IGNRIGFGFW
151 ACRSRVAAFE DGQNLGCVLA DLSHCVGRGG KCHADAQNTD AQCADEGGFF
201 HDVFPENGCV CLFCGFFRIA ALSVFLGEAG HEFTDQVFQN HCRTGYGDGV
251 AGSKVFRIAA LLQPDVLFQA KSRSQDLRGN VTAEILAVQ IKAHPRLIGF
301 RVKPSADAP DQYACGFDGG IDLQTADVAE IGINGVSFVR TAERRAARHA
351 ESEKGNRRRA DQDEQSDPKF QYVLFH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1581>:

m543.seq

```

1 ATGTTTGTG GGTATTGTC CGCCGTTTTT GGCTTCAAC TCGGCAATCA
51 GTCCGTCCAC GCCTTTCGCT TTGATAATT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 GTACGCCGAC TTCGGCGCGG ACGATGATT CTTTGCCCGC TTTATTGACG
251 ATGGGATTGT CTTTGACGTT GACGTTGGCG TTTTAAATT TCAGCATCGT
301 GCCGAATAG GTGCGGATCA GCAGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTGCGC GTCCGACGCG GTGCGCAAAG GGTGCGGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 GCGAGCGGTG TTGGCATCGC CGTTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTTGACG GATTGGCTT ACCGCGTCGG CAGGGCGGCG AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAGG AGGATTTTTT
601 CATGATTAAG TGTCTAGT TGAATATGAT GGCATACGTT TATTGCGCGG
651 CTTTTCCGC ATTGCCGCGC TCGGCATTT TCTCGCAA ACTCGTCATG
701 AATTGCGCA TAAGGTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCG GCAGCAAGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTGCGC GGAAACGTCG
851 CTGCTGAAT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTGCGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCCTG
951 CGGATTTGAC GGGGGCATG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCC CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAG CAACCGCCGC CGCGCAATC AGGACGAACA
1101 GTCCGACCCA AAATTCCAAT ATGTTCTTCT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1582; ORF 543>:

m543.pep

```

1 MVCRLFAAVF GFQLGNQSVH AFRFDNFEL VAVHGNQARA FDGDVVGTVF
51 TAALVGGEVH VDGFLPGYAD FGADDDFFAA FIDDGIVFDV DVGVFQFQHR
101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 ASGVGIAVFX DAQYLSGVLT DLAYRVGRGG KCHADAQNTD AQCADEGGFF
201 HDXVSXFEDY GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRGTGYD
251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQADV AEIGINGVSF VRTAERTAG
351 HAESEKGNRR RANQDEQSDP KFQYVLLH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng) from *N. gonorrhoeae*:

m543/g543

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNFELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
g543	MVCRLFAAVFGFQLGNQPVDAFGFDDFAELVAVHGNQARAFDGDVVGTVFAAALVGGKVH					
	10	20	30	40	50	60
m543.pep	VDGFLPGYADFGADDDFFAAFIIDDGIVFDVDVGVFQFQHRAGIGADQQGLKFFGQRLFLR					
g543	IDGLLTGDADFGTDDDFLAALIDDGIVFDVDGRVFEFQHRAGIGADQQGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

m543.pep  VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       VGRGTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLGVLADLSHCVGRGG
          130      140      150      160      170      180

          190      200      210      220      230      239
m543.pep  KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIA AVGIFLGKTRHEFADKV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       KCHADAQNTDAQCADEGGFFHDV---FPENGCVCLFCGFFRIAALSVFLGEAGHEFTDQV
          190      200      210      220      230

          240      250      260      270      280      290      299
m543.pep  FQNHCRRTGYGDGVAGSKVFRVAALLQPDVLLAQKRSRQDLRGNVAAELILAVQIEAHPRL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       FQNHCRRTGYGDGVAGSKVFRIAALLQPDVLFQKRSRQDLRGNVTAELILAVQIKAHPRRL
          240      250      260      270      280      290

          300      310      320      330      340      350      359
m543.pep  IGFRVKSDSADAPDQYACGFDGGIDLQTDVAEIGINGVSFVRTAERRTAGHAESEKGNR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       IGFRVKPDSADAPDQYACGFDGGIDLQTDVAEIGINGVSFVRTAERRAARHAESEKGNR
          300      310      320      330      340      350

          360      370      379
m543.pep  RRANQDEQSDPKFQYVLLHX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       RRADQDEQSDPKFQYVLFHX
          360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543.seq
1  ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTGGCG TTTTAAATT TCAGCATCGT
301 GCCGAATAG GTGCGGATCA GCAGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTTCGCG GTCGGACGCG GTGCGCCAAG GGTGCGGAC CGCCAATGCG
401 GTCATACGTT GGAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 GCGGGCGGTG TTGGCATCAC CGCTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTTTCGAC GATTGGTTT ACCGCGTCGG CAGGGCGCGG AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCGCG ATTGCCGCGG TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTGCCGA TAAGGTTTTC CAGAACCAT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCGG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTGCGC GGAAACGTCG
851 CTGCTGAAGT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTCGGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCGG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAG CAACCGCCG CGCGCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1  MAYGLLA VX SLQLXNQS VH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDFGLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITAF* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRRTGYGD
251 GVAGSKVFRV AALLQPDVLL AQKRSRQDLR GNVAAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQTDV AEIGINGVSF VRTAERRTAG

```

351 HAESEKGNRR RANQDEQSDP KFQYVLFH\*

m543/a543 96.0% identity in 378 aa overlap

m543.pep	MVCRLFAAVFGFQLGNQSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH
a543	MAYGLLAAVXSLQLXNQSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH
m543.pep	VDGFLPGYADFGADDDFFAAFIIDDGIVFDVDVGVFQHRAGIGADQQGLKFFGQRLFLR
a543	VDGFLPGXADFGADDDFFAAFIIDDXIVFDVDVGVFQHRAGIGADQQGLKFFGQRLFLR
m543.pep	VGRGAPRVADRQCGLTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
a543	VGRGAPRVADRQCGLTLEIEIGNRIGFGFLAGGVGITAFXDAQYLSGVLTDLVYRVGRGG
m543.pep	KCHADAQNTDAQADEGGFFHDXVSXFEYDGIRLFGGFFRIA AVGIFLGKTRHEFADKVF
a543	KCHADAQNTDAQADEGGFFHDXVSXFEYDGIRLFGGFFRIA AVGIFLGKTRHEFADKVF
m543.pep	QNHCRITGYDGVAGSKVFRVAALLQPDVLLAQKSRSDLRGNVAELILAVQIEAHPRLI
a543	QNHCRITGYDGVAGSKVFRVAALLQPDVLLAQKSRSDLRGNVAELILAVQIEAHPRLI
m543.pep	GFRVKSADSADPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERTAGHAESEKGNRR
a543	GFRVKSADSADPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERTAGHAESEKGNRR
m543.pep	RANQDEQSDPKFQYVLLHX
a543	RANQDEQSDPKFQYVLFHX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1585>:

g544.seq

```

1  atgaaaaaaa tactcaccgc cgccgccgctc gcaactgatcg gcatcctcct
51  cgccaccgctc ctcacccccg acagtaaaac cgccgccgcc ttctccctgc
101 ccgacctgca cggaataaac gtttccaacg ccgacctgca aggcaaatg
151 accctgatta atttttggtt tcctcctgtt ccgggttggtg tgagcgaaat
201 gcccaaagtc accaaaacgg caaacgacta caaaaataaa gatttccaag
251 tcctcgccgt tgcccagccc atcgatccga tagaaagcgt ccgccaatac
301 gtcaaagact acggactgcc gtttaccgctc atttatgatg cggacaaagc
351 cgtcggacag gcattcggca cacagggtta tccgacttcc gtccttatcg
401 gcaaaaaagg cgaaatcctc aaaacttatg tcggcgaaac cgatttcggc
451 aaactctacc aagaaatcga taccgcgctg gcgcaatag

```

This corresponds to the amino acid sequence &lt;SEQ ID 1586; ORF 544.ng&gt;:

g544.pep

```

1  MKKILTAAAV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGVK
51  TLINFWFPSC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

```

151 KLYQEIDTAL AQ\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1587>:

m544.seq

1	ATGAwAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCmTCCCCG	ACAGCAA AAC	CGCGCCCGCC	TTCmTGC
101	CCGACCTGCA	CGGAwAAAAAT	GTTTCCAAGC	CCGACCTGCA	AGGCAAAGTA
151	ACCTGATTA	ATTTTTGGTT	TCCCTCTGT	CCGGTTGTG	TGAGCGAwAT
201	GCCCAAAATC	ATTAAACCG	CAAATGACTA	TAAAwCAAA	AACCTCAAG
251	TACTTGCCGT	CGCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	GCGTTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCTTATCG
401	GCAAAATAGG	CGAAATCTTC	AAAACCTACG	TCCGCAACCC	CGATTTCCGC
451	AAACTCTACC	AAGAAATCGA	TACGCGCGTG	GCSCAATAG	

This corresponds to the amino acid sequence <SEQ ID 1588; ORF 544>:

m544 . pep

```

1  MXKILTAAAV ALIGILLAIV LXPDSKTTAPA FSXPDLHGKT VSNADLQGV
51 TLINFWPSPC PGCVSXMPKI IKTANDYKKK NFQVLAVAP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGK*GEIF KTYVGEPDFG
151 KLYQEIDTRV AQ*

```

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 544 shows 90.7% identity over a 162 aa overlap with a predicted ORF (ORF 544.ng) from *N. gonorrhoeae*:

m544/g544

	10	20	30	40	50	60
m544.pep	MXKILTA	AVVALIG	ILLAI	VLXPDS	KTAPAF	SXPDLHG
g544	MKKILTA	AAVALIG	ILLAT	VLIPDS	KTAPAF	SLPDLHG
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVS	XMPKI	I	KTAND	YKKXN	FQVLAV
g544	PGCVS	EMPKV	T	KTAND	YKNKD	FQVLAV
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQ	VYPTS	VLIGK	XGEI	FKTYV	GEPDFG
g544	AFGTQ	VYPTS	VLIGK	XGEI	LKTYV	GEPDFG
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1589>:

a544.seq

1	ATGAAAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCATCCCG	ACAGCAAAAC	CGCGCCCGCT	TTCTCCCTGT
101	CCGANCTGCA	CGGAAAAANC	GTTTNCACG	CCGACCTGCA	AGGCNAAGTT
151	ANCTGTGATTA	ANTTTTGGTT	TCCCTCCTGT	CGGGTTGTG	TGAGCGAAAT
201	GNCCANAATC	ATTAACACGG	CAATGACTA	TAAAAACAAA	AACCTTCAAG
251	TCCTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCTCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCCTG	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	CGGTTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCCTTATCG
401	GCAAAAAGAG	CGAATCTCCT	AAAATTTAT	TCGGCGAAC	CGATTTTCGGC
451	AAACTCTACC	AAGAAATCGA	TACCGCGCTG	GCACAATAG	

This corresponds to the amino acid sequence <SEQ ID 1590; ORF 544.a>:

a544.pcp

1 MKKILTAADV ALIGILLAIV LIPDSKTAPA FLSXLHGKX VXNADLQGXV  
51 XLIXFWFPSC PGCVSEMXXI IKTANDYKKN NFQVLVAQP IDPIESVRQY  
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPEDFG

151 KLYQEIDTAL AQ\*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544.pep	MXKILTAAVVALIGILLAIVLXPDSKTAPAFSXPDLHGKTVSNADLQGKVTLINFWFPSC					
a544	MKKILTAAVVALIGILLAIVLIPDSKTAPAFSLSXLHGKXVXNADLQGXVXLIXFWFPSC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVSXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
a544	PGCVSEMXXIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
a544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547.seq  
 1 atgttcgtag ataacggatt taataaaacg gtagcagatt ttgccccaaat  
 51 cgtcgaaaact ttcgacgtat tcttcttttag gaacgattgc gccttttttta  
 101 cgcagatgaa acagcgggtgc ggttgggtct gctcgttggg atattctcgtt  
 151 gatataattta caagatgcgg cttcgagatt ccgaaccgct cctttaaaga  
 201 gcttgggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg  
 251 ccgaagtcga gatggatgcc cattacttcc ccttactcag aaaatattta  
 301 aaattttataa tgttacatat agttacaaat attagagttt tttgtgtgtg  
 351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgtct ccaaaccgaa  
 401 aaaagcgggt tgttttttgt tggttaa

This corresponds to the amino acid sequence &lt;SEQ ID 1592; ORF 547.ng&gt;:

g547.pep  
 1 MFVDNGFNKT VASFAQIVET FDFVFFRND C AFFTQMKQRC GWVCSLVYLV  
 51 DIFTRCGFEI PNRSFKEGL LIQISLSERF RTNAEVEDMA HYFPLLRKYL  
 101 KFIMLHIVTN IRVFCVCVKE LLTILVKNL PNGKKRFVFC C\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547.seq  
 1 ATGTTTCGTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCAAAT  
 51 CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTSTA  
 101 CGCAGATGAA ACAGCGGTGC GGTGGGTCT GCTCGTTGGT ATATCTCGTT  
 151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCCT CTTTAAAGA  
 201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG  
 251 CCGAAGTCGA GATGGATGCT CATTACTTCC CTTACTCAG AAAATATTTA  
 301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTWTTGTGT  
 351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTG TCTCCAAACG  
 401 GAAAAAAGCG GTTTGTTTTT TGTGTGTTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1594; ORF 547&gt;:

m547.pep  
 1 MFVDNGFNKT VASFAQIVET FDFVFFRND C AFFTQMKQRC GWVCSLVYLV  
 51 DIFPRCGFEI PNRSFKEGL LIQISLSERF RTNAEVEDMA HYFPLLRKYL  
 101 KFIMLHIFTN IKVFXCVCKV ELLTILVKNL SPNGKKRFVF CC\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547



825

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
g547	ELLTILVKNLSPNGKKRFVFCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547.seq
1  ATGTTCTAG  ATAACGGATT  TAATAAACG  GTAGCGAGTT  TTGCCCAAT
51  CGTCGAACT  TTCGACGTAT  TCTTCTTAG  GAACAATTGC  ACCTTTT
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGGT  ATATCTCGT
151 GATATCTTTC  CAAGATGCGG  CTTCGAGATT  CCGAACCGCT  CCTTTAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAAT
251 CCGAAGTCGA  GATAGATGCT  CATTACTTCC  CCTTACTCAG  AAAATATTT
301 AAATTTATAA  TGTTACATAT  ATTTACAAAT  ATTAAAGTTT  TTTT.TGTGT
351 GTGCGTCAAG  GAATTGTTGA  CAATTTAGT  T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547.pep
1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNNC  TFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSFKELGL  LIQISLSERF  RTNAEVEIDA  HYFPLLRLKY
101  KFIMLHIFTN  IKVFXCVCVK  ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548.seq
1  atgttttccg  taccgcgttc  ctttttgccg  ggcgttttcg  tacttgccgc
51  gcttgccgcc  tgcaaacctc  aagacaacag  tgcggcgcaa  gccgtttctt
101 caagtgcac  cgcgccggct  gcggaaaatg  cggcaaagcc  gcaaacgcgc
151 ggtacggata  tgcgtaagga  agacatcggc  ggcgatttca  cactgaccga
201 cggcgaaggc  aagcctttca  gcctgagcga  ttgaaaggc  aaggtcgtga
251 ttctgtcttt  cggctttacg  cactgtcccg  atgtctgcc  gacagggctt
```

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```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggt ttctgcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acgggcgggc aaaacctgcc ggtcatcaag cagcaatacc gcgtggtttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccgggtg gtatcttata gataaaaacg gtgaggttgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1 MFSVPRSFLP GVFLAALAA CKPDNSAAQ AASSASAPA AENAAKPQTR
51 GTDMRKEDIG GDFLTLDGEG KPFSLDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVVV FVSIDPERDT PEIIGKYAQ FNPDFIGLTA
151 TGGQNLPIK QYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTCCG TACCGCGTTC CTTTTGCGG GCGTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCA AnACACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGATTTCa CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTATCAAG CAGCAATACc GCGTGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAATATTTC GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFLP GVFLAALAA CKPDNSAAQ VASSASASA AENAAKQXTR
51 GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVVV FVSIDPERDT PEIIGKYAQ FNPDFIXLTA
151 TGGQNLPIK QYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFLAALAAACKPDNSAAQVASSASASAAENAAKQXTRGTDMRKEDIG					
	:					
g548	MFSVPRSFLPGVFLAALAAACKPDNSAAQAASSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTPELLTYSIDLKQLGGQAKDVVV					
	:					
g548	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTGLLTYSIDLKQLGGQAKDVVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTPFIIGKYAKQFNPDFIXLTATGGQNLPIKQYRVVSAKVNQKDDSENYL					
	:					
g548	FVSIDPERDTPFIIGKYAKQFNPDFIGLTATGGQNLPIKQYRVVSAKINQKDDSENYL					
	130	140	150	160	170	180

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```

                190      200      210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLX
                |||||
g548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLX
                190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTC CG TACCGCGTTC CTTTTTGCCG GCGGTTTTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGCGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CCGCAAAGCC GCAAACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGGATTTC ACGTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTAGCA TCGATCCGGA ACGGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAACATTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSF L PGVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR
51  GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTTEL
101 LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

```

                10      20      30      40      50      60
m548.pep      MFSVPRSF L PGVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR GTDMRKEDIG
                |||||
a548          MFSVPRSF L PGVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR GTDMRKEDIG
                10      20      30      40      50      60

                70      80      90      100     110     120
m548.pep      GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTTEL LTYSDTLKQL GGQAKDVKVV
                |||||
a548          GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTTEL LTYSDTLKQL GGQAKDVKVV
                70      80      90      100     110     120

                130     140     150     160     170     180
m548.pep      FVSIDPERDT PEIIGKYAKQ FNPDFIXLTATGGQNLPIKQQYRVVSAKV NQKDDSENYL
                |||||
a548          FVSIDPERDT PEIIGKYAKQ FNPDFIGLTATGDQNLPIKQQYRVVSAKV NQKDDSENYL
                130     140     150     160     170     180

                190     200     210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLX
                |||||
a548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLX
                190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```

g550.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

m550.seq (partial)

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

m550.pep (partial)

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows \_\_\_\_% identity over a \_\_\_\_ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

m550/g550

```

m550.pep          10          20          30
                   DGIGKHALAVVFNGLVGLVHTVVFVAGLVN
                   |||:| |||||:|:|:| |||||
g550              DGFFVHRVQHFRRQQVCAGEAQEDVFANRIGKYAPAVVFNGLVEFFGFVHAVFVAGLVN
                   190          200          210          220          230          240

                   40          50          60          70          80          90
m550.pep          HAFGVANGHVFAFQAQIQQLXQAGNRGRTCAQTHQSREFFDFTAGKTXGVQYGGGGNDGRA
                   |||||:|:| ||||| ||||| ||||:||||| ||||| ||||| ||||| ||||| |||||
g550              HAFGVANGVYVFTFQAQIQQLVQAGNRGGTCAGAHQSREFFDFTAGITQGVQYGGGGNDGRA
                   250          260          270          280          290          300

                   100
m550.pep          VLVVVEYGDFAAFAX
                   |||::| |||||
g550              VLVIMKYGDFAAFAX

```

310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
  1 CTATATCAAT CTGACAGCAA AATGCCGCCCT GAAAACAGTT CAGACGGCAT
51 TTTAACC CGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCA AAT CTGCAATCGG ACGGTTGCC ACGCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGCGGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTC AAATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCGCA AAGCATACAC
301 GCAGGCGCGT TTCATTCTTT CGTGTATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTTGTCAC TTGGTTCTGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTTCG
451 CAGCGGCGCG AGGATTTCG GATTCCGGTT GGCCATAGCG AACACGATGG
501 GTTTTTCGTT CATGGTGTTC AGTATTTTAC GCGTCAGCAG GTTTCGCGCG
551 GAGAGCGCAA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CACGACCGG
601 CTGGCCGTTG TCTTCAATGG CGTAGAAGTG TTTGGACTCG TCCATACGGT
651 CTTTGCTTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTTCG GTTTC AAGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGCGCGCA CCTGCGCGCG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCCGTAAA AAGCAGGGCG TTCAATACGG CAGCGCGGAT AATGATGGCC
851 GTGCCGTGCT GGTCGTCGTG GAATACGGGG ATTTTGCATA GTTTGCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

a550.pep

1	LYQSDSKMPP	ENSSDGILTA	NGLQLPFAQL	GSVSFQICNR	TGCHAAAFHRK
51	FGGSRSRNAQ	QAGIERSRNQ	VFRAEFKFLT	VSGNHFFGYL	FHRQIRQSIH
101	AGAFHFFVDG	RRADIQRTAE	DEREAQYIVH	LVREVGAGT	DNHVRTGFFR
151	QRRQDGRFVR	GHSEHDGFFV	HGVQYFRRQQ	VRAGEAQEDV	FAFDGIGKAG
201	LAVVFNGVIL	<u>FGLVHTVFVF</u>	AGLVNHAFGV	ANGHVAFQV	YIQQLVQAGN
251	RGRTCAGTHQ	SRFFDFTAGK	TQGVQYGSFG	NDGRAVLVVV	EYGDFAFA*

**m550/a550 97.2% identity in 106 aa overlap**

```

m550.pep          10          20          30
                   DGIGKHALAVVFNGLVGLVHTVVFVAGL
                   |||||
a550               EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGLVGLVHTVVFVAGL
                   170          180          190          200          210          220

                   40          50          60          70          80          90
m550.pep          VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAQTHQSRFFDFTAGKTXGVQYGGGGNDG
                   |||||
a550               VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAQTHQSRFFDFTAGKTQGVQYGSGGNDG
                   230          240          250          260          270          280

                   100
m550.pep          RAVLVVVEYGDFAAFAX
                   |||||
a550               RAVLVVVEYGDFAAFAX
                   290          300

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

g552.seq

1	atgaagctga	aaaccttggt	attgcccttc	gccgcactgg	catttgtgtgc
51	caacgcattt	gccgccccgc	ccggcgacgc	gtcgttgga	cgttggtctg
101	atacgagaa	tttcgaccgg	gatatagaaa	aaaatatgat	tgaaggcttt
151	aatgccggat	ttaaaccgta	tgcggacaaa	gcccttgccg	aaatgccgga
201	agcgaaaaa	gatcaggcgg	cagaagcctt	taatcgttat	cgtgagaatg
251	ttttgaaag	tttgattacg	cccgaaagtga	aacaggctgt	ccgcaatacc
301	tatttgaaga	atgcccgtag	aatatacacg	caagaagaaa	ttgacggcat
351	gattgccttt	tacggttcgc	ctgtcgggtca	gtccgtcggt	gccaaaaaat
401	cgcgcttaat	caagaaatcg	atgagtgaag	tgcgggtatc	ttggactgc

451 ttgtcagggg aaatcgcgcg acatcatctg cccgagttta cggaagagtt  
501 acggcgcatc atctgcggcg gtatagtggg ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep

1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF  
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT  
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA  
151 LSGKIARHHL PEFTEELRRI ICGGIVD\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)

1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC  
51 CAATGCTTTT GCCGCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG  
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT  
151 AATGCCGGAT TTAACCGTA TGCGGACAAA GCCCTTGCCG AAATGCCGGA  
201 AGCGAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG  
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT  
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT  
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC  
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA  
451 TTGTGAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT  
501 GCGGCGCATC ATCTCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAG  
551 CCGGACAGGT TGGGAAAAG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)

1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF  
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT  
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA  
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	:     :     :     :     :     :					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	:     :     :     :     :					
g552	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
	:     :     :     :					
g552	YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIARHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
	190					
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq

1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC  
51 CAATGCTTTT GCCGCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG  
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT  
151 AATGCCGGAT TTAACCGTA TGCGGACAAA GCCCTTGCCG AAATGCCGGA

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```

201 AGCGAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

```

          10      20      30      40      50      60
m552.pep  IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
          |||||||
a552      IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
          10      20      30      40      50      60

          70      80      90     100     110     120
m552.pep  ALAEMPEAKKDQAAEAFNRYRENVLKDITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
          |||||||
a552      ALAEMPEAKKDQAAEAFNRYRENVLKDITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
          70      80      90     100     110     120

          130     140     150     160     170     180
m552.pep  YGSPVGQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
          |||||||
a552      YGSPVGQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
          130     140     150     160     170     180

          190
m552.pep  CKQAGQVGKRHQKX
          |||||||
a552      CKQAGQVGKRHQKX
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
 51 GTGCACCAAT GCTTTTGCCG CCCCGCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAA CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 LNIKLTLLL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
 51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKD LITPEVKQAVR
101 NTLKNAREI YTQEEIDGMI AFYGVSPVQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

832

```

1  TTGAATATTA AACTGAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCCGCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGCGGCCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEFN RYRENVKDL ITPEVKQAVR
101 NTLKLNAREI YTQEEIDGMI AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
m552-1	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a552-1.pep	DKALAEMPEAKKDQAAEFN RYRENVKDL ITPEVKQAVR NTLKLNAREI YTQEEIDGMI					
m552-1	DKALAEMPEAKKDQAAEFN RYRENVKDL ITPEVKQAVR NTLKLNAREI YTQEEIDGMI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a552-1.pep	AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPFTEELR RIICGGKNPD					
m552-1	AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPFTEELR RIICGGKNPD					
	130	140	150	160	170	180
	190					
a552-1.pep	AGCKQAGQVG KRHQKX					
m552-1	AGCKQAGQVG KRHQKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaacct gtctttgggc ttgacaaaaa agctgcccg
51  tatactgcaa acagaagtag cggagtgtgg cttggcatgt ctacggcgtg
101 tggccggatt ttatggtttc tatacggatt tgcgcgact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatg gggctgacgg gacgggctgt gaggtggat ttagacgaat
251 tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgctgg aatcggtatc ttcggacggg gctgccgtca tggatccggc
351 ttcgggacga cgcaaagtca agacggagga aatatcgcgc aagtttacgg
401 gaattgcttt ggaactgtgg ccaaacacgc gtttcgagga aggggaagaa
451 aagcaggaata tccgcatcct acccatgttg cgcgggattt ctgggctggg
501 gcggacattg tttcagcttt tggctttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgcttgcg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctcccgaat caggcaaaagt catgataaat gggcacgaca
701 tttacagctt accgccacct tttattccgc aatttgagtg cgatgggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccggt ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep



833

```

1 MDYLQNLISLG LTKKLPVILQ TEVAECGLAC LAAVAGFYGF YTDLRALRSK
51 YCLSLKGENL ADIVRFADDM GLTGRALRLD LDELGSLRLP CILHWDNLNH
101 VVLESVSSDG AAVMDPASGR RKVKTEEISR KFTGIALELW PNTRFEAGEE
151 KQEIRILPML RGISGLGRTL FQLLALAAAM EVFAFLQNVF FKIGRGESLA
201 LIGRSGCGKS TLLDILSGNL PPESGKVMIN GHDIYSLPPP FIPQFECDDGQ
251 GRTMFYSGLN LNR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1621>:

```

m553.seq (partial)
1 ATGGATTATT TATCAAGACT GTCCTTTGGA TTTAACAAAA AGCTACCTGT
51 CATTCTGCAA ACAGAAGTTG CTGAATGTGG TTTAGCATGC CTGACATCCA
101 TCTTGTCCTA TTATGGCTTT CACACTGATT TAAGAACGTT ACGCCAAAAA
151 TACACCCTGT CATTAAAGGG CGCAAATCTT GCAGACATCA TGAGATTG
201 CAATGAAATG AATTAAACGC CACGAGCTTT GCGTTTAGAG TTAGATGAGC
251 TGTCAAATTT ACAACTACCC TGCATTCTCC ATTGGAACCT AAACCATTTT
301 GTTGACTTTT GTTCCATTTC CAAAGACAGT ATCGTCATTA TGGACCCCTGC
351 TGTGCGTATG CGAAAAATCA AAATGGACGA AGTTTCACAA AAATTCACAG
401 GGATTGCCCT AGAATTATTC CCCAATACCC ATTTTGAAGA GAAAAAAGAA
451 ACAAAGAAAA TCAAATATAT ATCTCTATTA AGGGGGGG.T CAGGCTTAAA
501 ACGCTCTTTA ATTCAAATGC TTATATTAGC TATTCTTTG GAAGTCTTTG
551 CATTG...

```

This corresponds to the amino acid sequence <SEQ ID 1622; ORF 553>:

```

m553.pep (partial)
1 MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYGYF HTDLRTLQK
51 YTSLKGANL ADIMRFGNEM NLTPRALRLE LDELNLQLP CILHWNLNHF
101 VVLCISIKDS IVIMDPAVGM RKIKMDEVSQ KFTGIALELF PNTHFEKKE
151 TKKIKILSL RGXSGLKRSI IQMLILAI SL EVFAL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

m553/g553

	10	20	30	40	50	60
g553.pep	MDYLQNLISLGLTKKLPVILQTEVAECGLACLA	LAAVAGFYGFYTDLRALRSKYCLSLKGENL				
	:   : :	: : :				
m553	MDYLSRLSFGFNKKLPVILQTEVAECGLACLT	SILSYGYFHTDLRTLQKYLTLKGANL				
	10	20	30	40	50	60
g553.pep	ADIVRFADDMGLTGRALRLDLDELGSLRLPCILHWDNLNH	FVLESVSSDGA	AAVMDPASGR			
	:    : :	: : :				
m553	ADIMRFGNEMNLTPRALRLELDELNLQLPCILHWNLNHF	VVLCISIKDSIVIMDPAVGM				
	70	80	90	100	110	120
g553.pep	RKVKTEEISRKFTGIALELWPNTRFEAGEEKQEIRILPMLRGISGLGRTL	FQLLALAAAM				
	:  : : :	:  : : :				
m553	RKIKMDEVSQKFTGIALELFPNTHFEKKETKKIKILSLLRGXSGLKRS	LIQMLILAI SL				
	130	140	150	160	170	180
g553.pep	EVFAFLQNVSFKIGRGESLALIGRSGCGKSTLLDILSGNL	PPESGKVMINGHDIYSLPPP				
	:					
m553	EVFAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1623>:

```

a553.seq
1 ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAAA AGCTGCCTGT
51 TATCCTGCAA ACAGAAATAT CAGAATGCGG CTGGCATGT CTGGCGGCTG
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
151 TAC

```

This corresponds to the amino acid sequence <SEQ ID 1624; ORF 553.a>:

```
a553.pep
      1  MPHLQNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
      51  Y
```

m553/a553 62.7% identity in 51 aa overlap

	10	20	30	40	50	60
m553.pep	MDYLSRLSFGFNKKLPVILQTEVAECGLACLSILSYYGFTDLRTLRLQKYTLSLKGANL					
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
a553	MPHLQNLSLGLKKKLPVILQTEISECGLACLAAGVAGFHGFHTNLRALRSKY					
	10	20	30	40	50	
	70	80	90	100	110	120
m553.pep	ADIMRFGNEMNLTPRALRLEDELNLQLPCILHWNLNHFVVLCSISKDSIVIMDPVGM					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

```
g554.seq..
      1  atgacagcac ataaaatcct gcccgctcctt cttcccatca tcttaggcgt
      51  ttctcagca acggctgcat cgcccgcgcc caacagaccg acggtacacg
     101  ccgccccac gctccaaaca ccgaaaaccc tcacggcggc acacatcggt
     151  atcgaccttc aaagcaggca gactttatcc gccaaaaaca ccaatacccc
     201  tgtcgaaccg ggggcactaa cccaactgat gaccgcatat ttggttttca
     251  aaaacatgaa atcgggaaat atccaatctg aagaaaaactt aaaaataccc
     301  gaatccgcat gggcttcaga aggaagcaga atgtttgtac gtcccggcga
     351  tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
     401  acgatgccgc cctaaccctt gccgaccggc tgggcaacgg ctcgattgaa
     451  aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gcatgaagaa
     501  caccgtattc aaaaaccgca caggcttggg tagagaagga caggtttcca
     551  ccgccaaga cctctccctg ctgtctgaag cattgatgcg cgactttccg
     601  gaatattacc cgctgttttc catcaaatcg ttcaagttag aaaacataga
     651  acaaaacaac cgcaatatcc ttttatatag ggacaacaat gtaaacggcc
     701  tgaaagccgg gcacacagaa agcggcggct acaaccttgc cgtgtcatal
     751  tccggcaacg gcaggcacat ccttgtcatc acactagggt cggaatccgg
     801  ggaaaccgca gcatcggaca acagcaagct gctgaaccgg gcattgcagg
     851  ccttcgatac gcccaaaata tatccgaaag gcaaaaccgt tgcccaaatc
     901  caaatttccg gaggcagcaa aaaaaccgtc cgcgagggtc tcctcaaaga
     951  agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
    1001  tggaaaccat acagccgatt cccgccccgg taaaaaaagg gcagatttta
    1051  ggaaaaatca aaatcaggca aaacggacat accattgccg aaaaagaaat
    1101  cgctcgactg gaaaacgtag aaaaagaag ccggtggcaa aggcctttgga
    1151  cgcgtctgac agggcagtaa
```

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

```
g554.pep..
      1  MTAHKILPVL LPIILGVSHA TAASPAPNRP TVHAAPTLOT PETLTAAHIV
      51  IDLQSRQTL AKNTNTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
     101  ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LCANDAALTL ADRLNGSIE
     151  NFVQQMKEA RRLGMKNTVF KNPTGLGREG QVSTAKDLSL LSEALMRDFP
     201  EYYPLFSIKS FKFNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
     251  SGNRHLILVI TLGSESAETR ASDNSKLLNR ALQAFDTPKI YPKGKTVAQI
     301  QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKQIIL
     351  GKIIRQNGH TIAEKEIVAL ENVEKRSRWQ RLWTRLTGQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

```
m554.seq..
      1  ATGACAGCAC ATAAATCCT GCCCGTCTG CTTTCCATCA TCTTAGGCGT
      51  TTCTCAGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGTACACG
     101  CCGCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
     151  ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
     201  TGTGTAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTC
     251  AAAACATGAA ATCGGGCAAT ATCCAATCTG AAGAAAACCTT AAAAATACCC
```

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```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTG AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCGG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTGATC ACATTGGGTT CGGAATCGGC
801 GGAACACGCG GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAAATA TATCCGAAAG GCAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFQT PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQMLTAY LVFKNMKSGN IQSEENLKIP
101 ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LSANDAALT AGRLNGSIE
151 NFVQOMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHLVITL LGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKQIIL
351 GKIKIRQNGY TIAEKEIVAL ENVKRSRWQ RLWACL TGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554 . pep	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFQTPETLTAAHIVIDLQSKQILS					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTLPETLTAAHIVIDLQSRQTL					
	10	20	30	40	50	60
m554 . pep	AKNINTPVEPAALTQMLTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTVS					
g554	AKNTNTPVEPAALTQMLTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTVS					
	70	80	90	100	110	120
m554 . pep	AKNINTPVEPAALTQMLTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTVS					
g554	AKNTNTPVEPAALTQMLTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTVS					
	70	80	90	100	110	120
m554 . pep	TDKLLKGMIALSANDAALTLAGRLNGSIE NFVQOMNKEARRLGMKNTVFNPTGLSREG					
g554	TDKLLKGMIALCANDAALTADRLNGSIE NFVQOMNKEARRLGMKNTVFNPTGLSREG					
	130	140	150	160	170	180
m554 . pep	TDKLLKGMIALSANDAALTLAGRLNGSIE NFVQOMNKEARRLGMKNTVFNPTGLSREG					
g554	TDKLLKGMIALCANDAALTADRLNGSIE NFVQOMNKEARRLGMKNTVFNPTGLSREG					
	130	140	150	160	170	180
m554 . pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
m554 . pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
m554 . pep	SGGYNLAVSYSGNGRHLVITL LGSESAETR ASDNSKLLNWALQAFDTPKI YPKGKTVAQI					
g554	SGGYNLAVSYSGNGRHLVITL LGSESAETR ASDNSKLLNWALQAFDTPKI YPKGKTVAQI					
	250	260	270	280	290	300
m554 . pep	SGGYNLAVSYSGNGRHLVITL LGSESAETR ASDNSKLLNWALQAFDTPKI YPKGKTVAQI					
g554	SGGYNLAVSYSGNGRHLVITL LGSESAETR ASDNSKLLNWALQAFDTPKI YPKGKTVAQI					

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```
g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300

           310      320      330      340      350      360
m554.pep  QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPI PAPVKKGQILGKIKIRQNGY
           |||||
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPI PAPVKKGQILGKIKIRQNGH
           310      320      330      340      350      360

           370      380      390
m554.pep  TIAEKEIVALENVKKRSRWQRLWACL TGQX
           |||||
g554      TIAEKEIVALENVKKRSRWQRLWTRLTGQX
           370      380      390
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```
a554.seq
1   ATGACAGCAC  ATAAAATCCT  GCCCGTCCTG  CTTTCCATCA  TCTTAGGCGT
51  TTCTCAGGCA  ACGGCTGCAT  CGCCCGCGCC  CAACAGACCG  ACGGCACACG
101 CCGCCCCCAC  GTTCCAAACA  CCCGAAACCC  TCACAGCGGC  ACACATCGTT
151 ATCGACCTTC  AAAGCAAACA  GATTTTATCC  GCCAAAACA  TCAATACCCC
201 TGTCGAACCG  GCGGCACTAA  CCCAACTGAT  GACCGCATAT  CTGGTTTCA
251 AAAACATGAA  ATCGGGAAAT  ATCCGATCTG  AAGAAACTT  AAAAATACCC
301 GAATCCGCAT  GGGCTTCAGA  AGGAAGCAGA  ATGTTTGATC  GTCCCGGCGA
351 TACGGTCAGC  ACCGACAAAC  TCTTAAAGG  CATGATTGCA  CTATCCGCAA
401 ACGATGCCGC  CCTAACCCCT  GCCGGCCGGC  TGGGCAACGG  CTCGATTGAA
451 AATTTGTGTC  AACAAATGAA  CAAAGAAGCC  CGACGCTTGG  GCATGAAGAA
501 CACTGTATTC  AAAAATCCGA  CAGGCTTGAG  TAGAGAAGGA  CAGGTTTCCA
551 CCGCCAAAGA  CCTCGCCCAG  CTGTCTGAAG  CATTGATGCG  CGACTTCCCG
601 GAATATTACC  CGCTGTTTTC  CATCAAATCT  TTCAAATTCA  AAAATATAGA
651 GCAAAACAAC  CGCAATATCC  TTTTATATAG  GGACAACAAT  GTAAACGGTC
701 TGAAAGCCGG  ACACACAGAA  AGCGGCGGCT  ACAACCTTGC  CGTGTCTATC
751 TCCGGCAACG  GCAGGCACAT  CCTTGTCATC  ACATTGGGTT  CGGAATCGGC
801 GGAACACGCG  GCATCAGACA  ACAGCAAGCT  GCTGAAGTGG  GCATTGCAAG
851 CCTTCGATAC  GCCCAAATA  TATCCGAAAG  GCAAAACCGT  TGCCCAATC
901 CAAATTTCCG  GAGGCAGCAA  AAAAACCGTC  CGCGCAGGCT  TCCTCAAAGA
951 AGCCTACATC  ACTCTGCCAC  ATAAGGAAGC  GAAAAATGGC  GAACAATTC
1001 TAGAAACCAT  ACAGCCGATT  CCCGCCCCAG  TAAAAAAGG  GCAAATTTTA
1051 GGAAAAATCA  AAATCAGACA  AAACGATAC  ACCATTGCCG  AAAAAGAAAT
1101 CGTCGCACTG  GAAATGTAA  AAAAAGAAG  CCGGTGGCAA  AGGCTTTGGG
1151 CGTGTCTGAC  AGGGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```
a554.pep
1   MTAHKILPVL  LSIILGVSHA  TAASPAPNRP  TAHAAPTFQT  PETLTAAHIV
51  IDLQSKQILS  AKNINTPVEP  AALTQLMTAY  LVFKNMKSNG  IRSEENLKIP
101 ESAWASEGSR  MFVRPGDTVS  TDKLLKGMIA  LSANDAALTL  AGRLGNGSIE
151 NFVQQMNKEA  RRLGMKNVTF  KNPTGLSREG  QVSTAKDLAQ  LSEALMRDFP
201 EYYPLFSIKS  FKFKNIEQNN  RNILLYRDNN  VNGLKAGHTE  SGGYNLAVSY
251 SNGNRHILVI  TLGSESAETR  ASDNSKLLNW  ALQAFDTPKI  YPKGKTVAQI
301 QISGGSKKTV  RAGFLKEAYI  TLPHEAKMA  EQILETIQPI  PAPVKKGQIL
351 GKIKIRQNGY  TIAEKEIVAL  ENVKKRSRWQ  RLWACL TGQ*
```

m554/a554 99.2% identity in 389 aa overlap

```
           10      20      30      40      50      60
m554.pep  MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFFQTPETLTAAHIVIDLQSKQILS
           |||||
a554      MTAHKILPVLLSIILGVSHATAASPAPNRP TAHAAPTFFQTPETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554.pep  AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTVS
           |||||
a554      AKNINTPVEPAALTQLMTAYLVFKNMKSNGIRSEENLKIPESAWASEGSRMFVRPGDTVS
```

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	70	80	90	100	110	120
	130	140	150	160	170	180
m554.pep	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMNKEARRLGKNTVFKNPTGLSREG					
a554	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMNKEARRLGKNTVFKNPTGLSREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m554.pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNLKAGHTE					
a554	QVSTAKDLAQLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNLKAGHTE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m554.pep	SGGYNLAVSYSGNGRHILVITLGSESAETRASNKLLNWALQAFDTPKIYPKGKTVAQI					
a554	SGGYNLAVSYSGNGRHILVITLGSESAETRASNKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m554.pep	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGY					
a554	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGY					
	310	320	330	340	350	360
	370	380	390			
m554.pep	TIAEKEIVALENVKKRSRWQRLWACLTGQX					
a554	TIAEKEIVALENVKKRSRWQRLWACLTGQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcttgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccatcctgct tgcgcgcgtc atcgctgcgcg ccgctgcggg cggttttgtt
151 tggacatccc gccgacagca acgccagttt atcgaacgtc tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgcgcta
251 tgtaccacag cggcggacaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cacgctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC T GCGCTTGGGC GGCCTGATTT TACTGACCAC
51  CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTGTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCGGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTGCAAAA AATGTTCCGT GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

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101 LSQKCSVDEA HAMFKKRPT\* QEINQMAAKQ SRGQKRPHR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQF					
g556	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPT*					
g556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPT*					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
g556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAA	ACT	GCGCTTGGGC	GGCCTGATT	TACTGACCAC
51	CGCCGTTT	AGCCTCAT	TATGAT	TGTCGATTCC	TGGCCGCTTG	
101	CCATCCTGCT	TGCCGCGGTC	ATCGTCGCGG	CCGCTGCGGG	CGGCTTTGT	
151	TGGACATCCC	GCCGACAGCA	ACGCCAGTTT	ATCGAACGTC	TGAAAAAATT	
201	CGACATCGAT	CCCGAAAAAG	GCAGAAATCAA	CGAGGCAAAC	CTGCGCCGTA	
251	TGTACCACAG	CGGCGGACAA	CACCAAAAAG	ATGCGATTAC	CCTGATCTGC	
301	CTGTGCAAAA	AATGTTTCGGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG	
351	CCCGACACGT	CAGGAAATCA	ATCAAATGGC	GGCAAAACAG	TCGCGCGGTC	
401	AGAAACGTCC	GCACCGTTAA				

This corresponds to the amino acid sequence &lt;SEQ ID 1636; ORF 556.a&gt;:

a556.pep

1	MDNKTCLRGLG	GLILLTTAVL	SLIIVLIVDS	WPLAILLA	IVIAAAGGFV
51	WTSRRQQRQF	IERLKKFDID	PEKGRINEAN	LRRMYHSGGQ	HQKDAITLIC
101	LSQKCSVDEA	HAMFKKRPT*	QEINQMAAKQ	SRGQKRPHR*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQF					
a556	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPT*					
a556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPT*					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
a556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

g557.seq

1	atgaacaaaa	tattccttac	tgcgcgagcc	ttggtgctgg	gcgcgtgcgg
51	tttccacctg	aaaggtgcag	acggcatttc	tccgccgtg	acctaccgga
101	gctggtcacat	cgaaggcgga	caggcatgatc	aatttctt	ggaaaccgcg
151	ctgtatcagg	cttcgggcag	ggtagcattg	gctgccgcg	cgcagatgac
201	ctctcgctata	gacagcgttt	cccaaaaacaa	gaaacctat	accgttacc
251	gtgcggcagt	catcaacgaa	tatcttttga	tattgacggt	tgaagcgcag
301	gtattgaaac	gcggcgagcc	ggtcggcaaa	ccgatgaccg	tgctccgtccg
351	ccgcattttg	gattatgccc	acaacgaaat	tttgggcaaa	caggaagaag
401	aagaaaacct	gtgggcggaa	atgcggcagg	atgttgccga	acagattgtc
451	gcqccqctqa	cccttctqaa	qqcqqaatqa		

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pcp..

1 MNKIFLTAAL LVLGACGFHL KGADGISPP L TYRSHWIEGG QALQFPLETA  
51 LYQASGRVDD AAGAQM LTRI DSVSNKETY TVTRA AVINE YLLILTVEAQ  
101 VLKRGEFVGK PMTVSVRRIL DYADNEILGK QEEETLWAE MRQDVAEQIV  
151 RRLTELKAE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..

1	ATGAACAAAC	TGTTTCTTAC	TGCCGCAGTG	CTGATGCTGG	GCGCGTGCGG
51	TTTCCACCTG	AAAGGTGCG	ACGGCATTTC	TCCGCCGCTG	ACCTACCGGA
101	GCTGGCACAT	CGAAGGCGGA	CAGGCATTGC	GGTTTCCTTT	GGAAACCCGG
151	CTGTATCAGG	CTTCGGGCG	GGTGGACGAT	GCTGCCGCGG	CGCAGATGAC
201	CCTGCGTATA	GACAGCGTTT	CCCAAAACAA	GGAAACCTAC	ACCGTTATACC
251	GTGCGGCAGT	CATCAACGAA	TATCTTTTGA	TATTGACGGT	TGAAGCGCAG
301	GTATTGAAAC	GCGGCAGGCC	GGTCGGTAAA	CCGATGACCG	TGTCCGTCGG
351	CCGCGTCCTT	GCTTTATGCC	ACAACGAGAT	CTTGGGCAAA	CAGGAAGAGG
401	AAGCGGCATT	TGTGGCGGAA	ATGCGGCAGG	ATGCCGCCGA	ACAGATTGTC
451	CGCCGCGCTA	CCTTTCTGAA	GGCGGAATGA		

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pcp..

1	MNKLFLTAAL	LMLGACGFHL	KGADGISPP	TYRSWHIEGG	QALRFPLETA
51	LYQASGRVDD	AAGAQMTLRI	DSVSQNKETY	TVTRAAVINE	YLLILTVBAQ
101	VLKRGEFVGK	PMTVSRRVL	AYADNEILKG	QEEAAALWA	MRQDAAEQIV
151	RLRTFLKAE*				

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

	10	20	30	40	50	60
m557.pep	MNKLFLTAAV	MLGACGFHLK	GADGISPPLT	YRSWHIEGGQ	ALRFPLETAL	YQASGRVDD
	:	:	:	:	:	:
g557	MNKIFLTAAAL	VLGACGFHLK	GADGISPPLT	YRSWHIEGGQ	ALQFPLETAL	YQASGRVDD
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQM	TLRIDSV	SONKET	YTVTRA	AVINEY	LLILTVEA
g557	AAGAQM	TLRIDSV	SONKET	YTVTRA	AVINEY	LLILTVEA
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEIL	GKQEEEEA	LWAEMRQD	AAEQIVRR	LTFLKAEX	
g557	DYADNEIL	GKQEEETL	WAEMRQD	VAEQIVRR	LTFLKAEX	
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

840

a557.seq  
 1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG  
 51 TTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA  
 101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG  
 151 CTGTATCAGG CTTCGGGTAG GGTGGACGAT GCTGCCGCGC CGCAGATGAC  
 201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC  
 251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG  
 301 GTATTGAAAC GCGGCGAGCC GGTCGGCAAA CCGATGACCG TGTCCGTCGG  
 351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG  
 401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC  
 451 CGCCGCCTGA CCTTTCTGAA GGCGGAATGA

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

a557.pep  
 1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA  
 51 LYQASGRVDD AAGAQMTRLRI DSVSQNKETY TVTRA AVINE YLLILTVEAQ  
 101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV  
 151 RRLTFLKAE\*

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA	AVLMLGAC	GFHLKGAD	GISPPLTY	RSWHIEGG	QALRFPLE
a557	MNKLFLTA	AVLMLGAC	GFHLKGAD	GISPPLTY	RSWHIEGG	QALQFPLE
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTR	LIDSVSQN	KETYTVTR	AAVINEYL	LLILTVEA	QVLKRGE
a557	AAGAQMTR	LIDSVSQN	KETYTVTR	AAVINEYL	LLILTVEA	QVLKRGE
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEIL	GKQEEEA	ALWAEMRQ	DAAEQIVR	RRLTFLKA	EX
a557	AYADNEIL	GKQEEEA	ALWAEMRQ	DAAEQIVR	RRLTFLKA	EX
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

g558.seq..  
 1 ATGGATGCTT GTTTTTTCGT CATTCCCACA CAGGCGGGAA TTCGGAGATT  
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA  
 101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTCAACA GGGGACGGCA  
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG  
 201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA  
 251 AGTCCATTTC CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA  
 301 CTTTCAGACG GCATTGTTTA G

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

g558.pep..  
 1 MDACFFVIPA QAGIRRFIV FKRSGRILAG AGMMPLYTFS ELYMLQQGTA  
 51 HQAPHCVLPE RGCPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSNQSP  
 101 LSDGIV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

m558.seq..  
 1 ATGAATGCTT GTTTTTTCGT CATTCCCACA CAGGCGGGAA TTCGGAGATT  
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA  
 101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGTTCAACA GGGGACGGCA  
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG  
 201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA  
 251 AGTCCATTTC CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA  
 301 CTTTCAGACG GCATTGTTTA G

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:



m558.pep..

```

1  MNACFFVIPT QAGIRRFIV FKRSGRILAG AGMMPlyTFS ELYMFQOGTA
51  HQAPHCVLPE RDYPPIRFYR HKQTGFNRKG MGIKSISDIX RAMPSENQSP
101 LSDGIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

m558/g558

```

              10      20      30      40      50      60
m558.pep  MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPlyTFS ELYMFQOGTAHQAPHCVLPE
           |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g558      MDACFFVIPAQAGIRRFIVFKRSGRILAGAGMMPlyTFS ELYMLQOGTAHQAPHCVLPE
           10      20      30      40      50      60
              70      80      90     100
m558.pep  RDYPPIRFYRHKQTGFNRKGMGIKSISDIXRAMPSENQSP LSDGIVX
           | |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g558      RGCPPIRFYRYKQTGFNRKGMGIKSISDTSRAMPSENQSP LSDGIVX
           70      80      90     100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

```

a558.seq
1  ATGAATGCTT GTTTTTTCGT CATTCCCACA CAGGCGGGAA TTCGGAGATT
51  CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
101 TGCCCTTATA TATAGTGGAT TAAATTAAAT TCAGGACAAG GCGACGAAGC
151 CGCAGACAGT ACAAATAGTA CGGCAAGGCG AGGCAACGCC GTACTGGTTT
201 AAATTTAATC CACTATACTT TCTCCGAGCT TTATATGTTT CAACAGAGGA
251 CGGCACATCA AGCACCGCAC TCGGTGTTGC CCGAACGAGA CTGCCCTCCG
301 ATTAGATTCT ATCGCTATAA ACAGACGGGT TTCAACCGAA AAGGAATGGG
351 AATGAAGTCC GTTCCGACA CCTCTCGGGC GATGCCGTCT GAAAACCAAT
401 CTCCACTTTC AGACGCATT GTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

```

a558.pep
1  MNACFFVIPT QAGIRRFIV FKRSGRILAG AGMMPlyIVD *I*IRTRRRS
51  RRQYK*YGKA RQRTGLNLI HYTFSELYMF QQRTAHQAPH CVLPERDCPP
101 IRFYRYKQTG FNRKGMGMKS VSDTSRAMPS ENQSPLSDGI V*

```

m558/a558 70.2% identity in 141 aa overlap

```

              10      20      30
m558.pep  MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPly-----
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a558      MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPlyIVDXIXIRTRRRSRQYKXYGKA
           10      20      30      40      50      60
              40      50      60      70      80
m558.pep  -----TFSELYMFQOGTAHQAPHCVLPERDYPPIRFYRHKQTGFNRKGMGIKS
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a558      RQRTGLNLIHYTFSELYMFQRTAHQAPHCVLPERDCPPIRFYRYKQTGFNRKGMGMKS
           70      80      90     100     110     120
              90     100
m558.pep  ISDIXRAMPSENQSP LSDGIVX
           :|| |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a558      VSDTSRAMPSENQSP LSDGIVX
           130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1649>:

```

g560.seq
1  atgctcatca tccgcaacct gatttactgg ctgatactct gttccagcct

```

51	gattttcctc	tttcccttta	tgctgctcgc	ctcgcctttc	cgggacgggg
101	cgcacaagat	ggcgcggggc	tgggtcggca	tcctcaactg	gtcgtcctaaa
151	cacatcgtcg	ggctcaaaat	ccgcacatct	ggcgcggaac	acattccgga
201	ccgcctctcc	gtcatctcgc	ccaaacacca	aagcggctgg	gaaacgcctcg
251	cgctccaaga	gatttttccg	cgcagggtt	acggtgcaaa	gcgcgagttg
301	ttcaaaatcc	cctttttcgg	ctggggcttg	aaactggtca	aaaccatagg
351	catagaccgc	aacaaccgca	gcgaagccaa	cgaacagctc	ataaaaacagg
401	gtttggcgcc	caaaaacgaa	ggttatggaa	taccattttt	ccccgaaggc
451	acgcgccttg	gcgccggaaa	accgcggcaa	ttcaaaactcg	cgccgcgcgcg
501	catggcgaaa	atgtttgaga	tggacatcgt	ccccgtcgcc	ctcaacacgcg
551	gcgaattttg	gccgaaaaat	tcctttctga	aatatccggg	ggaaatcacc
601	gtcatcatct	gtccgaccat	cccgcacga	agcggcagcg	aagccgaatt
651	gatggaaaaa	tgcgaacacc	tcattgagca	gcaacaaccg	cttattttccg
701	gcgcgaagccc	gtttgcgcgc	gaaatgccgt	ctgaaaccgc	atga

This corresponds to the amino acid sequence <SEQ ID 1650; ORF 560.ng>:

g560.pep..

1	MLIIRNLIYW	LILCSSLIFL	FPFMLLASPF	RDGAHKMARV	VWGILNWSLK
51	HIVGLKYRII	GAEHIPDRPS	VICAKHQSGW	ETLALQEIFF	PQVYVAKREL
101	FKIPFFGWGL	KLVTGTIDIR	NMREANEQL	IKQGLARKNE	GWYITFFPEG
151	TRLAPGKRKG	YKLGGARMAC	MFENDIVPVA	LNSGEFWPKN	SFLKYPGEIT
201	VIICPTIPHA	SGSEAELEMEK	CEHLITTOQP	LISGAGPPFA	EMPET*

The following partial DNA sequence was identified in *N.meningitidis* <SEO ID 1651>:

m560.seq

1	ATGCTCATCA	TCCGCAACCT	GATTACTGG	CTGATACTCT	GTTCCACCCT
51	GATTTTCCTC	TTTCCCTTTA	TGCTGCTCGC	CTGCCTTTTC	CGGGACGGGG
101	CGCACAAAGAT	GGCGCGGGTC	TGGGTCTCGGCA	TTCTCAACTG	GTCTCTCAAA
151	CACATCGTCG	GGCTCAAATA	CCGCATCATC	GGCGCGGAAA	ACATCCCCGA
201	CGCCGCCGCC	GTCTCTTGGC	CCAAACACCA	AAGCGGCTGG	GAAACGCTCG
251	CCCTTCAGGA	CATTTTTCGG	CCGCGAGTTT	ACGTTGCCAA	ACGCGAGTTG
301	TTCAAAATCC	CCTTTTTCGG	CTGGGGCTTG	AAACTGGTCA	AAACCATAGG
351	CATAGACCGC	AACAACCGCC	GCGAAGCCAA	CGAGCAGCTC	ATAAAAACAG
401	GGTTTGGTCG	CAAAAACGAA	GGCTATTGGA	TTACCATTTT	CCCCGAAGGC
451	ACGCGCCTTG	CGCCCGGAAA	AGCGCGCAAA	TACAAACTCG	CGCGCGCGCG
501	CATGGCGAAA	ATGTTTGAGA	TGGACATCGT	CCCCGTCGCC	CTCAACAGCG
551	GCGAATTTTG	GCCGAAAAAC	TCCTTTCTGA	AATATCCGGG	GGAATCACC
601	GTCGTCATCT	GTCCGACCAT	CCGACAGGAA	AGCGGCAGCG	AAGCCGAATT
651	GATGGAAAAA	TGCGAACATC	CTCATCGAAC	GCAACAACCG	CTTATTTCCG
701	GCGCAGGCCC	GTTCGCGCC	AAAATGCCGT	CTGAAACCGC	ATGA

This corresponds to the amino acid sequence <SEQ ID 1652; ORF 560>:

m560.ppt

1	MLIIRNLIYW	LILCSTLIFL	PPFMLLASPF	RDGAHKMARV	VWGILNWSLK
51	HIVGLKYRII	GAENIPDRPA	VICAKHQSGW	ETLALQDIFP	PQVYVAKREL
101	FKIPFFGWGL	KLVTGTIDIR	NFREANEQEL	IKQGLVRKNE	GYWITIFPEG
151	TRLAPGKGRK	YKLGGARMAC	MMREANIPVA	LNSGFWFPKN	SFLKYPGEIT
201	VVICPTIPHA	SGSEAELEMEK	CEHLIETOOP	LISGAGFPAA	KMPSETA*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 560 shows 97.2% identity over a 246 aa overlap with a predicted ORF (ORF 560.ng)

from *N. gonorrhoeae*:

m560/g560

[illegible]

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMFEMDIVPVA					
	:					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	:					
g560	LNSGEFWPKNSFLKYPGEITVIICTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```
a560.seq
1  ATGCTCATCA TCCGCAACCT GATTACTGCG CTGATACTCT GTTCCACCCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGAGACGGGG
101 CGCACAAAGAT GGCGCGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCGG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAAATCC CCTTTTTCGG CTGGGGCTTG AAACGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAACAGG
401 GGTGGCGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCGAAGGC
451 ACACGCCTTG CGCCCGGAAA ACGCGGCAA TACAACTCG GCGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCGCGTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCGACCAT CCGCACGCA AGCGGACGCG AAGCCGAATT
651 GATGGGAAA TGCGAACACC TCATCGAAAC GCAGCAGCCG CTCATTCCG
701 GCGCAGGCC GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA
```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```
a560.pep
1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAQHSGW ETLALQDIFP PQVYVAKREL
101 FKIPFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGARMAM FEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMGK CEHLIETQQP LISGAGPFAA KMPSETA*
```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
a560	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVKILNLSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAQHSGWETLALQDIFPPQVYVAKRELFKIPFGWGLKLVKTIGIDR					
a560	GAENIPDRPAVICAQHSGWETLALQDIFPPQVYVAKRELFKIPFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMFEMDIVPVA					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMFEMDIVPVA					

844

	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
a560						
	190	200	210	220	230	240
m560.pep	KMPSETAX					
a560						
	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

```
m561.seq.
1  ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCAGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAC ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCCTGCGC AAATTGACAA TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCT
301 TCGGACACCC CTCTTGCTTA TGATTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCCTCCA GTCCTACCGG CGACCGACTC
401 AGGTGCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAATGAT CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTGCTC TGTACTGATG CTGTTTGGC
551 ACCAGATTTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTGCGGC GTTGTTCCTA TCAATGGGC GGCAGGTTGA
701 AAATTTTATA TGATGATTTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCTG CTGTACCAA CTACACGGGA
801 CTTGCACCAA TCCTACATAC CGCAACAGG TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTTC CATTATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTG GGAAGTACC ATGAGGAAAT CTTCCCATT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTTCTCTT
1051 GATGAAGACG ACCGCATCCT GCTTCAACA CTAGGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GGCACAAAAC AGGAGGAAGA AAAACGCCTG CTTGCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAC CCGCCTTTGC
1251 CGAAAAACAA CGGGAGGAAG CCGCAGAAAA CATCAGCTTT ATCAAAACAG
1301 GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTTCCGT
1351 ACCAAAATCA GCAATAAAGA ATTTCCCGAA GCGGTTGCCG ACCTATTCCG
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAAACG
1451 GTTCTGTTCT GCCGCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCCTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAAACAC GCCCAGGCCA CCCATGTAAA
1551 ATTACCCCTT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTGACACG GAGAAAATAG GAGAACCAC GGGCAGCCAT
1651 GTCGGAAGTC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA
```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

```
m561.pep
1  MILPARFSDG ISLSRLRLKL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLLKLYDDL EGQVAEQTRS
251 LEKQNQNLTL LYQTTRDLHQ SYIPQAAEH FLNRLPVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEERKL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFAENK REEAENISF IKTVQECYE DVRELLNFR
451 TKISNKEFFE AVADLFARFT QQTGITVETA WENGSLFPQ EAQLQMIFIL
```

501 QESLSNIRKH ARATHVKFTL SEHGGRFTMT IQDNGQGFDT EKIGEPTGSH  
 551 VGLHIMQERA KRIHAVLEIR SQAQQTTSV LTVASEESLK \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALS	VVLTLLLSRL	LENAASVIEE	EAGNLR	MQAY	
	:	:	:	:	:	:
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALS	VVLTLLLSFR	LENAASVIEE	EAGNLR	MQAY	
	10	20	30	40	50	60
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAE	FEKSLKRIAQSDAIH	PLIPSDTPLAYDLIQS	MLIIDWQA		
	:	:	:	:	:	:
g561	RLAYMAGEGSPRAQIDNQIAE	FEKSLKRISQSDAIH	PLIPSDNPLAYDLIQS	MLIIDWQA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYR	FAGNIELFLQALENANE	KNTWWLRRFQWAIM	MLTLVSSVLM		
	:     :	:     :	:     :	:     :	:     :	:     :
g561	NILPPLQAYRRPTQIELYR	FAGNIELFLQALENAGE	KNTWWLRRFQWVIM	MLTLVSSVLM		
	130	140	150	160	170	180
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGA	ERIGRRCFDIPVPEG	GTEFEKQVGR	CFNQMGGR	LKILYDDL	
	:	:	:	:	:	:
g561	LFWHQIWVIRPLQALREGA	ERIGQRHFDIPVPED	VRENSNRSGG	VSTKWRSGX		
	190	200	210	220	230	
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQNQNL	TLLYQTTDLHQSYIP	QQAAEHFLNRILPA	VGADSGR	VCLDG	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCTGGGT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTGCCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCTT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCCTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	GCCGGAACA	TCGAACTGTT	TTTGCAGGCA
451	TTGGAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCAATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCTGC	TGTAATGATG	CTGTTTGGCC
551	ACCAGATTTG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAATTCAAA	CAGGTCGGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCCTG	CTGTACCAAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATCCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCCGATTTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCCATT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTCTCTTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCTTG	CTTGCAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCTTTTGC
1251	CGAAAACAAA	CGGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTCCGCT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCCGAA	GCCGTTGCCG	ACCTATTCTC

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```

1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGGCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
1 MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51 EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIEFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQM GRLKILYDDL EGQVAEQTRS
251 LEKQONQLTL LYQTTLDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFNLQVQ MLETAFENK REEAAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQGFD T ENIGEPSGSH
551 VGLHIMQERA KRIHAVLEIR SQAQQTTS LTVASEESLK *

m561/a561 96.9% identity in 590 aa overlap

10 20 30 40 50 60
m561.pep MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSLRLLENAASVIEEAGNLRMQAY
a561 MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSLRLLENAASVIEEAGNLRMQAY
10 20 30 40 50 60

70 80 90 100 110 120
m561.pep RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA
a561 RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA
70 80 90 100 110 120

130 140 150 160 170 180
m561.pep HILPPLQSYRRPTQVDLYRFAGNIEFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
a561 HILPPLQSYRRPTQVDLYRFAGNIEFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
130 140 150 160 170 180

190 200 210 220 230 240
m561.pep LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLKILYDDL
a561 LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLKILYDDL
190 200 210 220 230 240

250 260 270 280 290 300
m561.pep EGQVAEQTRSLEKQONQLTLLYQTTLDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
a561 EGQVAEQTRSLEKQONQLTLLYQTTLDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
250 260 270 280 290 300

310 320 330 340 350 360
m561.pep GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT
a561 GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT
310 320 330 340 350 360

370 380 390 400 410 420
m561.pep LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFNLQVQMLETAFENK
a561 LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFNLQVQMLETAFENK

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847

	370	380	390	400	410	420
m561.pep	430	440	450	460	470	480
a561	430	440	450	460	470	480
m561.pep	490	500	510	520	530	540
a561	490	500	510	520	530	540
m561.pep	550	560	570	580	590	
a561	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

```

1 atggcaagcc cgctcagctct gcctttcaat tcgggcaaga ccaaaccgac
51 ggcttttgcc ggcgcggttt tggtcggaat catgttttcc acgccgctgc
101 gggcgcgccg caggtctttg tggcgcacgt cggtaacggt ttggtcgttg
151 gtcagtgctg ggatggtggt cattgcgcct ttgacgatgc cgacgcttcc
201 gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251 tggaaacgac ggatcatgtcg gcggtcagga cgctgtcggt caccgcttac
301 acgacggttg catcgacatc gtcgcccggc ggtgcggaat tgaggacttt
351 tttcgcgccc ctttcgaggt ggattttggc tttttctttg ctggtgaacg
401 cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451 tcggcagggg tgcgggtcga gaagaagggg attttgcgcg cgttgacgat
501 gaggttgccg ccgtcgtggg atacgtcgcc ttcaaagcgt ccgtgtacgg
551 tgtcgaattt ggtcagatgg gcgttggttt caaggctgcc gctggcggtg
601 acggcgacga tttggagttg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

```

1 MASPSSLPFN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51 VSAWMVVIAP LTMP TSLNT LATGERQLVV QEALTTVMS AVRTLSETPY
101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSM TSTPSSFHGS
151 SAGLRVEKKG ILSPLTMLRP PSWDTSASKR PCTVSNLVRW ALVSRPLPLAL
201 TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

```

1 ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51 GGCTTTTGCC GCGCCGTTT TGGTCGGAAT CATGTTTCC ACGCCGCTGC
101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGTCATGTCT GCGGTACAGG CGCTGTCTGT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCCGCCG GGTGCGGAAA TGAGGACTTT
351 TTTCCGCGCC CTTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TCGGGGTCGA GAAGAAGGGG ATTTTGTCTG CGTTGACGAT
501 GAGGTGCGCG CCGTCGTGGG ATACGTGCGC TTCAAAGCGT CCGTGCACGG
551 TGTCGAATTT GGTGAGATGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA GTTGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

```

1 MASPSSLPFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51 VSAWMVVIAP LTMP TSLNT LATGERQLVV QEALTTVMS AVRTLSETPY

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848

101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS  
 151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL  
 201 TATSWWS\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
g562	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
g562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTASAKR					
g562	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTASAKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRLPLALTATSWWSX					
g562	PCTVSNLVRWALVSRLPLALTATSWWSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

a562.seq  
 1 ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC  
 51 GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTTCC ACGCCGCTGC  
 101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG  
 151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC  
 201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT  
 251 TGGAAACGAC GGTCATGTCG GCGGTCAGGA TGCTGTCGTT CACGCCGTAC  
 301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT  
 351 TTTGCGCGCC CTTTCCAGAT GAACTTTGGC TTTTCTTTG CTGGTGAACG  
 401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT  
 451 TCGGCAGGGT TCGGGGTCNA GAAGAANGG ATTTTGTCGC CGTTGACGAT  
 501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG  
 551 TGTCGAATT GGTGAGGTGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG  
 601 ACGGCGACGA TTTGGAGTTG GTCTTGA

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

a562.pep  
 1 MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL  
 51 VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRMLSFTPY  
 101 TTVASTSSPP GAEMRTFFAP LSR\*TLAFSL LVNAPVHSMT KSTPSSFHGS  
 151 SAGLRVXXKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL  
 201 TATIWSWS\*

m562/a562 96.6% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
a562	MASPSSLSFN SGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60



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	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMASVRTLSTPYTTVASTSSPPGAEMRTFFAP					
a562	LTMPTLSLNTLATGERQLVVQEALETTVMASVRLSTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMKSTPSSFHGSSAGLRVEKKGILSPLTMLRPPSWDTSASKR					
a562	LSRXTLAFSLLVNAPVHSMKSTPSSFHGSSAGLRVKKXGILSPLTMLRPPSWDTSASKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRLPLALTATSWWSX					
a562	PCTVSNLVRWALVSRLPLALTATIWSWX					
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563.seq

```

1  ATGAACAAAA CCCTCTATCG TGTGATTTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAGC TGTGCCGATA
101 GTGGTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTCTTTTAT GTTTGGCTTT
201 GGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCCc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCCACTT GATGTGGGTA ATcgCGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GCGGTTGGA TTCAAGGCAA TCCTTGGTTG
451 ACAAGGGGCG AAGCACGTGT GGTGTAAAC CAAATCAACA GCAGCCATCC
501 TTCACAATG AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAAGTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTAAGATAA GGCAAGGCAA TGCTGTAATC GCCCGACACG
701 GTTTGGATGC CCGTGATACC GATTTCACAC GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTG GTAATCAAGG
801 GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCAGCATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAAGTCAA TATCCGCAGT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 ACATCGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTACAG CAAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAACTGGAT ATTGCGTTAC AAGATGATT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACCTTGC AAGCAGGAAA ACGATTTCGG
1351 ATTAAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CGGTACGACA GACATTGGCA CGCAGCACAA TTAAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAAACCAA ATCCAAGCCG GGCAAATGAA TAATATCGGT
1501 ACAGGTCGGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTTAGG CATTGAACAA TTAATAAACC GTGAAAACAG TCTGATTTAC
1651 AGCGGTAACG ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCCAAAGGA TACACAATGC CGGCGCAATC ATTGAAGCTG
1751 CAGGCAAAAT GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT
1801 TTGAAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATTG TTGATTACGA
1851 AGCATTGGA CGACACGAAT TATTGCGAGA AGGCAGGCAA CATGAATTAG
1901 GCTGGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAACGT CGCCTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

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2101 GCGGCCAAT TGCTTGTGCA AACAGAAAAA GACGGTTTGC ATAACGAGCA  
2151 AACCTTTGGC GAGAAGAAAG TCTTCAGCGA AAATGGTAAG TTGCACAAC  
2201 ACTGGCGTGC GCGTCGTAAA GGACATGATG AAACAGGGCA TCGTGAACAA  
2251 AATTATACTT TGCCGGAGGA AATCACACGC GACATTTCAC TGGGTTTCATT  
2301 TGCCTATGAA TCGCATAGCA AAGCATTAAAG CCGTCATGCG CCCAGCCAAG  
2351 GCACTGAGTT GCCACAAAGT AACCGGGATA ATATCCGTAC TGCGAAAAGC  
2401 AACGGTATTT CGTACCCTA TACGCCCAAT TCTTTTACCC CATTACCCGG  
2451 CAGCAGCTTA TACATTATCA ATCCTGCCAA TAAAGGCTAT CTTGTTGAAA  
2501 CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTTGGGTAG TGAATATATG  
2551 CTGGGCAGCC TCAAACTAGA CCCAAACAAT TTACATAAAC GTTTGGGTGA  
2601 TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA GAGCTGACAG  
2651 GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA ATTTAAAGCC  
2701 TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC TCAGCGTTGG  
2751 CATTGCATTA AGTGCCGAGC AAGCAGCGCA ACTGACCAGC GATATTGTTT  
2801 GGTTCGTACA AAAAGAAAGT AAACCTCCTG ATGGCGGCAC ACAAACCGTA  
2851 TTGATGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGGCA TAGACGGTAA  
2901 AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT TCAGGCAGCC  
2951 TGAAAAACTC AGGCACGATT GCAGGCGGCA ATGCGCTTAT TATCAATACC  
3001 GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA AATCAGCGGT  
3051 TACGGCCACA CAAGACATCA ATAATATTGG CGGCATTCTT TCTGCCGAAC  
3101 AGACATTATT GCTCAATGCG GGTAACAACA TCAACAACCA AAGCACGGCC  
3151 AAGAGCAGTC AAAATGCACA AGGTAGCAGC ACCTACCTAG ACCGAATGGC  
3201 AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA GCGCAGGCAG  
3251 GCAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA ATCAGATCAA  
3301 GGGCAAACCC GGCTGCAGGC AGGACGCGAC ATTAACCTGG ATACGGTACA  
3351 AACCGGCAAA TATCAAGAAA TCCATTTTGA TGCCGATAAC CATACCATCC  
3401 GAGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA AGGCGATGTT  
3451 ACCCtattGT CAGGGAATAA TCTCAATGCC AAAGCTGCCG AAGTCGGCAG  
3501 CGCAAAAGGC ACACCTGCGG TGTATGCTAA AAATGACATT ACTATCAGCT  
3551 CAGGCATCCA TGCCGGCCAA GTTGATGATG CGTCCAAACA TACAGGCAGA  
3601 AGCGGCGGCG GTAATAAATT AGTCATTACC GATAAAGCCC AAAGTCATCA  
3651 CGAAACTGCT CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT GTATTGCAGG  
3701 CAGGAAACGA TGCCAACATC CTTGGCAGTA ATGTTATTTT CGATAATGGC  
3751 ACCCGGATTC AAGCAGGCAA TCATGTTCGC ATTGGTACAA CCCAACTCA  
3801 AAGCCAAAGC GAAACCTATC ATCAAACCCA AAAATCAGGA TTGATGAGTG  
3851 CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA AGAAAACCAA  
3901 TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCC TGAAAGGCGA  
3951 TACCACCATT GTTGCAAGCA AACACTACGA ACAAACCGGC AGCAACGTTT  
4001 CCAGCCCTGA GGGCAACAAC CTTATCAGCA CGCAAAGTAT GGATATTGGC  
4051 GCAGCACAAA ACCAATTAAT CAGCAAAACC ACCCAAACCT ACGAACAAAA  
4101 AGGCTTAACG GTGGGCATTG AGTTCGCCCC TTACCGATTT GGCACAACAA  
4151 GCGATTGCCG TAGCACACAA AGCAGCAAAC AAGTCGGACA AAGCAAAAAC  
4201 GACCGCGTTA ATGCCATGGC GGCTGCCAAT GCAGGTTGGC AGGCCTATCA  
4251 AACAGGCAAA GGCGCACAAA ACTTAGCCAA TGGTACAACC AATGCCAAAC  
4301 AAGTCAGCAT CTCCATAACC TACGGCGAAC AGCAAAACCG ACAAAACCACC  
4351 CAAGTTCAAG CCAATCAAGC CCAAGCGAGT CAAATTCAAG CAGGCGGCAA  
4401 AACTACCCTT TATTGCCGAA GGTGCGGCGA ACAATCCAAT ATCAACATCA  
4451 CAGGCTCAGG TGTTTCAGGC AGAGCAGGAA CCGGCCTGAT TGCCGATAAG  
4501 CAAATCCATC TGCAATCAGC CGAGCAAAGC AATACCGAAC GCAGCCAAAA  
4551 CAAATCAGCA GGCTGGAACG CAGGTGCTGC CGTATCATTC GGACAAGGAG  
4601 GCTGGTCATT AGGCGTTGCC GCAGGCGGCA ATGTCGGCAA AGGCTACGGC  
4651 TATGGCGATA GCGTAACCCA CCGCCATAGC CATATTGGCG ACAAAAGCAG  
4701 CCAAACCTTT ATCCAAAGTG GTGGCGATAC CATCATCAAA GCGCGCAAG  
4751 TACGCGGCAA AGGCGTACAA GTCAATGCCA AAAACCTAAG CATTCAAAGT  
4801 GTACAAGATA GAGAACTTA TCAAAGCAAA CAACAAAACG CCGGTGCACA  
4851 AGTTACCGTA GTTTATGGCT TCAGTGCCAG TGGCGATTAC AGCCAAAGCA  
4901 AAATCCGAGC CGACCATGCT TCGGTAACCG AGCAAAGCGG TATTTATGCC  
4951 GGAGAAGACG GCTATCAAAT CAAGGTGCGA AACCATACAG GCCTCAAAGG  
5001 CCGCATCATC ACCAGCAGCC AAAGCGCAAA AGACAAGGGT AAAAACCGAT  
5051 TCAGCACAGG CACACTCGCC GGCAGTGATA TTCAAATTA CAGCCAATAC  
5101 GAAGGAAAAA GTTTTGGATT GGGTGCCAGC GTTGCCGTAA GCGGCAAAAC  
5151 ACTGGGACAG GGCGCAAAAA ATAAACCTCA AGACAAACAC CTGACAAGCA

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5201 TAGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC
5251 GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CCAAAAACAT
5301 TCAAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCGG
5351 CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA
5401 CGACATTCGG GCAGCCTGAA AAACATATTT GACAAAGATA GAGTGCAAAG
5451 TGAAGTGGAT TTACAAAgaa CCGTCAGCCA AGATTTTAGT AAAAATGTTC
5501 AACAAACCAA TACCGAGATT AACCAACATT TAGACAAACT CAAAGCAGAC
5551 AAAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT
5601 GGAAACTGCC AAACGCAAAG CCCATGAAGC TCAAGATGCG GCAGCAAAAG
5651 CAGATAATTG GCAACAAGGC AAAGTCATT CCAACATGTT AGCCTCAGGT
5701 TTAGCTGAGC CGACCCAAAG CGGAGCgggc ATCGCTGCGG CTACCGCATC
5751 GCCaagCGTA TCGTATGCGA TTGGACAGCA CTTTAAagaT TTAGCCGGTC
5801 AAAACGCGAA TGGCAAAC TAACCGCAGTC AagaAACCGC TCACGTTCTT
5851 GCCCAGCGCG TATTAGGAGC AGCGGTTGCC GCAGCATGAG GCAACAATGC
5901 CCGCGCAGGA GCATTGGGTG CGGGCGGGTc ggAagcggCC GCCCAATCA
5951 TCGGCAAAATG GCTGTACGGC AAAGGAGAcg gcggcagccT GAATgcggag
6001 gaaaAGaga CCGTTTCGGC GATTACAAGG ATGCTGggt cGgctGCCGG
6051 AGCAGCTGAG GGAAACTCGT CCGCCGATGC TGTGTGGGGT TGTTTTcaaa
6101 cggctTCaga TTTCGCTTCC TCTTTTTCAT ATCCTATAAA CATGTGA

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This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pep..

```

1 MNKTLRVIF NRKRGAUVAV AETTKREGKS CADSGSGSVY VKSVSFIPTH
51 SKAFCF SALG FSLCLALGTV NIAFADGIIT DKAAPKTQQA TILQTNGNIP
101 QVNIQTPTSA GVSVNQYQAF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL
151 TRGEARVVVN QINSSHPSQL NGYIEVGRRR AEVVIANPAG IAVNGGGFIN
201 ASRATLTGQ PQYQAGDFSG FKIRQGNVAV AGHGLDARDT DFTRILLYAN
251 KITLISTAEQ AGIRNQGLF ASSGNVAIDA NGRLVNSGTM AAANVQDMNN
301 TAEHKVNIRS QAFENSGTAV SQQGTQIHSQ SIQNTGKLLS AGTEDLAVSG
351 SLNNQNGEIA TNQQLIIHDG QQSTVVIDNT NGTIQSGRDV AIQAKSLSN
401 GTLAADNKLD IALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLQAGKRIR
451 IKANNLDNAV QGNIQSGGTT DIGTQHNLTN RGLIDGQOTK IQAGQMNIG
501 TGRIYGDNIA IAATRLDNQD ENGTGAAIAA RENLNLGIEQ LNNRENSLIY
551 SGNDMAVGGA LDTNDQATGK AQRIHNAGAI IEAGKMR LG EKLHNTNEH
601 LKTQLVETGR ERIVDYEAFG RHELLREGTQ HELGWFVYNN ESDHLRTPDG
651 VAHENWHKYD YEKVQETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA
701 GGQLLVQTEK DGLHNEQTFG EKKVFSENGK LHNWYRARRK GHDETGHREQ
751 NYTLPEEITR DISLGSFAYE SHSKALSRIA PSQGTLPQS NRDNIRTAKS
801 NGISLPYTPN SFTPLPGSSL YIINPANKGY LVETDPRFAN YRQWLGS DYM
851 LGSKLDPNN LHKRLGDGY EORLINEQIA ELTGHRRLDG YONDEEQFKA
901 LMDNGATAAR SMNLSVGIAL SAEQAAQLTS DIVVLVQKEV KLPDGGTQTV
951 LMPQVYVRVK NGGIDGKGAL LSGSNTQINV SGSLKNSGTI AGRNALIINT
1001 DTLDNIGGRI HAQKSAVTAT QDINNIGGIL SAEQTLNNA GNNINNQSTA
1051 KSSQNAQGS TYLDRMAGIY ITGKEKGVLA AQAGKDINII AGQISNQSDQ
1101 QTRLQAGRD INLDTVQTGK YQEIHFADN HTIRGSTNEV GSSIQTGKDV
1151 TLLSGNNLNA KAAEVGSAK TLAVYAKNDI TISSGIHAGQ VDDASKHTGR
1201 SGGGNKLVT DKAQSHHETA QSSTFEGKQV VLQAGNDANI LGSNVISDNG
1251 TRIQAGNHVR IGTQTQSQS ETYHQTQKSG LMSAGIGFTI GSKTNTQENQ
1301 SQSNEHTGST VGS LKGD TTI VASKHYEQTG SNVSSPEGNN LISTQSM DIG
1351 AAQNQLNSKT TQTYEQKGLT VGIQFARYR GTTSDCRSTQ SSKQVQGSKN
1401 DRVNAAAAAN AGWQAYQTGK GAQNLANGTT NAKQVSISIT YGEQQNRQT
1451 QVQANQAQAS QIQAGGKTTL YCRRCEQSN INITGSGVSG RAGTGLIADK
1501 QIHLQSAEQS NTERSQNKSA GWNAGAAVSF GQGGWSLGVA AGGNVKG YG
1551 YGDSVTHRHS HIGDKGSQTL IQSGGDTI IK GAQVRGKG VQ VNAKNLSIQS
1601 VQDRETYQSK QONAGA QVTV GYGFSASGDY SQSKIRADHA SVTEQSGIYA
1651 GEDGYQIKVG NHTGLKGGII TSSQSAKDKG KNRFTGTGLA GSDIQNYSQY
1701 EGKSFGLGAS VAVSGKTLGQ GAKNKPQDKH LTSLADKNKA SSSVGYGSDS
1751 DSQSSITKSG INTPKNIQIT DEAAQIRLTG KIAAQTKADI DTNVTIDTAE
1801 RHSGSLKNIF DKDRVQSELD LQRTVSQDPS KNVQQTNTET NQHLDKLAD
1851 KEAETA AAE ALANGDMETA KRKAHEAQDA AAKADNWQQG KVILNMLASG
1901 LAEPTQSGAG IAAATASPDV SYAIGQHF KD LAGQANANGKL TASQETAHVL
1951 AHAVLGA AAV AAXGNNAPAG ALGAGGSEAA APIGKWL YG KDGGSLSNAE
2001 EKETVSAITR MLGTAAGAAE GNSSADAVWG CFQTASDFAS SFSYPINM*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

```

1  ATGAATAAAA CTCTCTATCG TGTAATTTTC AACC GCAAAC GTGGGGCTGT
51  GGTAGCCGTT GCTGAAACTA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGATT CAGG CAGCGCTCAT GTGAAATCTG TTCCTTTTGG TACTACTCAT
151 GCACCTGTTT GTCGTTCAAA TATCTTTTCT TTTTCTTTAT TGGGCTTTTC
201 TTTATGTTTG GCTGTAGGTA CGGCCAATAT TGCTTTTGCT GATGGCATT A
251 TTGCTGATAA AGCTGCTCCT AAAACTCAAC AAGCCACGAT TCTGCAAACA
301 GGTAAACGGCA TACC GCAAGT CAATATTCAA ACCCTACTT CGGCAGGGGT
351 TTTCTGTTAAT CAATACGCCC AGTTTGATGT GGGTAATCGC GGGGCGATTT
401 TAAACAACAG CCGCAGCAAC ACCCAAACAC AGCTAGGCGG TTGGATTCAA
451 GGTAAATCCTT GGTGGAAG GGGCGAAGCA CGTGTGGTTG TAAACCAAT
501 CAACAGCAGC CATTCTTCAC AAATGAATGG CTATATTGAA GTGGGCGGAC
551 GACGTGCAGA AGTCGTTATT GCCAATCCGG CAGGGATTGC AGTCAATGGT
601 GGTGGTTTTA TCAATGCTTC CCGTGCCACT TTGACGACAG GCCAACCGCA
651 ATATCAAGCA GGAGACCTTA GCGGCTTTAA GATAAGGCAA GGCAATGTTG
701 TAATCGCCGG ACACGGTTTG GATGCCCGTG ATACCGATTT CACACGTATT
751 CTCAGTTATC ATTCCAAAAT TGATGCACCC GTATGGGGAC AAGATGTTGC
801 TGTCGTCGCG GGACAAAACG ATGTGGTCGC AACAGGTAAT GCACATTCGC
851 CTATTCTCAA TAATGCTGCT GCCAATACGT CAAACAATAC AGCCAACAAC
901 GGCACACATA TCCCTTTATT TGCGATTGAT ACAGGCAAAT TAGGAGGTAT
951 GTATGCCAAC AAAATCACCT TGATCAGTAC GGCCGAGCAA GCAGGCATT C
1001 GTAATCAAGG GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA
1051 AATGGCCGTT TAGTCAATAG TGGCACGATG GCTGCCGCCA ATGCGAAAGA
1101 TACGGATAAT ACAGCGGAAC ACAAGTCAA TATCCGCAGT CAGGGCGTTG
1151 AAAACAGCGG TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAG
1201 TCGATTCAAA AACTGGCAC ATTATTGTCC TCAGGCGAAA TATTGATTCA
1251 CAATTTCGGG AGCCTGAAAA ATGAAACATC AGGCACATT GAAGCGGCTC
1301 GTTTGGCTAT TGATACCGAC AACTTAATA ATCAAGGCAA ACTCTCTCAA
1351 ACAGGTTTCA AAAAATCCA TATTGATGCA CAAGGCAAAA TGGATAACCG
1401 TGGCCGCGAT GGTTTACAAG ATACCGCACC AACC GCGTCA AATGGTTCAA
1451 GCAATCAAAC CGGCAATAGT TACAATGCAT CTTTCCATT C ATCCACTACC
1501 ACACCAACAA CGGCAACAGG TACGGGTACT GCAACCGTTT CTATATCAAA
1551 CATAATCGCG CCTACCTTTG CTGATGGGAC AATTGCGACT CATGGTGCAC
1601 TGGATAATTC AGGCAGTATT ATTGCCAATG GTCAAACAGA TGTTAGTGCG
1651 CAACAAGGTT TAAATAATGC AGGACAAATA GACATTCATC AGTTAAATGC
1701 AAAAGGTTTC GCGTTTGACA ATCACAATGG AACAAATTATC AGTGTATGCG
1751 TCCACATTCA AGCCGGCAGC CTGAATAATC AAAATGGCAA CATCAACA
1801 CGCCAACAGT TAGAGATTGA AACC GATCAA CTGGATAACG CTCATGGCAA
1851 GTTATTATCA GCAGAAATAG CGGATTTAGC CGTTTCAGGC AGCCTGAACA
1901 ATCAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT TCACGATGGT
1951 CAGCAATCTA CCGCTGTCAT TGATAATACG AATGGCACGA TACAATCAGG
2001 CCGTGATGTT GCTATTCAGG CAAAATCGTT ATCCAACAAC GGCACACTTG
2051 CCGCTGATAA TAACTGGAT ATTGCGTTAC AAGATGATTT TTATGTAGAA
2101 CGCAATATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC GAGGCAGCCT
2151 GAAAAATTCA CATACTTTGC AAGCAGGAAA ACGCATTCCG ATTAAAGCAA
2201 ATAACCTTGA TAATGCAGCA CAAGGCAACA TTCAATCCGG CGGTACGACA
2251 GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA TTGACGGACA
2301 ACAAACAAA ATCCAAGCCG GGCAAATGAA TAATATCGGT ACAGGTCCGA
2351 TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA CAATCAAGAT
2401 GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGTGAAAACC TGAATTTAGG
2451 CATCGGACAA TTAAACAACC GTGAAAACAG TCTGATTTAC AGCGGTAACG
2501 ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGGCCAAGC CACAGGCAAA
2551 GCCCAAAGGA TACAATATGC CCGCGCAACC ATTGAAGCTG CAGGCAAAAT
2601 GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT TTGAAAACGC
2651 AGTTGGTAGA AACAGGGCGC GAGCATATTG TTGATTACGA AGCATTTGGA
2701 CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG GCTGGTCTGT
2751 CTATAACGAT GAATCAGACC ACTTACGCAC CCCTGATGGA GCGGCGCATG
2801 AAAATTGGCA TAAATACGAT TATGAAAAAG TCACCAAAAA AACCCAAGTT
2851 ACCCAAAC TG CAGCCAA AATCATTTCA GGTAATGATT TAACCATTGA
2901 TGGTAAAGAA GTATTTAATA CCGATAGCCA AATCATTGCT GGTGGCAATC
2951 TCATTGTACA AACAGAAAAA GACGGTTTGC ATAACGAGCA AACCTTTGGC

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3001 GAAAAGAAAG TATTCAGTGA AAATGGCAAA TTACACAGCT ATTGGCGTGA  
3051 GAAACATAAA GGACGAGACT CAACGGGACA TAGCGAACAA AATTACACTT  
3101 TGCCGGAGGA AATCACACGC AACATTTCAC TGGGTTTCATT TGCCTATGAA  
3151 TCGCATCGCA AAGCATTAAAG CCATCATGCG CCCAGCCAAG GCACTGAGTT  
3201 GCCGCAAAGC AACGGTATTT CGCTACCCTA TACGTCCAAT TCTTTTACCC  
3251 CATTACCCAG CAGCAGCTTA TACATTATCA ATCCTGTCAA TAAAGGCTAT  
3301 CTTGTTGAAA CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGGGGTAG  
3351 TGACTATATG CTGGACAGCC TCAAACCTAGA CCCAAACAAT TTACATAAAC  
3401 GTTTGGGTGA TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA  
3451 GAGCTGACAG GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA  
3501 ATTTAAAGCC TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC  
3551 TCAGCGTTGG CATTGCATTA AGTGCCGAGC AAGTAGCGCA ACTGACCAGC  
3601 GATATTGTTT GGTGGGTACA AAAAGAAAGT AAGCTTCCTG ATGGCGGCAC  
3651 ACAAACCGTA TTGGTGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGACA  
3701 TAGACGGTAA AGGTGCATTG TTGTACGGCA GCAATACACA AATCAATGTT  
3751 TCAGGCAGCC TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT  
3801 TATCAATACC GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA  
3851 AATCAGCGGT TACGGCCACA CAAGACATCA ATAATATTGG CGGCATGCTT  
3901 TCTGCCGAAC AGACATTATT GCTCAACGCA GGCAACAACA TCAACAGCCA  
3951 AAGCACCACC GCCAGCAGTC AAAATACACA AGGCAGCAGC ACCTACCTAG  
4001 ACCGAATGGC AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA  
4051 GCGCAGGCAG GAAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA  
4101 ATCAGAGCAA GGGCAAACCC GGCTGCAAGC AGGGCGCGAC ATTAACCTAG  
4151 ATACGGTACA AACCAGCAA CATCAAGCAA CCCATTTTGA TGCCGATAAC  
4201 CATGTTATTG GCGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA  
4251 AGGCGATGTT ACCCTATTGT CAGGGAATAA CCTCAATGCC AAAGCTGCCG  
4301 AAGTCAGCAG CGCAAACGGT ACACCTCGTG TGTCTGCCAA AAATGACATC  
4351 AACATCAGCG CAGGCATCAA CACGACCCAT GTTGATGATG CGTCCAAACA  
4401 CACAGGCAGA AGCGGTGGTG GCAATAAATT AGTCATTACC GATAAAGCCC  
4451 AAAGTCATCA CGAAACCGCC CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT  
4501 GTATTGCAGG CAGGAAACGA TGCCAACATC CTTGGCAGCA ATGTTATTTC  
4551 CGCAATGCGC ACCCAGATTG AAGCAGGCAA TCATGTTTCG ATTGGTACAA  
4601 CCCAAACTCA AAGCCAAAGC GAAACCTATC ATCAAACCCA GAAATCAGGA  
4651 TTGATGAGTG CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA  
4701 AGAAAACCAA TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCT  
4751 TGAAAGGCGA TACCACCATT GTTGACGGCA AACACTACGA ACAAATCGGC  
4801 AGTACCGTTT CCAGCCCGGA AGGCAACAAT ACCATCTATG CCCAAAGCAT  
4851 AGACATTCAA GCGGCACACA ACAAATTAAA CAGTAATACC ACCCAAACCT  
4901 ATGAACAAAA AGGCCTAACG GTGGCATTCA GTTCGCCCCG TACCGATTG  
4951 GCACAACAAG CGATTGCCGT AGCACAAGC AGCAAACAAG TCGGACAAAG  
5001 CAAAAACGAC CGCGTTAATG CCATGGCGGC TGCCAATGCA GGCTGGCAAG  
5051 CCTATCAAAC AGGTAAGAGT GCACAAAACCT TAGCCAATGG TACAACCAAT  
5101 GCCAAACAAG TCAGCATCTC CATAACCTAC GCGGAACAGC AAAACCGACA  
5151 AACCACCCAA GTTCAAGCCA ATCAAGCCCA AGCGAGTCAA ATTCAAGCAG  
5201 GTGGTAAAC CACATTAATC GCCACAGGCG CAGCAGAACA ATCCAATATC  
5251 AACATCGCAG GCTCAGATGT TGCCGGCAAA GCAGGCACAA TCCTGATTGC  
5301 CGATAACGAC ATCACACTCC AATCAGCCGA GCAAAGCAAT ACCGAACGCG  
5351 GCCAAAACAA ATCGGCAGGC TGGAACGCAG GTGCTGCCGT ATCATTGGGA  
5401 CAAGGAGGCT GGTCAATAGG CGTTACCGCA GGCGGCAATG TCGGCAAAGG  
5451 CTACGGCAAT GCGACAGCA TCACCCACCG CCATAGCCAT ATCGGCGACA  
5501 AAGGCAGCCA AACCTTATC CAAAGCGGTG GCGACACTAC CATCAAAGGC  
5551 GCGCAAGTAC GCGCAAAGG CGTACAAGTC AATGCCAAAA ACCTAAGTAT  
5601 TCAAAGCGTA CAAGATAGAG AAACCTATCA AAGCAAACAA CAAACGCCA  
5651 GTGCACAAGT TACGTAGGT TATGGCTTCA GTGCCGGTGC CGATTACAGC  
5701 CAAAGCAAAA TCCGAGCCGA CCATGTTTCA GTAACCGAGC AAAGCGGTAT  
5751 TTAGTCCGGA GAAGACGGCT ATCAAATCAA GGTCGGAAAC CATAAGACC  
5801 TCAAAGGCGG CATCATCACC AGTACCCAAA GCGCAGAAGA CAAGGGTAAA  
5851 AACCGCTTTC AGACGGCCAC CCTCACCCAT AGCGACATCA AAAACCCACG  
5901 CCAATACAAA GGCAGAAAGT TTGGATTGGG CGCAAGTGCG TCCATAAGCG  
5951 GCAAAAACACT GGGACAGGGC GCACAAAATA AACCTCAAAA CAAACACCTG  
6001 ACAAGCGTAG CCGATAAAAA CAGCGCAAGT TCATCAGTGG GTTATGGCAG  
6051 CGACAGCGAC AGTCAAAGCA GCATCACAAA AAGCGGCATC AACACCCGCA

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6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
6151 GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
6201 CGAACGACAT TCGGGCAGCT TGAAGAACAC CTTCAACAAA GAAGCGGTGC
6251 AAAGTGAAC TGGATTACAA AGAACCCTCA GCCAAGATTT TAGTAAAAAT
6301 GTTCAACAAG CCAATACCGA GATTAAACCA CATTTAGACA AACTCAAAGC
6351 AGACAAAGAA GCAGCCGAAA CAGCAGCAGC CGAGGCATTA GCCAATGGCG
6401 ATATGGAAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TGCGGCAGCA
6451 AAAGCAGATA ATTGGCAACA AGGCAAAGTC ATTCTCAACA TGTTAGCCTC
6501 AGGTTTAGCT GCGCCGACCC AAAGCGGAGC GGGCATCGCT GCGGCTACCG
6551 CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCACTTTAA AGATTAGCC
6601 GGTCAAACG CGAATGGTAA ACTAACC GCC AGTCAAGAAA CCGCACACGT
6651 TCTTGCCAC GCGGTATTAG GAGCAGCGGT TGCCGCAGTA GGAGACAACA
6701 ATGCTCTAGC AGGAGCATTG AGTGCGGCGC GGTCCGGAAGC GGCTGCGCCT
6751 TACATCAGCA AATGGTTATA CCGCAAAGAA AAAGGAAGCG ACTTAACGGC
6801 GGAAGAGAAA GAGACTGTAA CAGCGATTAC AAATGTATTG GGTACGGCTA
6851 CGGGTGCGGC AGTCGGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
6901 AATGCGCAA GTGCGGTGGA GAATAATGAT ACTGTAGAGC AAGTGAAATT
6951 TGCTCTTAGC CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
7001 ATCCTGGCTC TACATTAGAG CCTAATATTT CAACAATTGC TTCAACTTTT
7051 CAATTAAATT TATTTCTTAA TAGTGAATTT GGTGGTGAAG GTGGAGTTGG
7101 CAATGCATTC AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTG
7151 GCAAAGATAT TGCTGTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAATACCA
7301 ATAGGTAA CACAAAAGAG TTAGTTGGAT TAATTCTGGA AACTTATAAA
7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
7401 TGTAAGAAAA AGATTATCTG AAAAAGATTA CCAGAATACA AGCAATATAT
7451 TGATTCACCT AGATAATACT GGTGCCGGAT TAAAATTCA GCAGAGGAGA
7501 AAACAAATCA GAGCACAAT TTCAGCCAGA CAATGGAGAA GATAA

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This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pep..

```

1 MNKTLRYRVIF NRKRGAVVAV AETTKREGKS CADSDSGSAH VKSVPFQTTH
51 APVCRSNIFS FSLLGFSLCL AVGTANIAFA DGIIADKAAP KTQQATILQT
101 GNGIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRSN TQTQLGGWIQ
151 GNPWLARGEA RVVVNQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
201 GGFNASRAT LTTGQPQYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
251 LSYHSKIDAP VWGQDVRVVA QQNDVVATGN AHSPILNNA ANTSNNTANN
301 GTHIPLFAID TGKLGMYAN KITLISTAEQ AGIRNQQLF ASSGNVAIDA
351 NGRLVNSGTM AAANAKDNDN TAEHKVNIRS QGVNSGTAV SQQGTQIHSQ
401 SIQNTGTLLS SGEILIHNSG SLKNETSGTI EAARLAIDTD TLNNQKLSQ
451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSSTT
501 TPPTATGTGT ATVSISNITA PTFADGTIRT HGALDMSGSI IANGQTDVSA
551 QQGLNNAGQI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
601 RQQLIEITDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNQQLIHDG
651 QQSTAVIDNT NGTIQSGRDV AIQAKSLSN GTLAADNKLD IALQDDFYVE
701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
751 DIGTQHNLTN RGLIDGQQTK IQAGQMNNIG TGRIYGDNIA IAATRLDNQD
801 ENGTGAAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGA LDTNGQATGK
851 AQRHINAGAT IEAAGKMLRG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG
901 RHELLREGTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
951 TQTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEEITR NISLGSFAYE
1051 SHRKALSHHA PSQGTQLPQS NGISLPYTSN SFTPLPSSSL YIINPVNKGY
1101 LVETDPRFAN YRQWLGSDDY LDSLKLDPNN LHKRLGDGYY EQRLINEQIA
1151 ELTGHRRLDG YQNDEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
1201 DIVWLQKEV KLPDGGTQTV LVPQYVVRVK NGDIDKGAL LSGSNTQINV
1251 SGSLKNSGTI AGRNALINT DTLDNIGGRI HAQKSAVTAT QDINNIGGML
1301 SAEQTLNNA GNNINSQSTT ASSQNTQGS TYLDRMAGIY ITGKEGVLA
1351 AQAGKDINII AGQISNQSEQ QQTRLQAGRD INLDTVQTSK HQATHFDADN
1401 HVIRGSTNEV GSSIQTGKDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
1451 NISAGINTTH VDDASKHTGR SGGGNKLVIT DKAQSHHETA QSTFEGKQV
1501 VLQAGNDANI LGSNVISDNG TQIQAGNHVR IGTTQTQSQS ETYHQTQKSG

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855

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1551 LMSAGIGFTI GSKTNTQENQ SQSNEHTGST VGSCLKGDTTI VAGKHYEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNKLNST TQTYEQKGLT VAFSSPVTDL
1651 AQQAIAVAQS SKQVQSKND RVNAMAANA GWQAYQTGKS AQLANGTTN
1701 AKQVSISITY GEQQNRQTTQ VQANQAQASQ IQAGGKTTLI ATGAAEQSNI
1751 NIAGSDVAGK AGTILIADND ITLQSAEQSN TERGQNKASG WNAGAAVSFG
1801 QGGWSLGVTA GGNVKGKGYGN GDSITHRSH IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDKKG
1951 NRFQATLTH SDIKNHSQYK GESFGLGASA SISGKTLGQG AONKPQNKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQQANTEINQ HLDKLGADKE AAETAAEAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQGGKV ILNMLASGLA APTQSGAGIA AATASPAVSY AIGQHFCDLA
2201 QONANGKLT SAQTAHVLAH AVLGAAVA AV GDNNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTAITNVL GTATGAAVGN SATDAAQGS
2301 NAQSAVENND TVEQVKFALR HPRIAIAIGS VHKDPGSTLE PNISTIASTF
2351 QLNLFNPNSEF GEGGVGNF RHVLWQATIT REFGKDIQV VGNSHESGK
2401 INYSIRRLS LDKADEMIDQ LNNEIGREIA LNTNRLNTKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILHLDNT GAGFKIQRR
2501 KQIRAQISAR QWRR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

```

              10      20      30      40      50
g563.pep      MNKTLRYVIFNRKRGAVVAVAETTKREGKSCADSGSGSVYKVSFIPTH-----SKAFC
              |||||
m563.pep      MNKTLRYVIFNRKRGAVVAVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
              10      20      30      40      50      60

              60      70      80      90      100     110
g563.pep      FSALGFSLCLALGTVNIAFADGIIITDKAAPKTQQATILQTGNGIPQVNIQTPTSAGVSVN
              |||||
m563.pep      FSLGFLSLCLAVGTANIAFADGIIADKAAPKTQQATILQTGNGIPQVNIQTPTSAGVSVN
              70      80      90      100     110     120

              120     130     140     150     160     170
g563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE
              |||||
m563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQMNGYIE
              130     140     150     160     170     180

              180     190     200     210     220     230
g563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIRQGNVVIAGHGL
              |||||
m563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLSGFKIRQGNVVIAGHGL
              190     200     210     220     230     240

              240
g563.pep      DARDTDFTRIL-----
              |||||
m563.pep      DARDTDFTRILSYHSKIDAPVWGQDVRVVAGQNDVVATGNAHSPILNNAANTSNTANN
              250     260     270     280     290     300

              250     260     270     280     290
g563.pep      -----LYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGTM
              :|||
m563.pep      GTHIPLFAIDTGKLGMYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGTM
              310     320     330     340     350     360

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856

	300	310	320	330	340
g563 . pep	AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----				
	::  :				
m563 . pep	AAANAKDNTDAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLSSGEILIHNSG				
	370	380	390	400	410
	420				
g563 . pep	-----				
m563 . pep	SLKNETSGTIEAARLAIDTDTLNNQGKLSQTGSQKLHIDAQGMNDRGRMGLQDTAPTAS				
	430	440	450	460	470
	480				
g563 . pep	-----				
m563 . pep	NGSSNQTGNSYNASFHSSTTTPTTATGTGTATVSIENITAPTADFAGTIRTHGALDNSGSI				
	490	500	510	520	530
	540				
g563 . pep	-----				
m563 . pep	IANGQTDVSAQQGLNNAQGIDIHQLNAKGSAFDNHNGTIIISDAVHIQAGSLNNQNGNITT				
	550	560	570	580	590
	600				
			350	360	370
g563 . pep	-----EDLAVSGSLNNQNGEIATNQQLIIHDGQQSTVVIDNT				
m563 . pep	RQOLEIETDQLDNAHGKLLSAEIAIDLAVSGSLNNQNGEIATNQQLIIHDGQQSTAVIDNT				
	610	620	630	640	650
	660				
	390	400	410	420	430
g563 . pep	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERKIVAGNELSLSTRGSLKNS				
m563 . pep	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNS				
	670	680	690	700	710
	720				
	450	460	470	480	490
g563 . pep	HTLQAGKRIRIKANNLDNAVQGNIQSGGTTDIGTQHNLTNRGLIDGQQTKIQAGQMNNIG				
m563 . pep	HTLQAGKRIRIKANNLDNAAQGNIQSGGTTDIGTQHNLTNRGLIDGQQTKIQAGQMNNIG				
	730	740	750	760	770
	780				
	510	520	530	540	550
g563 . pep	TGRIYGDNIAIAATRLDNQDENG TGAAIAARENLNLGIEQLNNREN SLIYSGNDMAVGGA				
m563 . pep	TGRIYGDNIAIAATRLDNQDENG TGAAIAARENLNLGIGQLNNREN SLIYSGNDMAVGGA				
	790	800	810	820	830
	840				
	570	580	590	600	610
g563 . pep	LDTNDQATGKAQRIHNAGAIIEAAGKMRLGV EKLHNTNEHLKTQLVETGRERIVDYEAFG				
m563 . pep	LDTNGQATGKAQRIHNAGATIEAAGKMRLGV EKLHNTNEHLKTQLVETGREHIVDYEAFG				
	850	860	870	880	890
	900				
	630	640	650	660	670
g563 . pep	RHELLREGTQHELGW FVYNNESDHLRTPDGV AHENWHKYDY EKVTQETQVGTAPAKIIA				
m563 . pep	RHELLREGTQHELGWSVYNDES DHLRTPDGA AHENWHKYDY EKVTQKTQVGTAPAKIIS				
	910	920	930	940	950
	960				
	690	700	710	720	730
	740				



857

g563.pep	GSDLIIDSKAVFNSDSRIIAGGQLLVQTEKDGLHNEQTFGEKKVFSSENGKLHNYWRARRK
m563.pep	GNDLTIDGKEVFNTDSQIIAGGNLIVQTEKDGLHNEQTFGEKKVFSSENGKLHSYWREKHK
	970 980 990 1000 1010 1020
g563.pep	GHDETGHREQNYTLPEEITRDISLGSFAYESHKALSRHAPSOGTELPQSNRDNIRTAKS
m563.pep	GRDSTGHSEQNYTLPEEITRNISLGSFAYESHKALSHHAPSOGTELPQSN-----
	1030 1040 1050 1060 1070
g563.pep	NGISLPYTPNSFTPLPGSSLYIINPANKGYLVETDPRFANYRQWLGS DYMLGSLKLDPNN
m563.pep	-GISLPYTSNSFTPLPSSSLYIINPVNKG YLVETDPRFANYRQWLGS DYMLDLSKLDPNN
	1080 1090 1100 1110 1120 1130
g563.pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
m563.pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
	1140 1150 1160 1170 1180 1190
g563.pep	SAEQAAQLTSDIVWLQKEVKLPDGGTQTVLMPQVYVRVKNGGIDGKGALLSGSNTQINV
m563.pep	SAEQVAQLTSDIVWLQKEVKLPDGGTQTVLVPQVYVRVKNGDIDGKGALLSGSNTQINV
	1200 1210 1220 1230 1240 1250
g563.pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQSAVTATQDINNIGGILSAEQTLLLNA
m563.pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQSAVTATQDINNIGGMLSAEQTLLLNA
	1260 1270 1280 1290 1300 1310
g563.pep	GNNINNQSTAKSSQNAQGSSTYLDRMAGIYITGKEKGVLAQAQKDINI IAGQISNQSDQ
m563.pep	GNNINSQSTTASSQNTQGSSTYLDRMAGIYITGKEKGVLAQAQKDINI IAGQISNQSEQ
	1320 1330 1340 1350 1360 1370
g563.pep	GQTRLQAGR DINLDTVQTGKYQEIHFADADNHTIRGSTNEVGSSIQTKGDVTL LSGNNLNA
m563.pep	GQTRLQAGR DINLDTVQTSKHQATHFDADNHHVIRGSTNEVGSSIQTKGDVTL LSGNNLNA
	1380 1390 1400 1410 1420 1430
g563.pep	KAAEVGSAKGT LAVYAKNDITISSGIHAGQVDDASKHTGRSGGGNKLVI TDKAQSHHETA
m563.pep	KAAEVSSANGT LAVSAKNDINISAGINTTHVDDASKHTGRSGGGNKLVI TDKAQSHHETA
	1440 1450 1460 1470 1480 1490
g563.pep	QSSTFEKGQVVLQAGNDANILGSNVISDNGTRIQA GNHVRIGTTQTQSQSETYHQTKSG
m563.pep	QSSTFEKGQVVLQAGNDANILGSNVISDNGTQIQAGNHVRIGTTQTQSQSETYHQTKSG
	1500 1510 1520 1530 1540 1550
g563.pep	LMSAGIGFTIGSKTNTQENQSQSNEHTGSTVGS LKGDTTIVASKHYEQTGSNVSSPEGN
	1290 1300 1310 1320 1330 1340

[illegible]

859

	1950	1960	1970	1980	1990	2000
g563.pep	TASQETAHVLAHAVLGA AVAAAXGNNAPAGALGAGGSEAAAPIIGKWLYGKGDDGGSLSNAE					
m563.pep	TASQETAHVLAHAVLGA AVAAVGDNNALAGALSAGGSEAAAPYISKWLYGKEKGSDDLTAE					
	2210	2220	2230	2240	2250	2260

  

	2010	2020	2030	2040	2049	
g563.pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFQTASDFASSFSYPINMX					
m563.pep	EKETVTAITNVLTATGA AVGNSATDAAQGSLSNAQSAVENNDTVEQVKFALRHPRIATAI					
	2270	2280	2290	2300	2310	2320

  

m563.pep	GSVHKDPGSTLEPNISTIASTFQLNLFNSEFGGEGGVGNAFRHLVWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

m564.seq

1	ATGAACCGCA	CCCTGTACAA	AGTTGTATTT	AACAAACATC	GAAACTGCAT
51	GATAGCCGTT	GCTGAAAATG	CCAAACGCGA	GGGCAAAAAC	ACAGCCGACA
101	CCCAAGCTGT	AGGTATTTTG	CCAAATGATA	TTGCGGGCTT	TGCGGGTTTT
151	ATCCATTCTA	TCTCTGTTAT	CTCATTCTCC	CTTTCATTAC	TGCTCGGTTC
201	TGCCCTTATC	CTGACTTCTT	CTTCTGCTAC	TGCCCAAGGT	ATCGTTGCCG
251	ACAAATCCGC	ACCTGCACAG	CAACAGCCTA	CCATCCTGCA	AACAGGTAAC
301	GGCATACCGC	AAGTCAATAT	TCAAACCCCT	ACTTCGGCAG	GGGTTTCTGT
351	TAATCAATAC	GCCCAGTTTG	ATGTGGGTAA	TCGCGGGGCG	ATTTTAAACA
401	ACAGTCGCAG	CAACACCCAA	ACACAGCTAG	GCGGTTGGAT	TCAAGGCAAT
451	CCTTGGTTGG	CAAGGGGCGA	AGCACGTGTG	GTTGTAAACC	AAATCAACAG
501	CAGCCATTCT	TCACAACTGA	ATGGCTATAT	TGAAGTGGGC	GGACGACGTG
551	CAGAAAGTCG	TATTGCCAAT	CCGGCAGGGA	TTGCAGTCAA	TGGTGGTGGT
601	TTTATCAATG	CTTCCCGTGC	CACTTTGACG	ACAGCCCAAC	CGCAATATCA
651	AGCAGGAGAC	CTTAGCGGCT	TTAAGATAAG	GCAAGGCAAT	GTTGTAATCG
701	CCGGACACGG	TTTGGATGCA	CGTGATACCG	ATTACACACG	TATTCTCAGT
751	TATCATTTCA	AAATTGATGC	ACCCGTATGG	GGACAAGATG	TTCGTGTCGT
801	CGCGGGACAA	AACGATGTGG	CCGCAACAGG	TGATGCACAT	TCGCCTATTC
851	TCAATAATGC	TGCTGCCAAT	ACGTCAAACA	ATACAGCCAA	CAACGGCACA
901	CATATCCCTT	TATTTGCGAT	TGATACAGGC	AAATTAGGAG	GTATGTATGC
951	CAACAAAATC	ACCTTGATCA	GTACGGTCGA	GCAAGCAGGC	ATTCGTAATC
1001	AAGGGCAATG	GTTTGCCCTCA	GCCGGCAATG	TGGCAGTGAA	TGCTGAGGGT
1051	AACTGGTCA	ACACGGGCAT	GATTGCAGCG	ACGGGAGAAA	ATCATGCGGT
1101	TTCATTTCAT	GCCCGCAATG	TTCATAATAG	CGGTACGGTT	GCCTCACAGG
1151	ATGATGCCAA	TATTCACAGC	CAGACGCTGG	ACAATTCAGG	TACGGTCTTA
1201	TCCTCAGGTC	GATTGACTGT	TCGTAATTTA	GGCCGTCTGA	AAAACCAAAA
1251	CAACGGTACG	ATCCAGGCTG	CCCGCTTAGA	TATGTCAACA	GGTGGTTTGG
1301	ATAACACAGG	TAATATTACT	CAAACAGGTT	CACAAGCATT	GGATTTGGTA
1351	TCTGCCGGCA	AATTCGATAA	CAGTGGAAG	ATTGGTGTA	GTGACGTTCC
1401	ACAGACCGGT	TTGAATCCCA	ATCCATCAGT	CATACCACAG	ATTCCGAGTA
1451	CTGCAACAGG	TTCAGGCAGC	AGCACTGTCT	CGGTATCTAA	GCCTGGTTCA
1501	AACAATCCCG	TTTCACCTAC	AGCACCTGCA	AAAAACTACG	CCGTAGGACG
1551	CATTCAAACA	ACAGGAGCAT	TTGACAATGC	AGGATCAATT	AATGCGGGTG
1601	GGCAAATTGA	CATTGCCGCC	CAAAACGGTT	TGGGAAATTC	GGGTAGTCTG
1651	AATGCGGCTA	AACTACGAGT	ATCAGGCGAT	TCATTTAACA	ATACGGTAAA
1701	AGGCAAACTC	CAGGCACACG	ATCTGGCTGT	TAACACTCAA	ACTGCTAAAA
1751	ACAGCGGTCA	CTTATTAATC	CAAACCGGCA	AGATTGATAA	CCGTGAAGTG
1801	CATAATGCCG	GAGAAATTGC	CGCCAACAAT	CTGACACTCA	TTCATTCCGG
1851	CCGCTTGAGC	AATGATAAAA	AAGGCAATAT	TCGAGCTGCA	CATTACAGC
1901	TTGATACCGC	CGGTTTACAT	AATGCAGGTA	ACATTCTTGC	CGATAGTGGA
1951	ACCGTTACCA	CCAAGAATAA	TCTTCGCAAT	ACAGGAAAAG	TTTCTGTTGC
2001	ACGACTGAAT	ACCGAAGGTC	AGACTCTAGA	TAATACGCGC	GGACGTATAG
2051	AGGCTGAAAC	GGTTAACATC	CAAAGTCAGC	AACTGACTAA	CCAAAGCGGC
2101	CATATTACTG	CTACCGAACA	ACTGACTATC	AATAGTCGAA	ATGTAGACAA
2151	CCAAAACGGC	AAACTCCTAT	CTGCAAACCA	AGCACAATTA	GCTGTTTCAG
2201	ACGGCCTATA	CAACCAACAT	GGTGAAATTG	CCACCAACCG	GCAGTTGTCT

2251 ATTACAGATA AAAATCAAAA CACTTTGGCG TTAAACAATG CGGATGGCAC  
2301 GATTCAATCT GCCGGTAATG TATCGCTACA AGCCAAATCA CTCGCCAACA  
2351 ATGGCACATT AACAGCCGGT AACAACTGG ATATTGCTTT GACGGACGAT  
2401 TTCGTCGTAG AGCGCGACCT CACTGCAGGC AAACAATTAA ATCTAAGCAT  
2451 AAAAGGCCGT CTGAAAAATA CCCATACCCT ACAAGCAGGC CATACGCTCA  
2501 AACTCAATGC CGGCAATATA GATAACCAAG TTACAGGCAA AATTATTGGT  
2551 GGAGAACAAA CGGACATCAC ATCCGAACAG CATGTTGACA ACAGGGGCTT  
2601 GATCAACAGC GACGGTTTGA CCCACATCGG TGCAGGTCAA ACCCTGACCA  
2651 ACACCGGGAC AGGCAAAATC TATGGCAACC ATATTGCCCT GGACGCGCAA  
2701 ATACTGCTTA ACCGGGAAGA AACGACGGAA GGCAGTACCA AAGCGGGGGC  
2751 AATAGCTGCA AGGAAACGTT TGGATATTGG AGCGAAAGAG ATTCTAATCC  
2801 AAGAAGGTGC CCTACTATCC AGCGAAGGTA TTTTGGCCGT AgGTAATCGA  
2851 CTGGATGAAC AACATCATGC GGCAGGCATG GCCGATACCT TTGTTAATGG  
2901 CAGTCCGGT TTGGAAGTAC AAGGTGATGC ATTGATGTCC GTTCGGAATA  
2951 TGCAGAAAT CAATAATCAC TTTAAACAG AGACATACTT AGCCAAAGCG  
3001 GAAAAGCAAG TCCGCGACTA CACCGTACTG GGGCAAAATA CCTACTATCA  
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3101 CTAATGCTAC GTTCCATTTA AAAAATGGTT CTCGTATTGA GGCCAACCAA  
3151 TGGCATGTCC GAGACTACCA CATCGAGACT TATAAAGAAC GCATCATCGA  
3201 AAACCGGCCG GCACACATTA CTGTGGGCGG TGATTGACT GCCTCAGGTC  
3251 AAAATTGGCT GAACAAGAC AGCCGGATTG TAGTAGGCGG GCGTATTATC  
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3351 AGGTGCGACA GATGCTGTGC GCACACAGTG GGATTGAGT ACAAAAAAAG  
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3451 CTTTACCATG ATACCCAAT ATTTACCCAC GACTTCGACA CGCCTGTATC  
3501 CGTCATCCAA CAGAATGCCG CCTCCCTTC CTTTCAACCC GCCGCATCTG  
3551 CAATCAAAT GATTGACGGA GTATCCACGG CAGCCGTCAA TGGTCAGCGC  
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3701 AAACCGATCC TCAATTGCA GACTACCGCC GCTGGTTGGG CAGCGATAC  
3751 ATGTTGCAAC AACTGCAATT GGACACCAAT CATCTACACA AACGGCTTGG  
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3901 GATCTGATGG ACAACGGCCT TACTGCTGCC AAAACATTCT GTCTCAGCCC  
3951 AGGTATCGCC TTGAGTGCAG AGCAAGTTGC CCGCTTAACT TCAGATATCG  
4001 TTTGGATGGA AAATCAAACC GTCACCTGT CTGACGGTTC GACTCAAACC  
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4151 GCAACCTGAC TAACAGCGGT ACCATTGCGG GCGGACAGGC CGTACTATC  
4201 CAGGCACGGA ATATTAACAG CAACGGTAAC ATTCAAGCCG ACCAAATCGG  
4251 CTTAAAAGCT GAAAAAAGTA TCAATATCGA CGGCGGGCAG GTACAAGCAG  
4301 GCAGACTGCT GACTGCCCAA GCGCAAAATA TCAACCTTAA CGGTACAACC  
4351 CAAACTTCCG GTAATGAACG TAACGGCAAT ACCGCCATCG ATCGTATGGC  
4401 CGGCATTAAC GTGGTCGGAA GCCATACTGA ACAAGTAGAT AACAGAACTT  
4451 CAGACGGCAT CCTATCCCTG CATGCCAGCA ACGATATCAA CCTCAATGCG  
4501 GCCACCGTCT CTAACCAAGT TAAAGACGGC ACTACCCAAA TTACCGCCGG  
4551 CAATAATCTC AACCTCGGCA CCATCCGTAC CGAACATCGC GAAGCCTATG  
4601 GTACATTAGA TGACGAGAAC CATCGCCATG TCCGCCAAAG TACCGAAGTC  
4651 GGCAGCAGTA TCCGCACGCA AAACGGCGCA CTGCTTAGAG CCGGTAACGA  
4701 CTTAAAAATC CGCCAAGGCG AACTGGAGGC CGAAGAAGGC AAAACCGTCC  
4751 TTGCCGCGAG ACGTGATGTC ACTATCAGCG AAGGACGCCA AATAACCGAA  
4801 CTGGATACCT CGGTAAGCGG AAAAAAGCAA GGCATCCTTT CCAGTACCAA  
4851 AACACACGAC CGCTACCGCT TCAGTCATGA TGAAGCAGTC GGCAGCAACA  
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5051 AGAGCAAAAA ATCAGGCGTC ATGGGTACTG GCGGATTGGG CTTTACTATC  
5101 GGTAAACCGA AAATACCGA TGACACTGAT CGTACCAATA TTGTCCATAC  
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5251 ACCGTACAG CCAAAAGCAT AGATGTAGAG TTCGCAACA ACCGGTATGC  
5301 CACTGACTAC GCCCATACCC AGGAACAAAA AGGCCTTACC GTCGCCCTCA  
5351 ATGTCCCGGT TGTCCAAGCT GCACAAAAT TCATACAAGC AGCCCAAAAT  
5401 GTGGGCAAAA GTAAAAATA ACGCGTTAAT GCCATGGCTG CAGCCAAATG  
5451 TGCAATGGCAG AGTTATCAAG CAACCAACA AATGCAACA TTTGCTCCAA  
5501 GCAGCAGTGC GGGACAAGGT CAAAACAACA ATCAAAGCCC CAGTATCAGT

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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CCGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAGG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAAA AACAAAAGCA
5801 GTGGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
5851 GGAATTACCG CCGGAGGAAA TATCGGTAAA GGTAAAGAGC AAGGGGGAAG
5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
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6051 TGAACCTAT CAGAGCAAAC AGCAAAACGG CAATGTCCAA GTTACTGTCTG
6101 GTTACGGATT CAGTGAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAACCCAC AGCCGCTACG AAGGCAGAAG
6351 CTTCGGCATA GCGGCGAGTT TCGACCTGAA CGGCGGCTGG GACGGCAGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
6451 TACGGCAGCG ACGGAGACAG CAAAACAGC ACCACCCGCA GCGGCGTCAA
6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACAG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCGG CATCGACACC
6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAAAACAGT TCGACAAAGA
6651 CGCGGTCGCC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCC
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCCG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGCG TGAGGCCGCA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAAA AGCCGCCTTC CGGCGATCCC
6851 TCGGCCAAGT AAACGCCTAT CTGCGCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
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7001 TTGCCGCACC GTATTGGAC AAAGCGGCGG AAAACCTCGG TCCGCGGGCG
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7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAAGTTGG AACAAATAGG
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7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
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7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
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7651 ACCGGCAGCG ATCCCTTATT GCGGGGTGCG GGGGAATATCC GTATCCCTGC
7701 AAACGGCAAT GTTGCGAAGG GGGACAGGAT TCCGGATACG GCATTGGTCA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

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1  MNRTLYKVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51  IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QOPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIOQN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQFPYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW QGDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWQFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVSQVPTQG LNPNPVPIQ IPSTATSGS STVSVPKPS
501 NNPVSPAPFA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL
551 NAAKLRVSGD SFNNTVKGKL QAHD LAVNTQ TAKNSGHLT QTGKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILADSG
651 TVTTKNNLRN TGKVSVARLN TEGQTLNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVNQNG KLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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901	ILLNREETTE	GSTKAGAIAA	RKRLDIGAKE	IHNQEGALLS	SEGIFAVGNR
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1001	EKQVRDYHTV	GKNTYYQAGK	DGLFDNSQSQ	KDQTTATFHL	KNGSRLEANQ
1051	WHVRDYHIET	YKERIENRNP	AHITVYGDLT	ASQGNWLKND	SRIVVQGRII
1101	TDDLNQKEIT	NQSTTGKGR	DVAGTQWDSV	TKKGWYSGRK	RQRRTERNHT
1151	PYHDTQLFTH	DFDTPVSVIQ	QNAASPSFQP	AASAIKLIDG	VSTAAVNGQR
1201	IHTGNVSLTN	NATVTLPNSS	LYTTHPDNKG	WLVTEDPQFA	DYRRWLGSFY
1251	MLQQQLDLTN	HLHKRLGDGY	YEQKLVNEQI	HQLTGYRRLD	GYRSDDEEQD
1301	ALMDNGLTAA	KTFGLTPGIA	LSAEQVARLT	SDIVWMENQT	VLTSDBGSTQT
1351	VLVPKVYALA	RKGDNLNTSG	LISAEQVLLK	LQNGNLNTSG	TIAGRQAVLI
1401	QARNINSNGN	IQADQIGLKA	EKSINDIGGG	VQAGRLLTAL	QASININLGTT
1451	QTSNGERNNG	TAIDRMAGIN	VVGSHTEQVD	NRTSDGLISL	HASNDINLNA
1501	ATVSNQVKDG	TTQITAGNNL	NLGTIRTEHR	EAYGTLDDEN	HRHVRQSTEV
1551	GSSIRTQNGA	LLRAGNDLKI	RQGELEAEEG	KTVLAAGRDV	TISEGRQITE
1601	LDTSVSGKSG	GILSSTKTHD	RYRFSHDEAV	GSNIYGGKMI	VAAGQDINVR
1651	GSNLISDKGI	VLKAGKTHDI	STAHNRITYGN	EYHESKKSGV	MGTTGGLGFTI
1701	GNRKTDTDDT	RTNIVHTGSI	IGSLNGDTVT	VAGNRYRQTG	STVSSPEGRN
1751	TVTAKSIDVE	FANNRYATDY	AHTQEOKGLT	VALNVPVVQA	AQNFIQAAQN
1801	VGKSKNKRVN	AMAAANAAWQ	SYQATIQMQQ	FAPSSSAGQG	QNNNQSPSIS
1851	VSITYGEQKS	RNEQKRLHYE	AAASQIIGKG	QTTSLAATGS	EQSNINITGS
1901	DVIGHAGTAL	IADNHRKHQS	AKQDGSQESK	KTLSSWAGNV	AVKIGNGRFR
1951	GITAGNIGIK	GKEQGGSTTH	RHTHVGSTTG	KTTIRSGGDT	TLKGVQLIGK
2001	GIQADTRNLH	IESVQDTEYI	QSKQQGNVQ	VTVGYGFSAS	GSYRQSKVKA
2051	DHASVTGQSG	IYAGEDYQYI	KVRDNTLQKG	GIITSSQSAE	DKGNLNFQTA
2101	TLTASDIQNH	STRYEGRSFGI	GGSEFDLNGW	DGTVTDKQGR	PTDIRISPAAG
2151	YGSDBGSKNS	TRYSGVNTNH	IHITDEAGQL	ARTGRTAKET	EARIYTGIDT
2201	ETADQHSGHL	KNSFDKDAVA	KEINLQREVT	KEFGRNAAQA	VAAVADKLG
2251	TQSYERYQEA	RTLLEAELQN	TDSEAEKAAF	RASLGQVNAV	LAENQSRYDT
2301	WKEGGIGRSI	LHGAAGGLTT	GSLGKILAGG	GTSLAAPYLD	KAAENKSGFAG
2351	KAAVNALGGA	AIGYATCGSG	GAVGANVNDV	NNRQLHPKEM	ALADKYAEAL
2401	KREVEKREGR	KISSQEAMMR	IRRQILRWVD	KGSQDGYTDQ	SVISLIGMKG
2451	EDKALGYTWD	YRDYQAGARNP	TYNDPKLEE	YRRQDKPEYR	NLTWLHSGTV
2501	DTKIRQYGER	NEEFALNVAE	GLTSLVNP	RIKVPILAGI	RNLKNISKPT
2551	TGSDPPLLAGA	GNIRIPANGN	VAKGDRIPTD	ALASKGIHKH	KDRDQLEKK*

Computer analysis of this amino acid sequence gave the following results:

## Homology with fha

m564/fha

ID FHAB BORPE STANDARD; PRT; 3591 AA.

AC P12255;

DT 01-OCT-1989 (REL. 12, CREATED)

DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE FILAMENTOUS HEMAGGLUTININ. . . . .

SCORES      Init1:    190   Initn:    524   Opt:    594

Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

```
m564      .pep    MNRTLYKVVFENKHKRNCMIAVAENA KREGKN TADTQAVGILPNDIAGFAGFIHSISVISFS  
           ||::|::||:: |:: ::||:   ||  :: | : : | : |: :::  
fhab_borpe MNTNLYRLVLFSSHVRGM LVPVSEHCTV-G-NTFCGRTRG---QRSGARATSLSVAPNALA  
          10       20       30       40       50       60
```

```

              70      80      90      100      110      119
m564 .pep    L S L L G - S A L I L T S S S A T A Q G I V A D K S A P A Q Q Q P T I L Q T G N G I P Q V N I Q T P T S A G V S V N Q
              : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
fhab_borpe  W A L M L A C T G L P L V T H - - - A Q G L V - - - - P - Q G Q T Q V L Q G N K V P V V N I A D P N S G G V S H N K
              60      70      80      90      100

```

```

      120      130      140      150      160      170      179
m564 .pep  YAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQLNGYIEV
      : |||:| | :||:| : : :||| : || |:| :| :| :| :| :| :| :| :|
fhab_borpe FQGFNVANPGVVFNNGLTDGVSRIIGGALTKNPNLTR-QASAILAEVTDTSPSRLAGTLEV
      110      120      130      140      150      160

```

		180	190	200	210	220	230	239
m564	.pep	GGRRAEVVIANPAGIAVNGGGFINASRATLTTAQPPQYQAGDLSGFKIRQGNVVVIAGHGLD						
fhab_borpe		:   ::          :     : :           : :   :   :   :   :   :   :						
		YGKGADLI IANPNGISVNLSTLNASNLTLTTRPSVNGGRI-GLDVQQGTVTIERTGGVN						
		170	180	190	200	210	220	
		240	250	260	270	280	290	
m564	.pep	ARDTDYTRILSYHSKIDAPV---WGQ---DVRVVAGQNDVAATGDAHSPILNNAANTS						
fhab_borpe		:   : : :   : :   : :   : :   : :   : :   : :   : :   : :   :						
		ATGLGYFDVVARLVKLQGAVSSKQGPLADIADVAGANRYDHATRRTPI----AAGARG						
		230	240	250	260	270	280	
		300	310	320	330	340	350	
m564	.pep	NTANNNGTHIPLFAIDTGKLGMYANKITLISTVEQAGIRNQGWAFASAGNVAVNAEGLKV						
fhab_borpe		:   : : :   :   : : :   :   :   :   :   :   :   :   :   :   :						
		AAAGA-----YAIDGTAAGAMYGKHITLVSSDSGLGVRLGS-LSSPSAITVSSQGEIA						
		290	300	310	320	330		
		360	370	380	390	400	410	
m564	.pep	NTGMIAATGENHAVSLHARNVHNSTVASQDDANIHSQTLDNSGTVLSSSRLTVRNLR						
fhab_borpe		:     : :   : : :   : :   :     : : : :   : : :   : : :   :						
		---LGDATVQRGPLSLKGAGVVSAGKLASGGGAV---NVAGGGAVKIA---SASSVG						
		340	350	360	370	380		
		420	430	440	450	460	470	
m564	.pep	KNQNNGTIQAARLDMSTGGDLNTGNITQTGSQALDLVSAGKFDFNSGKIGVSDVPQTGLNP						
fhab_borpe		:   :   :   : : :   : : :   :   :   : :   : : :   : : :   :						
		AVQGGGKVQATLLNAG-----GTLVSGRQAVQLGAASSRQALSVDAGALKADKALSA						
		390	400	410	420	430		
		480	490	500	510	520	530	
m564	.pep	NPSV-I PQIPSTATSGSGSSTVSVSKPGSNPVSPATAKKNYAVGRIQTTGAFF-NAGSIN						
fhab_borpe		:   : : :   :   :   : : :   : : :   :   :   : :   : : :   :						
		TRRVDVDGKQAVALLGSASSNALSVRAGGA-----LKAGKLSATGRDLVDGKQAVTLG						
		440	450	460	470	480	490	
		540	550	560	570	579		
m564	.pep	AGGQIDIAAQNGLNSGSLNAAKLRSVSG-----DSFNNT-----VKGKLQAHDLAVNT						
fhab_borpe		:   : : :   :   : : :   :   :   :   :   : : :   :   :   :   :						
		SDGALSVSAGGNLRANELVSSAQLEVRGQREVALDDASSARGMTVVAAGALAARNLQSKG						
		500	510	520	530	540	550	
		580	590	600	610	620	630	
m564	.pep	QTAKNSGHLLTQTGKIDNRELH--NAGEIAANNLTLIHSGRSLNDKKGNIRAHLQLDTA						
fhab_borpe		: :   : : : : :   : : : : :   : : : : :   : : : : :   : : : :						
		AIGVQGGAEVSVANANSDAELRVGRGQVDLHDLSAARGADISGEGRVNIAGRSDSDVK						
		560	570	580	590	600	610	
		640	650	660	670	680	690	
m564	.pep	GLHNAGNILADSGTVTTKNNLRNTGKVSVARLNTTEGQTLDNTRGRIEATVNIQSQQLTN						
fhab_borpe		:   : :       : : :   :   : : :   : : :   : : :   :   : :						
		-VSAHGALSIDSMTALGAIGVQAGGSVSAKDMRSRGAVTVSGGG-----AVNLGDVQ---						
		620	630	640	650	660		
		700	710	720	730	740	750	
m564	.pep	QSGHITATEQLTINSRNVDNQNGKLLSANQAQLAVSDGLYNQHGEI						

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m564	.pep	760	770	780	790	800	810
		TLALNNADGTIQSAGNVSLQAKSLANNGTLTAGNKLDIALTDDFVVERDLTAGKQL-NLS					
fhab_borpe		RL-----DGA-HAGGQLRVSSDQAALGSLAAKGELTVSAAARAATVA-EL---KSLDNIS					
			720	730	740	750	760
m564	.pep	820	830	840	850	860	870
		IKGRLEK-NTHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLINS DGLT					
fhab_borpe		VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE---GWGAVGADSL-					
			770	780	790	800	810
m564	.pep	880	890	900	910	920	930
		HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETEGSTKAGAIARKRLDI-GAKEIHN					
fhab_borpe		--GSDGAISVSGRDAVRVDQARSLADISLG---AEGGATLGAVEAAGSIDVRGGSTV--					
			820	830	840	850	860
m564	.pep	940	950	960	970	980	990
		QEGALLSSEGI FAVGNRLDEQHHAAGMADTFVNGSAGLEVQGDALMSVRNMQNINNHEFT					
fhab_borpe		AANSLHANRDVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV					
			870	880	890	900	910
m564	.pep	1000	1010	1020	1030	1040	1050
		ETYLAKAEK--QVRDYTEVLGQNTYYQAGKDGLEFNSQGGKQDQTTATFHLKNGSRIEANQ-					
fhab_borpe		ALQSAKASGTLHVQGGHELDLGLTAAVGAVDV----NGTGDVVRVAKLVSDAGADLOAGRS					
			930	940	950	960	970
m564	.pep	1060	1070	1080	1090	1100	
		--WHVRDYHIETYKERIENRPAHITVGGDLTASGQNLNKSRIVVGGRIITDDLNQKE					
fhab_borpe		MTLGIVDTTGDQLQARAQQKLELGSVKSDDGGLQAAAGGALSALAAEVAGALELS---GQGV					
			980	990	1000	1010	1020
m564	.pep	1110	1120	1130	1140	1150	1160
		ITNQSTTGKGRDVAVGTDQWDSVTKKGWY--SGRKRQRRTERNHPTPYHDTQLFTHDFDTPV					
fhab_borpe		TVDRASASRARIDSTGSGVIGALKAGAVEAASPRRARRALR-----QDFFTPG					
			1040	1050	1060	1070	1080
m564	.pep	1170	1180	1190	1200	1210	1220
		SVI---QQNAASPSFQPAASAIKLIDGVSTAANGQRIHTGNVSVLNNATVTLPNSSLYT					
fhab_borpe		SVVVRAQGNVTVGRGDPHQGVLAQGDIIIMDA--KGGTLLLRNDALTENGTVTISADSAVL					
			1090	1100	1110	1120	1130
m564	.pep	1230	1240	1250	1260	1270	1280
		THPDNKGWLVETD-PQFADYRRWLGS DYMLQQLQDLTNHLHKRLGDGYEQLVNEQIHQ					
fhab_borpe		EHSTIESKISQSVLAAGDKGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRQIDV					
			1150	1160	1170	1180	1190
m564	.pep	1290	1300	1310	1320	1330	1340
		LTGYRRLDGYRSDEEQFKALMDNGLTAAKTFGLTPG-IASAEQVARLTSDIVWMENQTV					
fhab_borpe		VDGRPQI---TDAVTGEARKDES SVVSDAALVADGGPIVVEAGELVSHAGGIGNGRNK--					
			1200	1210	1220	1230	1240



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      1350      1360      1370      1380      1390      1400
m564 .pep  TLSDGSTQTVLPKYYALARKGDLNTSGGLISAEQVLLKLQNGNLNLSGTIAGRQAVLIQ
      :|:: || :      |::| : :| :|:: :| ||| : : : :| :
fhab_borpe --ENGASVTVRTT-----GNLVNKGYSAGKQGVLEV-GGALTNEFLVGS DGTQRIE
      1260      1270      1280      1290      1300

      1410      1420      1430      1440      1450
m564 .pep  ARNINSNGNIQ-----ADQIGLKAESINIDGGQVQAGRLLTAQ-----AQNINLNGTT
      |: |:: |::| | : :| :| :| || : :| : : : :| : : : :| :
fhab_borpe AQRIENRGTFQSQAPAGTAGALVVKAAEAIVHDGVMATKGEMQIAGKGGGSPVTVAGAKA
      1310      1320      1330      1340      1350      1360

      1460      1470      1480      1490      1500
m564 .pep  QTSGNERNGNTAI-DRMAGINVV-GSHTQVDNRTSD-GILSLHASNDINLNAATVSNQV
      ||::| : :| | : : : :| : :| :| :| : : : :| : : :| ||
fhab_borpe TTSANKLSVDVASWDNAGSLDIKKGGAQVTVAGRYAEHGEVSIQGDYTVSADAIALAAQV
      1370      1380      1390      1400      1410      1420

      1510      1520      1530      1540      1550
m564 .pep  --KDGTTQITAGNNLNLGT-IRTE---HREAYGTLDDENHRHVRQST-----EVGS
      : |:::| : : : :| : :| :| : : : :| : : : :| : : :| :| :
fhab_borpe TQRGGAANLTSRHDTRFSNKIRLMGPLQVNAGGPVSNLTGNLKVREGVTVTAASFNETGA
      1430      1440      1450      1460      1470      1480

      1560      1570      1580      1590      1600
m564 .pep  SIRTQNGALLRAGNDLKIRQGELEAEEGKTVLAAGR DV--TISEGRQITELDTS---VSG
      : : : : :| :| : :| : : : :| :| : :| :| : :| :| : :| :| :
fhab_borpe EVMAKSATLTTSGAARN--AGKMVQKEAATIVAASVSNPGTFTAGKDITVTSRGGFDNEG
      1490      1500      1510      1520      1530

      1610      1620      1630      1640      1650      1660
m564 .pep  K---SKGILSSTKTHDRYRF---SHDEAV-GSNIGGGKMIVAAGQDINVRGSNLISDKGI
      | :| | : :| : :| :| :| :| :| : : : :| :| :| :| :| :| :| :
fhab_borpe KMESNKDIVIKTEQFSNGRVLDKHDLTVTASGQADNRGSLKAGHDFTVQAQRI--DNSG
      1540      1550      1560      1570      1580      1590

      1670      1680      1690      1700      1710
m564 .pep  VLKAGHDIDISTAHNRYTG-----NEYHESKSKSGVMGTGGLGFTIGNRKTDDTDRTNIV
      : :| | | : : :| | | : :| : : : :| :| :| :| :| :| :| :
fhab_borpe TMAAGHDATLKAHLRNTGQVVAGHDIHIINSKLENTGRV--DARNIALDVADFTN--
      1600      1610      1620      1630      1640      1650

      1720      1730      1740      1750      1760      1770
m564 .pep  HTGSIIGSLNGDVTTVAGNR YRQT---GSTVSSPEGRNTVTAKSIDVEFANNRYATDYA
      ||| : : :| :| :| :| : :| :| :| :| :| :| :| :| :| :| :| :
fhab_borpe -TGSLYAEHDA-TLTLAQGTQDRLVVDQDHILPVAEGTLRVKAKSLTTEIETGNPGSLIA
      1660      1670      1680      1690      1700      1710

      1780      1790      1800      1810      1820      1830
m564 .pep  HTQEQKGLTVALNVPVQAQNFQAQNVGKSKNKR VNAMAAANAA-WQSYQATQOMQ
      :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :
fhab_borpe EVQE-----NIDNKQA-----IVVGKDLTSL-SAHGNVANEANALLWAAGELTVKAQN
      1720      1730      1740      1750

      1840      1850      1860      1870      1880      1890
m564 .pep  FAPSSSAGQGQNNNQSPSISVSITYGEQKSRNEQKRHYTEAAASQIIGKGQTTLAATGSG
      : : : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| :
fhab_borpe ITNKRAALIEAGGNARLTAVALNKLGRIRAGEDMHL D---APRI----ENTAKLSGEV
      1760      1770      1780      1790      1800      1810

      1900      1910      1920      1930      1940      1950
m564 .pep  EQSNINITGSDVIGHAGTALIADNHIRLQSAKQDGSEQSKNKGWAGVAVKIGNGIRF
      : : : : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| :
fhab_borpe QRKGVQDVGGGEHGRWSGIGYVNYWLRAGNGKKAGT-----IAAPWYGGDLTAEQSLIEV
      1820      1830      1840      1850      1860
```

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		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGKEQGGSTTHRHVHGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGIGG-----DVDNRSV-					
		1870	1880	1890	1900		

  

		2020	2030	2040	2050	2060
m564	.pep	IESVQDTETYQSKQQNGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE				
		:::	:	:	:	:
fhab_borpe		VRTVSAMEYFKTPLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRXEYIWGLYPTY				
		1910	1920	1930	1940	1950

  

		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGNLFQTATLTASDIQNH--RYEGRSFGIGGS					
		::::	:	:	:	:	:
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPMPKA-----PELDLRGHTLESAGEGRKI-FGEY					
		1970	1980	1990	2000	2010	

  

		2130	2140	2150	2160	2170
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYGSDDGSKNSTTRSGVNTNHIHITDEAG				
			:	:	:	:
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRRVHDQLG-----QRYGKALGGMDAETKEVDGIIQ				
		2020	2030	2040	2050	2060

  

		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKETEARIYTGIDTETADQHSGLKNSFDKDAVAKEINLQREVTKEFRNAA					
		:	:	:	:	:	:
fhab_borpe		EFAADLRITVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPGRVT--LAKALS					
		2080	2090	2100	2110	2120	

  

		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAYL-----					
			:	:	:	:	:
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKQETVLAAGAGLTLNNGAIHNGENA					
		2130	2140	2150	2160	2170	2180

  

		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGS LAAPYLDKAAENLGPAKG					
			:	:	:	:	:
fhab_borpe		AQNRGRPEGLKIGAHSA TSVSGSFDALRDVGLEKRLDIDDALAAVLVNPHIFTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1  atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accattttcg cccgtcccag accggcggct tccaatactt
101 ccctgcgttt cgcacgcgcg aacgacaccg gctcgcctgc acttctggct
151 acctgcacgc gtgcgatgac caagtcgagc gcgaaatagc gaatatcctc
201 tttgggcgaa gacgcgtccg accgtctgcc cgccccctgc gaagccgaca
251 atcagcacat gatcagactt gctcatcgct tccaccaaca tgctgtgcag
301 atcgagcgac ttcattgtccc agcttga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1  MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1  ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

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251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCCG CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGT AGGCTGTGCG CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSAF NTSSIAN SIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||||
g565           MDSTLSKTCCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
                10      20      30      40      50      60

                70      80      90     100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
                |||||
g565           AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
 51 CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCGG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCG GCCCTGCGC AAGCCGACAA
251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCCG CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGT AGGCTGTGCG CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSAF NTSSIAN SIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||||

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a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60
m565.pep  AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSIILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
a565      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSIILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
m565.pep  PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
a565      PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
m565.pep  KAMANTTSAFNTSSIANSTINCRQPPINAX
           190     200     210
a565      KAMANTTSAFNTSSIANSTINCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct tttcagacgg cattttgtat gggggttaac
51  ggttgttcag cccgagtacg tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggtc
151 gccggctttg tgggtgattt ccacgcgttc gccgtcgggt gcgaagaggg
201 cgggtgtggc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcgacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgccggc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAHSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGCTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTTGTTCAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTGTCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACCG GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGC GCACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCCGA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
51  AGLVGDFFHAL AVGGEEGGVV ADDVACADGG KADGRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAHSA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||

```

869

```

g566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60
           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g566      AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566.seq
1  ATGCCGCTCTG  AACAATATCT  TTTCAGACGG  CATTTTGTAT  GGGGGTTAAC
51  GGTGTGTTTACG  CCCGAGTACG  TCCTGCATAT  CGTACAAACC  CGTTTACCAG
101 TTTACCCAAA  CTGCGGCGCG  GACGGCGCCG  GCGGCAAAGG  TCATGCGGCT
151 GCTTGCCTTG  TGGGTGATTT  CCACGCGCTC  GCCGTCGGTG  GCGAAGAGGG
201 CGGTGTGGTC  GCCGACGATG  TCGCCCGCGC  GGACGGTGGC  AAAGCCGATG
251 GTGGACGGAT  CGCGCGGGCC  GGTGTGGCCT  TCGCGCCCGT  AAACGGCGCA
301 TTGTTTGAGG  TCTCTGCCGA  GCGCGCCGCG  GATGACTTCG  CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566.pep
1  MPSEQYLFRR  HFVWGLTVVQ  PEYVLHIVQT  RFTVYPNCGA  DGAGGKGHAA
51  ACLVGDFHAL  AVGGEEGGVV  ADDVARADGG  KADGGRIARA  GVAFAAVNGA
101 LFEVSAERAG  DDFAHA*

```

m566/a566 94.0% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
           10      20      30      40      50      60
           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567.seq.
1  atgcgacgac  gggcagcgcc  atcgacaagg  cgggtttgca  gtccggcggt
51  tatcaggtct  tattggcgca  tgcggacgtg  cagtcggcgg  cggtacgcag
101 caaagagggc  ggatacgcg  tgttgggtgc  gaacgcgcgc  gcttgccggc
151 gcggaaatcg  agctgggtgc  ggaaatcgcc  cgggaagtgc  gtttgaaaaa
201 cgcgctcaag  gcagtggcgg  aagattacga  ctttatcctg  atcgactgtc
251 cgccttcgct  gacgctgttg  acgcttaacg  gcttggtggc  gccgggcggc
301 gtgattgtgc  cgatgtttg  cgaatattac  gcgctggaag  ggatttccga
351 tttgattgcg  accgtgcgca  aaatccgtca  gccggtcaat  cccgatttgg
401 acatcacggg  catcgtgcgt  acgatgtacg  acagccgcag  caggctgggt
451 gccgaagtca  gcgaacagtt  gcgcagccat  ttcggggatt  tgctttttga
501 aaccgccatc  ccgcgcaata  tccgccttgc  ggaagcgccg  agccacggta
551 tgccggtgat  ggcttacgac  gcgcaggcaa  agggtgccaa  gccgtatctt
601 gccttggcgg  acgaactggc  gccgagggtg  tcggggaaat  ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567.pep
1  MRRRAAATR  RVCSPAFIRS  YWAMRTCSRR  RYAAKRADTA  CWVRTRALAG
51  AEIELVQEIA  REVRLLKALK  AVAEDYDFIL  IDCPPSLTLL  TLNGLVAAGG
101 VIVPMLCEYY  ALEGISDLIA  TVRKIRQAVN  PDLDTGIVR  TMYDSRSLV
151 AEVSEQLRSH  FGDLLFETAI  PRNIRLAEAP  SHGMPVMAYD  AQAKGAKAYL
201 ALADELAARV  SGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTGCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGCACTCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
251 CTGTGTTGGG TCGCAACCGC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTGAAA AACGCGCTCA AGGCAGTGGA
351 AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGACATCACG GGCATCGTGC
551 GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTGCGGGA TTTGCTTTTT GAAACCGTCA TCCCGGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701 ACGCGCAGGC AAAGGTACC AAGCGTATC TTGCCTTGCG GGACGAGCTG
751 GCGGCGAGGG TGTCGGGGA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
1  MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101 QEIAREVRLK NALKA VEEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAGT KAYLALADEL
251 AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

60      70      80      90      100     110     119
m567.pep GYVYQVLLGDADVQSAAVRSKEGGYAVLGNALAGAEIELVQEIAREVRLKNALKAVEED
g567      AFIRSYWAMRTCSRRRYAAKRADTACWVRTRALAGAEIELVQEIAREVRLKNALKAVAE
           20      30      40      50      60      70

120     130     140     150     160     170     179
m567.pep YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
g567      YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
           80      90      100     110     120     130

180     190     200     210     220     230     239
m567.pep TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAG
g567      TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAG
           140     150     160     170     180     190

240     250
m567.pep TKAYLALADELAARVSGKX
g567      AKAYLALADELAARVSGKX
           200     210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTGCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
```

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```

251 GCGTGTGGG TCGAACC GCCTGGCCG GCGCGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TCGCAATATT ACGCGCTGGA AGGGATTTCG GATTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGCCGAGGG TGTCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
  1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGRVVLVVDL DPQGNATTGS
 51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GYGVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

m567/a567 97.7% identity in 257 aa overlap

              10      20      30      40      50      60
m567.pep  MSANILAIANQKGGVGKTTT TVNLAASLASRGRVVLVVDLDPQGNATTGSGIDKASLQSG
a567      MSANILAIANQKGGVGKTTT TVNLAASLASRGRVVLVVDLDPQGNATTGSGIDKASLQSG
              10      20      30      40      50      60

              70      80      90      100     110     120
m567.pep  VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
a567      VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
              70      80      90      100     110     120

              130     140     150     160     170     180
m567.pep  DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
a567      DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
              130     140     150     160     170     180

              190     200     210     220     230     240
m567.pep  GIVRTMYDSRSRLVAEVSQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
a567      GIVRTMYDSRSRLVAEVSQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
              190     200     210     220     230     240

              250
m567.pep  KAYLALADELAARVSGKX
a567      KAYLALADELMARVSGKX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
  1 atgtctcaggg tcagaccggt attattttgcc gtcaaggcgt ccgcctcttc
 51 gataccttgc agaattctgcc gattaaagcg ttcgcggctg cccaatatatt
101 tcaggcgcatt attgttttcg tgcaggcggc gtacctgttt ttgcaaaaggc
151 tgtaaaaaca gcccacacag gaacgaaact tcgtcttcgg ggcgacgccca
201 gtttttcggt gaaaaggcaa acacggctcag atattgcacg cccagtttgg
251 cgcaatgctt caccatattt tccaacgcgt ccaagccgct tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggccgt tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg

```

401 tgctgctctt catatctgcc tttcgcgggt cggcggtcaa atgccgtctg  
451 aacgccgcgc cgtga

This corresponds to the amino acid sequence <SEQ ID 1690; ORF 568.ng>:

g568.pep  
1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA  
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP  
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL  
151 NAAP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1691>:

m568.seq  
1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC  
51 GATGCCTTGC AGAATCTGCC GGTGAAGCG TTCGCGGCTG CCCAATATCT  
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC  
151 TGTA AAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGGCCA  
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCAGTTTGG  
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC  
301 ATTATGCGCG GGAGGAAACG TTTTTCGCG CAACGGCCGT TGCCGTCCAT  
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGGCCTGCG  
401 TGCTGCTTTT CATGTCTGCC TTTGCGGTT CCGCATTCAA ATGCCGTCTG  
451 AACGCCGAAC CGTGCAGGT AAATTGCCAT CAAATCTTCT TCTTTGGCAG  
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTGCGTCAG TTTTGAACC  
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTCTT TGTCTTTGAG  
601 GAGTTTTTTG ATGTGGTCTG TGGCATCGCG GCGCACGTTG CCGATAGAGA  
651 CCGGCGCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG  
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CCGATCAGGT CCGCGACAGC  
751 TGCCGGGTTC AGTCCCAAGT TTGA

This corresponds to the amino acid sequence <SEQ ID 1692; ORF 568>:

m568.pep..  
1 MLRVRPVLFA VNASASSMPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA  
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP  
101 IMRGRKRFFA QRPLPSIITA ICLGMVCSK TACVLLFMSA FRGSAFKCRL  
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE  
201 EFFDVVGIA AHVADRDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS  
251 CRVQSQV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m568/g568 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	:    :					
g568	MLRVRPVLFAVKASASSIPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFITFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
	:    :					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFITFSNASKPRLCPIIRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
	:     :    :					
g568	MCLGMVCSKMVCVLLFISAFRGSFAFKCRLNAAPX					
	130	140	150			
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADRDAFFRFAAYDFNQVFAAFLGQHG					



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51 GATGCCCTTC AGGATTGAC GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTAAAAACA GCCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATGACACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCG CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGGCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTGCGGTT CGGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGCAGGTT AAATGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTGCTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG .CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CCGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1 MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFDVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVKASASSMPFRIXRLKRSRLPSIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADRDAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADGDAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADRDAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADGDAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	HRHADQVADSCRVSQVX					
a568	HRHADQVADSCRVSQVX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1 atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51 gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgcgggc
101 tgattgcctt gaccgccttg tgggagtatg cccgatggc cggtttgctg
```

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```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgcctatgcg ggcggctgga tgetgctaa ttggtttgg tatgttgttt
251 tggcattttg gctcgccgtt atgcctttgt ggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgetcatgcc
351 gttttggttc gcgtcgtat ccctggcgcc cgcattccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRPKWR
101 LGGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGC GGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATTG CCTCGCCGCA ACCTTGCTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCTTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGTTTTC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTA TACAGGCTGG
601 TTCGATACCG TGTAAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAAGCTGCT GCCCGGACAC GCGGCGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRPKWR
101 LGGGWQVYAV GWLLMPFWF ALVSLRPHPD DALPELLAVMG LVWVADICAY
151 FSGKAFGKHK IAPASPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVDRTDSL
251 IAVISVYAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRPKWRLNGGWQVYAVGWLLVMPFWF					
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRPKWRLNGGWQVYAVGWLLMPFWF					
	70	80	90	100	110	120
m569.pep	ALVSLRPHDDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPASPGKSWEGAIGGAVC					
g569	ALVSLAPASRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGC GGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

```

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGGTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCCCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACC GG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTGA TACAGGCTGG
601 TTCGATACCG TGTAAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GGCAGCGTGT TCGACCGCAC CGACAGCTAC
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569.pep
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFTDGTW
201 FDTVLI GLVL TVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRTDSL
251 IAVISVYAAM MSVLN*

m569/a569 99.6% identity in 265 aa overlap

      10      20      30      40      50      60
m569.pep MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCIKIKTNHYLAA
|||||
a569      MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCIKIKTNHYLAA
      10      20      30      40      50      60

      70      80      90      100     110     120
m569.pep TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
|||||
a569      TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
      70      80      90      100     110     120

      130     140     150     160     170     180
m569.pep ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC
|||||
a569      ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC
      130     140     150     160     170     180

      190     200     210     220     230     240
m569.pep VAVYMTAVRSAGWLAFTDGTWFDTVLI GLVL TVSVCGDLL ESWLKRAAGI KDSSKLLPGH
|||||
a569      VAVYMTAVRSAGWLAFTDGTWFDTVLI GLVL TVSVCGDLL ESWLKRAAGI KDSSNLLPGH
      190     200     210     220     230     240

      250     260
m569.pep GGVFDRTDSL IAVISVYAAMMSVLNX
|||||
a569      GGVFDRTDSL IAVISVYAAMMSVLNX
      250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

g570.seq..

```

1  atgatccggtt tgaccgcgcg gtttgccgcc gccctgatcg gtttatgctg
51  caccacaggc gcgcacgcgc acacctcca aaaaatcggc tttatcaaca
101 ccgagcgcgt ctacctgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc cgtcaggac gaattgcaaa aactgcaacg
201 cgaaggcttg gatttgaaa ggcagctcgc cggcgcaaaa cttaaggacg
251 caaaaaaggc gcaagccgaa gaaaaatggc gcggcgctgt cgaagcgctt
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaacgcaaa ccgcgtcatc gtcaaaatcg

```

876

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac  
 451 acccaatcag acgttaccga cagcgtcatt aaagaaatga acgcccgcgtg  
 501 a

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

1 MIRLTRAFAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT  
 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF  
 101 RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN  
 151 TQYDVTDSVI KEMNAR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

1 ATGACCCGTT TGACCCGCGC GTTGTCCGCG GCTCTGATCG GTTGTGCTG  
 51 CACCGCAGGC GCGCAGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA  
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG  
 151 CTGGACAGCG AATTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG  
 201 CGAAGGTCTG GATTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG  
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC  
 301 CGCAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA  
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG  
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC  
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG  
 501 A

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

1 MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT  
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAP  
 101 RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQNVYVN  
 151 TQYDVTDSVI KEMNAR\*

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLTLDSEFSARQD					
g570	MIRLTRAFAAALIGLCCTTAGAHADTFQKIGFINTERIYLESKQARNIQKTLTLDGEFSARQD					
	10	20	30	40	50	60
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAPFRKKQAQFEEDYNLRRNEEFA					
g570	ELQKLQREGLDLERQLAGGKLDKAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRRNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVIKIAKQEGYDVILQNVYVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

1 ATGACCCGTT TGACCCGCGC GTTGTCCGCG GCTCTGATCG GTTGTGCTG  
 51 CACCGCAGGC GCGCAGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA  
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG  
 151 CTGGACAGCG AATTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG  
 201 CGAAGGTCTG GATTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG  
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC  
 301 CGCAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA  
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG  
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC  
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
  1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101  RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151  TQYDVTDSVI KEMNAR*

m570/a570  97.6% identity in 166 aa overlap

              10      20      30      40      50      60
m570.pep    MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTL DSEFSARQD
a570        MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTL DSEFSARQD
              10      20      30      40      50      60

              70      80      90     100     110     120
m570.pep    ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA
a570        ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA
              70      80      90     100     110     120

              130     140     150     160
m570.pep    SLQQNANRVIVKIAKQEGYDVILQNVYVNTQYDVTDSVIKEMNARX
a570        SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
  1  atgcgcgttt tccgagtaaa ccgatttgtt gttaccgttt tcggcggcgg
 51  tataggttct gccgtcccac acgctgcctg cgtcggcaaa caggctcagg
101  cggacgggtg gtgcgtcttt cgcaccgggc atcgggaaga gcagctcggc
151  ggagacgttg gcttttttgt tgcgcgta gctgattttt tcgcggtatt
201  cgtcatacac ttccgggccc agcgtgccgc ttctgtagcc gcgcaccgaa
251  cccaggccgc cgccgtagaa gttttcaaag aaggggattt ctttggttct
301  gccgtagccc cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351  ttttgc...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
  1  MRVFRVNRV VTVFGGIGS AVPHAACVVK QAQADGACVF RTGHRREEQLG
 51  GDVGFFVAAV ADFFAVFVIH FRAERAFAVA AHRTQAAAVE VFKEGDFFGS
101  AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCCCTGCCG CCGGTCGCCG
 51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101  GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201  TTTTTCGCCG GTATTCGTCA TAGACTTTTG GACCGAGCGT GCCGCTTTTG
251  TATCCGCGCA CCGAACCAGG GCCGCCGCCG TAGAAGTTT CAAAGAAGGG
301  GATTTCCTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351  GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACCAGGT TTGTTGTGG
401  GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTGCGCGTT
451  CACGCCCGTC AGGTAGCCGC GCGTCGCCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
  1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
 51  EEQLGGDVGF FVAADVFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101  DFFGSAVAAR NADFAAEHQR EGFAQGEEPG LVVGGGVVLQ FAARQGDFFGV
151  HARQVAARRP *

```

878

m571/g571 93.1% identity in 102 aa overlap

	10	20	30	40	50	60
m571.pep	MGIAGAVNVLPAAAGRGTA VVVGVFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF					
g571	MRVFRVNRFFVTVFGGGIGSAVPHAACVKGQAQADGACVFRTHREEQLGGDVGF					
	10	20	30	40	50	
	70	80	90	100	110	120
m571.pep	FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ					
g571	FVAAVADFFAVFVIHFRAERAAAFVAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ					
	60	70	80	90	100	110
	130	140	150	160		
m571.pep	EGFAQGEPEGLVVGGGVVLQFAARQDGFVHARQVAARRPX					
g571	EGFA					
						119

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCCG CCGGTCGCGG
51  AACTGCTGTT GTCGTCGTAG GTTTGCGCT CCCACACGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201 TTTTTCGCC GTATTCGTCA TACACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCCAG GCCGCCCGCG TAGAAGTTT CAAAGAAGGG
301 GATTTCTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGGTTTTG CTTAAGGGGA AGAACCAGGT TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTTGCTGCCG GGCAGGGCGA TTTCGGCGTT
451 CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1712; ORF 571.a&gt;:

```

a571.pep
1  MGIAGAVNVLPAAAGRGTA VVVGVFAVPHA ACVKGQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFVIHFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQ EGFA*GEEPG LVVGGGVVLQ FAAGQDGFV
151 HARQVAARRP *

```

m571/a571 98.1% identity in 160 aa overlap

	10	20	30	40	50	60
m571.pep	MGIAGAVNVLPAAAGRGTA VVVGVFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF					
a571	MGIAGAVNVLPAAAGRGTA VVVGVFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m571.pep	FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ					
a571	FVAAVADFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ					
	70	80	90	100	110	120
	130	140	150	160		
m571.pep	EGFAQGEPEGLVVGGGVVLQFAARQDGFVHARQVAARRPX					
a571	EGFAXGEPEGLVVGGGVVLQFAAGQDGFVHARQVAARRPX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq..

879

```

1  atgtgcgcca tcgtcggggc ggccggggctg ccttcgcgcg tcgcagcggc
51  gcaaaaaggc aaaaccattt atctggcaaa caaagaaacg ctggtgggtt
101 cggcgcggtt gtttatggaa accgcccgcg caaacggcgc ggcaagtgtt
151 cccgtcgaca gcgaacacaa cgccattttc caagttttgc cgcgcgatta
201 cacagaccgt ctgaacgaac acggcatcga ttcgattatc ctgaccgcct
251 ccggcggccc gtttttaaca accgatttaa gcacgttcga cagcattacg
301 cccgagcagg cgttcaaaca cccaattggc cgtatggggc gcaaaatctc
351 cgtcgattca gccactatgg caaacaaggg cttggaactg attgaagcgc
401 attggctgtt caactgtccg cccgacaaac tcgaagtcgt catccatccc
451 caatccgtga tacacagtat ggtgcgctac cgcgacggct ccgtgctggc
501 gcaactgggc aatcccgata tgcgaacgcc catcgccatg tgtttgggct
551 tgcccgcgag catcgattcg ggtgtcggca aactcgattt cgcgcgattg
601 tccgcgctga ccttccaaaa gcccgacttc ggccgcttcc cctgcctgaa
651 gttcgcctat gaaaccataa acgcaggcgg agccgcgccc tgcgtattga
701 acgcgcgcaa cgaaacccgc gtcgccgctt ttttgacggg acagattaag
751 ttaccgcaca ttgcccacaa cgtcgcccac tgtcttcgac aagacttttc
801 aaacggcatg ggcgatatag aaggactgtt ggcgcaagat gcccgacac
851 gcgcacaagc gcgggcattt atcggcacac tgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1714; ORF 572.ng>:

g572.pep..

```

1  MCAIVGAAGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAIF QVLPRDYDTR LNEHGIDSII LTASGGPFLT TDLSTFDSIT
101 PEQAVKHPNW RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGKLDLFDAL
201 SALTFOKPDF GRFPCLKFAY ETINAGGAAP CVLNAANETA VAAFLDGQIK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1715>:

m572.seq..

```

1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATT TATCTGGCAA CAAAGAAACG CTGTTGGTTT
101 CCGCGCGGTT GTTTATGGAA ACCGCCCGTG CAAACGCGCG GGCAGTGCTG
151 CCGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTCG CGCGCGATTA
201 CGCGCGCGCT CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGCGGCCCC GTTCTGACC GCCGATTTAA ACACGTTTCA CCGCATACG
301 CCGCCCCAAG CGGTCAAACA CCAATTTGG CGTATGGGAC GCAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCCGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGCTGGC
501 GCAACTGGGC AATCCCGATA TGCGAACGCC CATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCT GGTGTCGGCG ACCTGGATTG CGACGCATTG
601 TC CGCGCTGA CCTTCCAAA GCCCGACTTT GACCGCTTCC CCGCCTGAG
651 GCTCGCCTAT GAAGCCATGA ACGCAGCGCG AGCCGCGCCC TCGGTATTGA
701 ACGCGGCCAA CGAAGCCGCC GTCGCGCCT TTTTGACCG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCAC TGTCTTCAC AAGACTTTTC
801 AGACGGCATA GCGGATATAG GGGGCTCTT GCGCAAGAT GCCCGACAC
851 GCGCACAAAG GCGAGCATTT ATCGGCACAC TCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1716; ORF 572>:

m572.pep..

```

1  MCAIVGAAGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAIF QVLPRDYAGR LNEHGIIASII LTASGGPFLT ADLNTFDRIT
101 PAQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFOKPDF DRFPCLRLAY EAMNAGGAAP CVLNAANEA VAAFLDGQIK
251 FTDIKTVAH CLAQDFSDGI GDIGGLAQD ARTRAQARAF IGTLR*

```

m572/g572 92.9% identity in 295 aa overlap

```

10      20      30      40      50      60
m572.pep  MCAIVGAAGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAIF
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572      MCAIVGAAGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAIF
          10      20      30      40      50      60

70      80      90      100     110     120
m572.pep  QVLPRDYAGRLNEHGIIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572      QVLPRDYDTRLNEHGIDSII LTASGGPFLTDLSTFDSITPEQAVKHPNWRMGRKISVDS

```

880

	70	80	90	100	110	120
	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDPKLEVVHPQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
g572	ATMMNKGLELIEAHWLFNCPDPKLEVVHPQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDLFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVSKLDFGALSALTFQKPDFGRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
g572	VAAFLDGGQIKFTDIAKTVAHCLAQDFSNMGMDIEGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```

a572.seq
1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGGCGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCCGTG CAAACGGCGC GGCAGTGC TG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTCG CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCCC GTTCTGACC GCCGATTAA ACACGTTTCA CAGCATTACG
301 CCGACCAAG CGGTCAAACA CCCAATTGG CGTATGGGAC GCAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATGAAGCGC
401 ATTGCTGTT CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTTGGC
501 GCAACTGGGC AATCCCGATA TCGCAACGCC TATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTG GGTGTCGGCG ACCTGGATTT CGACGCATTG
601 TCCGCGCTGA CCTTCCAAA GCGCGACTTT GACCGCTTCC CCTGCCTGAA
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCCT TTTTGACGG ACAGATTAG
751 TTTACCGACA TTGCCAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTTC
801 AGACGGCATA GCGGACATAG GGGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGCACAAAG CGGGGCATTT ATCGGCACAC TGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```

a572.pep
1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGA AVL
51  PVDSEHNAV FQVLPRDYTGR LNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALT FQKPDF DRFPCLKLAY EAMNAGGAAP CVLNAANEAA VAAFLDGGQIK
251 FTDIAKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*

```

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572.pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAV F					
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAV F					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572.pep	QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
a572	QVLPRDYTGRLNEHGIASII LTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS					
	70	80	90	100	110	120



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	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSVMVRYRDGSVLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSVMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGDLDFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIKTVAHCLAQDFSDGIGDIGGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIKTVAHCLSDQDFSDGIGDIGGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1  atgccctggt tgtgccgcct taatcgcaat atcggcagtt tccaaatcac
51  gaatctcacc gaccataatg atgtccgggt cctgacgcag gaaagacttc
101 aaagcagcgg caaaagtcag accctgctta tcattgacgt taacctgatt
151 gatgcccgcc aggttaatct cggcagggtc ttccgccgtt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga caccgtctta
251 cccgaacccg tcggaccggt taccagcacc atcccgtaag gacggtgaat
301 cgcttccaac aacaattttt tctggaacgg ctcaaaacgg agctggtcga
351 tgttcaaaga cgcggcatcg gaattcaaaa tccgcatcac gaccttttcg
401 ccaaacagcg tcggcaatgt gctgacacgg aaatcgacag gcttgccgcc
451 cttttgaaag gtcagctgca tcctaccgtc ctggcgatc cgtttttcgg
501 aaatgtccaa acgcgacatt accttaatcc ggggaagcaag ctgccccctt
551 accgcaatgg gcggctgaac cacctcgagg agctgcccgt ccacacggaa
601 acggatacgc gcatttgtgt cgtaaaactc gaaatggatg tcggatgccc
651 cgctacgcaa ggcatccgac aaagttttat ggataaacct cggaacaggg
701 ccgtcttctg cctcctcgtc gtcgataata aggggtgtgc ttctctcttc
751 ctcttgcccc tccccaagct cctgaagcag cgatgtcgaa cggaaccca
801 ccaatcgag caaacccgcc aactggtcat cctcgacaat gaccaactca
851 accgcaatcc ctgcggcaga aaccgttttc tgaatttgcg gcattctggg
901 cggatcgga accgcaaaaa atactttgtc gccccacgg aaaaccggca
951 cacagtggaa ctccaccatc tgcctctccg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgaataac tgaacaccct
1051 cgcaatcaat gccgcaagcg acttgggcga aatgacaccg tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1  MPCLRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNL
51  DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHPVVRTVN
101 RFQQQFFLER LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPTV LRYPFPGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTRIVFVKL EMDVGCPATQ GIRQSFMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNRNPGCR NRFLNLRHIG
301 RIGNRKKYFV APTENRHIVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1  ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGGTACCAAC aCaw.TTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGAAGG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT

```

```

551 ACCGCAATGG GCGGCTGAAC CACCTGCGG AGCTGCCCCG CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCTGCCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACGGCAAAAA ATACTTGTG GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

```

m573.pep..
  1 MPCLCLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
 51 DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXFFLKR LKTELVDVQR RGIGIQNPHH DLFQKRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

m573.pep	10	20	30	40	50	60
	MPCLCLNRNIGSFQITNLDHNDVRVLTQERLQSSGKSQALLIIDVNLDARQVNLGRV					
g573	MPCLCLNRNIGSFQITNLDHNDVRVLTQERLQSSGKSQTLIIDVNLDARQVNLGRV					
	10	20	30	40	50	60
m573.pep	70	80	90	100	110	120
	FRRCNLYRLRIQNIQTGIERHRLTRTRTGYQHHPVGTNRYQHXFFLKRKTELVDVQR					
g573	FRRCNLYRLRIQNIQTGIERHRLTRTRTGYQHHPVRTVNRVQQQFLERLKTELVDVQR					
	70	80	90	100	110	120
m573.pep	130	140	150	160	170	180
	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK					
g573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPFGNVQTRHYLNPXSK					
	130	140	150	160	170	180
m573.pep	190	200	210	220	230	240
	LPPYRNGRLNHLAELPVHTE TDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
g573	LPPYRNGRLNHLAELPVHTE TDRIVFVKLEMDVRCPAAGGIRQSFMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	250	260	270	280	290	300
	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
g573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNRNPGCRNRFNLRHLG					
	250	260	270	280	290	300
m573.pep	310	320	330	340	350	360
	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

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a573.seq

```

1 ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCCGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAAATTTT TCTGAAACGG CTCAAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGAAGCAAG CTGCCCCCTT
551 ACCGAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCCTCTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTT TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATAATTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCACCATC TGCTCCTCCG TCAACACCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCTT
1051 CGCAATCAAT GCCGAAGCG ACTTGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```

1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51 DARQVNLRV FRRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHFVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFQRRQC ADTEIDRLAA
151 LLKQLHPAV LRYFFFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIROSLMDKP RNRAVFCLLV VDIQGVAFLF
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQTLLIIDVNLI DARQVNLRV					
	10	20	30	40	50	60
m573.pep	FRRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHFFLKR LKTELVDVQR					
a573	FRRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
m573.pep	FRRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHFFLKR LKTELVDVQR					
a573	FRRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFFGNVQTRHYLNPGSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFFGNVQTRHYLNPGSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIROSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIROSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIROSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIROSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300
m573.pep	VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300

884

	310	320	330	340	350	360
m573.pep	RIGNRK	KYFVAPT	ENRHTVELH	HLHLLRQHP	HPVARIMTQ	IKNRITEHPRNQCRKRLGR
a573	RIGNRK	KYFVAPT	ENRHTVELH	HLHLLRQHP	HPVARIMTQ	IKNRITEHPRNQCRKRLGR
	310	320	330	340	350	360
m573.pep	NDTVX					
a573	NDTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1  atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51  attgtggatt atcctgctgc cgattatcct tttgcccgtc ttcttcacga
101 tgggctgggt tgccgcccgc gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc cttcgggatt ttataaaagc ctggacgctt tggtcgaccg
201 caacagcggg cgcgcggcaa gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaac cttaccctcg gcaaaactta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccaaa ggcgggtttg gtcgatcggt ccgaacagat ttttttgggg
451 ctgcaagacg gtgaaatggc gcgtgaaagg agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcggtt
651 caatgtcgcc aaggcactcg aagccaacaa aaaatgcacc cgcgcccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tggccgcgct
751 gaagccctat ccgccatcga gcagcaaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaacgg tctgacagga tatatgcaga cgtttccga acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg ctttaaggcg agaaagaagc
951 cgcgcaaaac gccgtcgagc ttgtccgccc caagcccgac cttaacggcg
1001 tgtaccgcct gctcgggttg aaactcagcg atttggatcc ggcttggaaa
1051 gccgatgccg acatgatgcg ttcggttacc ggacggcagc tccagcgcag
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgcctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagtttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1  MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREB RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFEIAQFYC
201 ELAQAALEFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMOTFPELDL
301 INVVYEKSL LKGEKEAAQT AVELVRRKPD LNGVYRLGL KLSDLDPAAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1  ATGCGCCCGA ATCTACCAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCCGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GGCGAAAACG ACAAAGCCAT CAACATACAC CGGACAATGC TCGATTCTCC
351 CGATACGGTC GCGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTTCGGG
451 CTGCAAGACG GTAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG TCGCGCGTTT

```

```
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGGCAGAGAAG CTTTACGAAG CCTATGCCGC GCAGGAAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AAACCTAGCG ATATGAATCC GGCTTGGAAA
1051 GCCGATGCCG ACATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCT
1151 GGCACTGCCC CGCCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```
1 MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51 KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GKPEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSDMNPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

m573/g573 97.8% identity in 402 aa overlap

```
10 20 30 40 50 60
m574.pep MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA KSIPSGFYKS
g574 MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA KSIPSGFYKS
10 20 30 40 50 60

70 80 90 100 110 120
m574.pep LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQ GENDKAINIH RTMLDSPDTV
g574 LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQ GENDKAINIH RTMLDSPDTV
70 80 90 100 110 120

130 140 150 160 170 180
m574.pep GEKRARVLF ELAQNYQSAGL VDRAEQIFLG LQDGKMAREARQHLLNIYQQ DRDWEKAVET
g574 GEKRARVLF ELAQNYQSAGL VDRAEQIFLG LQDGEMAREARQHLLNIYQQ DRDWEKAVET
130 140 150 160 170 180

190 200 210 220 230 240
m574.pep ARLLSHDDQT YQFEIAQFYC ELAQALFKS NFDVARFNVG KALEANKKCT RANMILGDIE
g574 AQLLSHDEQT YQFEIAQFYC ELAQALFKS NFDVARFNVG KALEANKKCT RANMILGDIE
190 200 210 220 230 240

250 260 270 280 290 300
m574.pep HRQGNFPAAV EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GKPEEGLNRLTG YMQTFPELDL
g574 HRQGNFPAAV EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GKPEEGLNRLTG YMQTFPELDL
250 260 270 280 290 300

310 320 330 340 350 360
m574.pep INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSDMNPAWK ADADMRSVI
g574 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSDLPAWK ADADMRSVI
310 320 330 340 350 360

370 380 390 400
m574.pep GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI EVX
g574 GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI EVX
370 380 390 400
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1 ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51 ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GGCAGAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TCGGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTGATG CCGCGCGTTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGCGGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGC AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCAGC CTCAACGGCG
1001 TGTACCGCCT GCTTGGTTTG AAATCAGCG ATTTGGATCC GGCTTGGAAA
1051 GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACA GTCTTTTCT
1151 GGCATTGTCC TGCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1 MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51 KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLDSPDTT GAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSLDPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

m574/a574 97.5% identity in 402 aa overlap

          10      20      30      40      50      60
m574.pep MRPNLPNSLKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a574      MRPNLPNSLEKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS
          10      20      30      40      50      60

          70      80      90      100     110     120
m574.pep LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a574      LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINMHQTLDSPDTT
          70      80      90      100     110     120

          130     140     150     160     170     180
m574.pep GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET
          | |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a574      GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET
          130     140     150     160     170     180

          190     200     210     220     230     240
m574.pep ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a574      ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE
```

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	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGVMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGVMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDINGVYRLGLKLSDMNPAWKADADMRSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPDINGVYRLGLKLSDLDPWKADADMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFQSQVFFWHCPACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFQSQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

```

g575.seq (partial)
1 ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51 cccgtcaaac gtcgcgtttc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggcaacttc actggctgtt tccgcaacag
151 gttcggaac ggtgttaccg gtttcgtcgg tcggcgtgtc gatggcagaa
201 gcggcggctt cttggggggg cggattcggc agcgggttcc gatgcggcag
251 tatttgcagc ggttacaggt ccgggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt gggttcgggt cgaacggccg gttttccgc
351 ttttgcctcg ggccgggcaa ctttgccttc aggtttttca accggttttt
401 cgacaggttt ctctatcggt ttctccacag ttgctgttt ggacgggtca
451 gacggcatgg atgcagtttc ggtttgggt ttcgccgttt gcggtttggg
501 ttgttccgct ttgattttt tgggtgctgc cgctttgatc ctgttcagat
551 tcggaatgtg a*

```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

```

g575.pep (partial)
1 ..MPCLRQQAAR CTNRRTDROT VRFRLLRQK PVRQVRQVR RQLHNLFPQQ
51 VRKRCYRFR SACRWQKRRL LGGADSAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGS RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDGS
151 DGMDAVSALG FAVCGLGCSA LIFLGAALI LFRFGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

```

m575.seq..
1 ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51 GCGAGGTTTT GCGGAAGCTG TTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTGTGC GGAGAAATCG GTATCGACGG TTTCGGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201 GTTGTAACGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAAATGCC GTTTGCGCG GCTGCCAGGC TGTCGAAATC
351 CAAGTCGATG CGGTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGT
401 TTGCCGATAA CTCTTCTTCA GATTCCCCAT CTAAGGCAAG TGTGTCGTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601 GCAGAAAGCA GCAGCAGGGC GATTAATGCC GCGCCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACGCCGA ACAGACCGTC AACAGTCCG CTTTCGGTTT
701 CTCTTTCGGC AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGGTCG GCGTGTCTGAT GGCAGAAGCG GCGGCTTCTT GGGGGCGGGA
801 TTCGGCAGCG GTTTCGGATG CGGCAGTATT TGCAGCGGGT ACAGGTTTCG
851 GTCGAAACGC CGGTTTTTCC GCTTTTGCTT CGGGCGCGGC AACTTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTCGGGTT
1001 GTTCGCTTTT GATCCTGTTC AGATTCGGA TGTGA

```

888

This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

m575.pep  
 1 MVSGEAEFRK PASPEGEAGF AEA VSSVPIW LFEGR LSEKS VSTVSGLFSA  
 51 VWATDSGSGV SMTISTGLYG LKVS GSYTLS VDSMAFQSAS ARFWVSSSCV  
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVC FADN SSS DSPSKASVSF  
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR  
 201 RKSSSRAINA APPPASSKVY EPPNRPNSP LSVSSSAETC STGSETALPV  
 251 SSVGVSMAEA AASWGADSA VSDAAVFAAG TSGRTAGFS AFASGAATFA  
 301 SGFSTGFSTV ACLDGS DGM DAVSALGFAVC GLGCSALILF RFGM\*

m575/g575 70.2% identity in 114 aa overlap

	240	250	260	270	280
m575.pep	SSAETCSTGSETALPVSSVGVSMAEAAAASWGADSAVSDAAVFAAGTG-----				
g575	LHWLFPQVRKRCYRFRRSACRWQKRLLGGADSAVSDAAVFAAGTGPGRSVAEAGVS				
	50	60	70	80	90 100

  

	290	300	309	310	320
m575.pep	-----SGRTAGFSAFASGAATFASGFSTGFST-----VACLDGSDGMDAVSALGFA				
g575	DTAGLGSGRTAGFSAFASGAATFASGFSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA				
	110	120	130	140	150 160

  

	330	340
m575.pep	VCGLGCSALI-----LFRFGMX	
g575	VCGLGCSALIFLGAAALILFRFGMX	
	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

a575.seq  
 1 ATG GTT TCGG GCGAGGAAGC CTT CAGGAAG CCTGCCAGTC CGGAGGGTGA  
 51 GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG  
 101 GCAGGTGTCT GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA  
 151 GTTTGGGCGA CAGATCCCG TFCGGGCGTG TCGATGACGA TTTCGACAGG  
 201 GTTG TACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA  
 251 TGGCGTTCCA ATCGGCATCC GCGCGTTTT GGGTTTCTTC ATCCTGCGTA  
 301 AGTGCCCGG ATAAATGCC GTTTTGCGCG GCTGCCAGGC TGTCGAAATC  
 351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT  
 401 TTGCCGACAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTTT  
 451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CGACTTCGGC  
 501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT  
 551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG  
 601 CGCAAAAGCA GCAGCAGGGC GATCAATGCC GCGCCTCCGC CGGCAAGCAG  
 651 CAAGGTGTAC GAACCGCCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG  
 701 AAACCTGTTC GACAGGTCG GAAACGGCGT TACCGGTTTC GTCGGTCGGC  
 751 GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT  
 801 TTCCGATGCG GCAGTATTTG CAGCGGGTAC AGGTTGCGGT CGAACGCGCG  
 851 GTTTTTCGCG TTTTGCTTCG GCGCGGCAA CTTTGTCTTC AGGTTTTTCA  
 901 ACCGTTTCT CTACCGTTGC CTGTTTGGAC GGTTCCGACG GCATGGATGC  
 951 GGTTCGGCT TTGGGTTTCG CCGTTTGGCG TTTGGGTTGT TCCGCTTTGA  
 1001 TCCTGTTTCA ATTCCGAATG TGA

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

a575.pep  
 1 MVSGEAEFRK PASPEGEAGF AEA VSSVPIW LFEGR LSEKS VSTVSGLFSA  
 51 VWATDSGSGV SMTISTGLYG LKVS GSYTLS VDSMAFQSAS ARFWVSSSCV  
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVC FADN SSS DSPSKASVSF  
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR  
 201 RKSSSRAINA APPPASSKVY EPPNRPNSP LSVSSSAETC STGSETALPV  
 251 VSMAEAAASW GADSAVSDA AVFAAGTGS RTAGFSAFAS GAATFASGFS  
 301 TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM \*



889

m575/a575 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
m575.pep	MVSGEAAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
a575	MVSGEAAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m575.pep	SMTISTGLYGLKVSGSYTLSDMAFQASARFWVSSSCVSPDKMPFCAAARLSKSKSM					
a575	SMTISTGLYGLKVSGSYTLSDMAFQASARFWVSSSCVSPDKMPFCAAARLSKSKSM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m575.pep	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSSAASSR					
a575	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSSAASSR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m575.pep	SGSSSGTDSSVRRARLDWARRKSSSRAINAAPPPASSKVYEPNRPNSPLSVSSSAETC					
a575	SGSSSGTDSSVRRARLDWARRKSSSRAINAAPPPASSKVYEPN----SPLSVSSSAETC					
	190	200	210	220	230	
	250	260	270	280	290	300
m575.pep	STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTSGSRTAGFSAFASGAATFA					
a575	STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTSGSRTAGFSAFASGAATFA					
	240	250	260	270	280	290
	310	320	330	340		
m575.pep	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
a575	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1 ..atggcgctgg acatcggacg ctcctgaaa caaatgaagg aacagggcgc
51 ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttcttgacag agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttcgggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcggtt ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccgcc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactggtca aaatcggcgc acccgaaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence &lt;SEQ ID 1738; ORF 576.ng&gt;:

g576.pep.. (partial)

```

1 ..MGVDIGRSLK QMKEQGAEID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51 FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVDSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1 ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

```

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```

51   GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301  CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451  GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCCA
501  AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGGCG
551  GCGACAAATC CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1   ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMMKFLO  EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITKQGE  GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ  LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVVKLV
201 KIGAPENAPA  KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

```

              10      20      30      40      50      60
m576.pep      MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLO
              |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g576           MGVDIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLO
              10      20      30      40      50

              70      80      90      100     110     120
m576.pep      EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTAS GLQYKITK QGEGKQPTKDDIV
              |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g576           EQQAKAVEKH KADAKANKEK GEAFLENAA EDGVKTTAS GLQYKITK QGEGKQPTKDDIV
              60      70      80      90      100     110

              130     140     150     160     170     180
m576.pep      TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ VIPGWTEGV QLLKEGGEATF YIPSNLAYRE
              |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g576           TVEYEGRLID GTVFDSSKAN GPATFPLSQ VIPGWTEGV RLLKEGGEATF YIPSNLAYRE
              120     130     140     150     160     170

              190     200     210     220
m576.pep      QGAGDKIGPN ATLVDVVKLV KIGAPENAPAK QPAQVDIKK VN*
              |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g576           QGAGEKIGPN ATLVDVVKLV KIGAPENAPAK QPDQVDIKK VN*
              180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCGGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCGGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA

```

```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
  1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
  51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

                                10      20      30
m576.pep                                MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
a576                                CGKKEAAPAS ASEPAASSA QGDTSSIGST MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m576.pep                                FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
a576                                FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
                                90     100     110     120     130     140

                                100     110     120     130     140     150
m576.pep                                KDGVKTTASGL QYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
a576                                KDGVKTTASGL QYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m576.pep                                VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
a576                                VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
                                210     220     230     240     250     260

                                220
m576.pep                                KQPAQVDIKK VN
a576                                KQPAQVDIKK VN
                                270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

```

g576-1.seq
  1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
  51 ACTTTCGCCG TCGGCGAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
 101 CTGCCGCCCG TTCTGCCGCG CAGGCGGACA CCTCTTCAAT CGGCAGCAGC
 151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
 201 ACAATGAAG GAACAGGCGC CGGAAATCGA TTTGAAAGTC TTTACCGATG
 251 CCATGCAGGC AGTGATGAC GGCAAGAAAA TCAAAATGAC CGAAGAGCAG
 301 GCCCAGGAAG TGATGATGAA ATTCTGCAG GAGCAGCAGG CTAAGCCGT
 351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
 401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTCCGGT
 451 CTGCAGTACA AAATCACCAA ACAGGGTGAA GGCAACAGC CGACAAAAGA
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
 551 TCGACAGCAG CAAAGCCAAC GCGGCGCCGG CCACCTTCCC TTTGAGCCAA
 601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
 651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
 701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTGACGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

## g576-1.pep

```

1  MNTIFKISAL  TLSAALALSA  CGKKEAAPAS  ASEPAAASAA  QGDTSSIGST
51  MQQASYAMGV  DIGRSLKQMK  EQGAEIDLKV  FTDAMQAVYD  GKEIKMTEEQ
101 AQEVMKFLQ  EQQAKAVEKH  KADAKANKEK  GEAFLENAA  KDGVKTTASG
151 LQYKITKQGE  GKQPTKDDIV  TVEYEGRLID  GTVFDSSKAN  GGPATFPLSQ
201 VIPGWTEGVR  LLKEGGEATF  YIPSNLAYRE  QGAGEKIGPN  ATLVDVKLV
251 KIGAPENAPA  KQPDQVDIKK  VN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

## m576-1.seq

```

1  ATGAACACCA  TTTTCAAAT  CAGCGCACTG  ACCCTTTCCG  CCGCTTTGGC
51  ACTTTCCGCC  TGCAGCAAAA  AAGAAGCCGC  CCCCAGCATCT  GCATCCGAAC
101 CTGCCGCCGC  TTCTTCCGCG  CAGGCGCACA  CCTCTTCGAT  CGGCAGCAGC
151 ATGCAGCAGG  CAAGCTATGC  GATGGGCGTG  GACATCGGAC  GCTCCCTGAA
201 GCAAATGAAG  GAACAGGCGC  CGGAAATCGA  TTTGAAAGTC  TTTACCGAAG
251 CCATGCAGGC  AGTGTATGAC  GGCAAGAAAA  TCAAAATGAC  CGAAGAGCAG
301 GCTCAGGAAG  TCATGATGAA  ATTCCTTCAG  GAACAACAGG  CTAAAGCCGT
351 AGAAAAACAC  AAGGCGGACG  CGAAGGCCAA  TAAAGAAAAA  GGCGAAGCCT
401 TTCTGAAAGA  AAATGCCGCC  AAAGACGCCG  TGAAGACCAC  TGCTTCCGGC
451 CTGCAATACA  AAATCACCAA  ACAGGCGGAA  GGCAACACAG  CGACCAAGAA
501 CGACATCGTT  ACCGTGGAAT  ACGAAGGCCG  CCTGATTGAC  GGTACGGTAT
551 TCGACAGCAG  CAAAGCCCAAC  GGCAGCCCGG  TCACCTTCCC  TTTGAGCCAA
601 GTGATTCCGG  GTTGGACCGA  AGGCGTACAG  CTTCTGAAAG  AAGGCGGCGA
651 AGCCACGTTT  TACATCCCGT  CCAACCTTGC  CTACCGCGAA  CAGGGTGCGG
701 GCGACAAAAA  CGGTCCGAAC  GCCACTTTGG  TATTGTATGT  GAAACTGGTC
751 AAAATCGGCG  CACCCGAAAA  CGCGCCCGCC  AAGCAGCCGG  CTCAGTCCA
801 CATCAAAAAA  GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

## m576-1.pep

```

1  MNTIFKISAL  TLSAALALSA  CGKKEAAPAS  ASEPAAASSA  QGDTSSIGST
51  MQQASYAMGV  DIGRSLKQMK  EQGAEIDLKV  FTEAMQAVYD  GKEIKMTEEQ
101 AQEVMKFLQ  EQQAKAVEKH  KADAKANKEK  GEAFLENAA  KDGVKTTASG
151 LQYKITKQGE  GKQPTKDDIV  TVEYEGRLID  GTVFDSSKAN  GGPVTFPLSQ
201 VIPGWTEGVQ  LLKEGGEATF  YIPSNLAYRE  QGAGDKIGPN  ATLVDVKLV
251 KIGAPENAPA  KQPAQVDIKK  VN*

```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASAAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEQVMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEQVMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLEKGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

## a576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGCGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGC GG
701 GCGACAAAT CCGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAGTCTGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

**a576-1.pep**

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLO EQQAKAVEKH KADAKANKEK GEAFLENAE KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

**a576-1/m576-1** 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pep	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	KADAKANKEKGEAFLENAEKDGVKTTASGLQYKITQGEKGKPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAEKDGVKTTASGLQYKITQGEKGKPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAEKDGVKTTASGLQYKITQGEKGKPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAEKDGVKTTASGLQYKITQGEKGKPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

### Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipathic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577.seq..
1  atggaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcggt
151 tttatttacg gagcaaacat gaaacttatc tataccgtca tcaaatcat
201 tatcctgctg ctcttcctgc tgcttgccgt cattaatatg gatgccgtta
251 ccttttcta tctccgggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cgtttgtcgt cggcatcgtg ttcggaatgt ttgccctgtt
351 cggcgggctg ctgtccttgc gggcgaaaa cagccgctg cgtgcggaag
401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgcgata
451 caaatgctg ccgaatctgc caaacagcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
1  MERSGVFGKI VGNRILRMPS EHAAAFYPKP CKSFKLTQSW FRVRSCPCGV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINM DAVTFSYLPQ QSVNPLPLIV
101 LFGAFVVGIV FGMFALFGRL LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAESAQKP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577.seq..
1  ATGGAAGGA ACGGTGTATT TGGTAAATT GTCGGAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAGTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTACG GAGCAACAT GAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAATACG GATGCCGTTA
251 CCTTTTCTA CTGCGGGGG CAAAATTCTG ATTTGCCGCT GATTGTCTGA
301 TTGTTCCGCG CATTTGTAGT CGGTATTATT TTTGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGCV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIV
101 LFGAFVVGII FGMFALFGRL LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m577/g577 88.1% identity in 160 aa overlap

	10	20	30	40	50	60
m577.pep	MERNVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCLGCVFIYGANMKLI					
g577	MERSGVFGKIVGNRILRMPSEHAAAFYPKPCKSFKLTQSWFRVRSCPCGVFIYGANMKLI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m577.pep	YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIIFGMFALFGRL					

895

```

|||||
g577      YTVIKIIILLFLLAVINMDAVTFSYLPQSVNLPLIVVLFGAFFVVGIVFGMFALFGRL
          70      80      90      100     110     120
          130     140     150     160
m577.pep  LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||:|||||:|||||:|||||:|||||
g577      LSLRGENSRLRAEVKKSARLSGQKLTAPPIQNAESAQKPX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1  ATGGAAAGGA  ACGGTGTATT  TGGTAAAT  GTCGGCAATC  GCATACTCCG
51  TATGTCGTCC  GAACACGCTG  CCGCATCCTA  TCCGAAACCG  TGCAAATCGT
101  TTAAACTAGC  GCAATCTTGG  TTCAGAGTGC  GAAGCTGTCC  GGGCGGCGTT
151  TTTATTTACG  GAGCAAACAT  GAAACTTATC  TATACCGTCA  TCAAAATCAT
201  TATCCTGCTG  CTCTTCCTGC  TGCTTGCTGT  CATTAAATACG  GATGCCGTTA
251  CCTTTTCCTA  CCTGCCGGGG  CAAAATTCG  ATTTGCCGCT  GATTGTCGTA
301  TTGTTGCGCG  CGTTTGTCGT  CGGCATCGTG  TTCGGAATGT  TTGCCTTGTT
351  CGGACGGTTG  TTGTCGTTAC  GTGGCGAGAA  CGGCAGGTTG  CGTGCCGAAG
401  TAAAGAAAAA  TGC GCGTTTG  ACGGGGAAGG  AGCTGACCGC  ACCACCGGCG
451  CAAATGCGC  CCGAATCTGC  CAAACAGCCT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.pep
1  MERNGVFGKI  VGNRILRMSS  EHAAASYPKP  CKSFKLAQSW  FRVRSCPGGV
51  FIYGANMKLI  YTVIKIILL  LFLLLAVINT  DAVTFSYLPQ  QKFDLPLIVV
101  LFGAFVVGIV  FGMFALFGRL  LSLRGENGR  LRAEVKKNAR  LGKELTAPPA
151  QNAPESAKQP  *

```

m577/a577 98.1% identity in 160 aa overlap

```

          10      20      30      40      50      60
m577.pep  MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCLGGVFIYGANMKLI
          |||||
a577      MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCPGGVFIYGANMKLI
          10      20      30      40      50      60
          70      80      90      100     110     120
m577.pep  YTVIKIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFFVVGIIIFGMFALFGRL
          |||||
a577      YTVIKIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFFVVGIVFGMFALFGRL
          70      80      90      100     110     120
          130     140     150     160
m577.pep  LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||
a577      LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq
1  atgggaaagc  tcgacatcgg  gatattgttt  gccgatttct  tcaaagattt
51  cgcgccacag  ttcggtggtt  tccaaaacgt  tggctttgcc  tacggagcag
101  acttttttgc  tgcgtttttg  ggcggattgg  aaggccacgt  gggcgatgcy
151  gcggatttcg  ctttcgctgt  atttcaggtt  gttgtagcct  tcgtgttcgc
201  cgtttttcaa  aacacggatg  ccgcgcggtt  cgcgaaata  aatatcgccg
251  gtaagtctgc  gcacaatcaa  aatatccaaa  ccggcaacga  ttccaggctt
301  gagcgtggag  gcgttggtta  a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.pep
1  MGKLDIGILF  ADFFKDFAPQ  FGGFQNVGFA  YGADFFAAFL  GGLEGHVGD
51  ADFAFAVFG  VFAVFAVFG  NTDAARFAEI  NIAGKFAHNQ  NIQTGNDPRL

```

896

101 ERGGVG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

m578.seq..

```

1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTCT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTCG TCGTTTTCG GCGGATTGG AAGGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCAG AACGCGGATG CCGCGCGGTT CGCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGGCAACGA TTTCAGGCTT

```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

m578.pep..

```

1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMGNT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGGVG*

```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
	:                         :         :					
g578	MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGHVGDADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQNTDAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	:         :         :         :					
g578	VVAFAFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

a578.seq

```

1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTCT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTCG TCGTTTTCG GCGGATTGG AAGGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCAG AACACGGATG CCGCGCGGTT CGCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

a578.pep

```

1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGNT
51  ADFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*

```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
	:                         :         :					
a578	MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGDVGNTADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQNTDAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	:         :         :         :					
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

g579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT

```



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```

51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCGC
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTGTCCCTTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCCGTTCAAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT TAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCCGCGG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

g579.pep..

```

1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLTTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

m579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCGC
101 CATTGGGACG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCCG CCCGTTCAAA GTCGGCGACT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT TAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

m579.pep..

```

1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLTTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

```

          10      20      30      40      50      60
m579.pep  MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL
          |||||
g579       MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL
          10      20      30      40      50      60

          70      80      90     100     110     120
m579.pep  KDQLSNFAAGALIIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM
          |||||
g579       KDQLSNFAAGALIIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM
          70      80      90     100     110     120

```

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	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	:     :     :     :     :					
g579	GNSIVNRSSLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	:     :     :     :     :					
g579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```

a579.seq
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGC GCGGGT TGGCGGTGGC GTTGTCTTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCCGTTCAAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCCACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```

a579.pep
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLTTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCQDLNEQVVE NLRKVNINIP FPQORDIHIIN S*

m579/a579 100.0% identity in 231 aa overlap

      10      20      30      40      50      60
m579.pep MRAAMTRAQVDATLISFLCNVANIGLLILV IIAALGRLGVSTTSVTALIGGAGLAVALSL
      |||||:|||||:|||||:|||||:|||||:|||||
a579      MRAAMTRAQVDATLISFLCNVANIGLLILV IIAALGRLGVSTTSVTALIGGAGLAVALSL
      10      20      30      40      50      60

      70      80      90      100     110     120
m579.pep KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM
      |||||:|||||:|||||:|||||:|||||:|||||
a579      KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM
      70      80      90      100     110     120

      130     140     150     160     170     180
m579.pep GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
      |||||:|||||:|||||:|||||:|||||:|||||
a579      GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
      130     140     150     160     170     180

      190     200     210     220     230
m579.pep DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX
      |||||:|||||:|||||:|||||:|||||:|||||
a579      DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX
      190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:  
g579-1.seq

```
1 ATGGACTTCA AACAAATTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51 GGGGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTCTTGGTC GGGAAATGGG CGGCGAAACG CATTGTGCGC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGG ACGGTTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGT GCGTGTGCC TTAAGAAC AGCTGTCCAA
351 TTTTGCCGCC GCGCGCTGA TTATCTGTT CCGCCCGTTC AAAGTCGGCG
401 ACTTTATCCG TGTGCGCGT TTTGAAGGAT ATGTCCGGA AATCAAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCACG CTGCCGCTTT
551 GCGCGGCCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCCGCC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGCCCG CCGCTACAT CACCGCCTTG GCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGT GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACGCGACAT ACACATCATC AATTCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```
1 MDFKQDFDLH LISVSGWHL AEKAWAFGLN LAAALLIFLV GKWAARKRIVA
51 VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVVLPSNVV MGNSIVNRSS LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAA EHPLSVQNEE RQPAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```
1 ATGGACTTCA AACAAATTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51 GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTCTGGTC GGGAAATGGG CGGCGAAACG CATTGTGCGC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGT GCGTGTGCC TTAAGAAC AGCTGTCCAA
351 TTTTGCCGCC GCGCGACTGA TTATCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCACG CTGCCGCTGT
551 GCGCGGCCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCTG CCGCTACAT CACCGCCTTG GCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGT GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACGCGACAT ACACATCATC AATTCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```
1 MDFKQDFDLH LISVSGWEHL AEKAWAFGLN LAAALLIFLV GKWAARKRIVA
51 VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVVLPSNVV MGNSIVNRST LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAHV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*
```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAARKRIVAVMRAAMTRAQ					
g579-1	MDFKQDFDLHLISVSGWHLAEKAWAFGLNLAAALLIFLVGKWAARKRIVAVMRAAMTRAQ					
	70	80	90	100	110	120
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	130	140	150	160	170	180
m579-1.pep	GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPSNVVMGNSIVNRST					

900

```

g579-1      |||||:
             G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M V Q T S L R T T D N E E V L P N S V V M G N S I V N R S S
             130      140      150      160      170      180

m579-1.pep  190      200      210      220      230      240
             L P L C R A Q V I V G V D Y N C D L K V A K E A V L K A A V E H P L S V Q N E E R Q A A Y I T A L G D N A I E I T L W
             |||||:

g579-1      L P L C R A Q V I V G V D Y N C D L K V A K E A V L K A A E H P L S V Q N E E R Q P A A Y I T A L G D N A I E I T L W
             190      200      210      220      230      240

m579-1.pep  250      260      270      280
             A W A N E A D R W T L Q C D L N E Q V V E N L R K V N I N I P F P Q R D I H I I N S X
             |||||:

g579-1      A W A N E A D R W T L Q C D L N E Q V V E N L R K V N I N I P F P Q R D I H I I N S X
             250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

```

a579-1.seq
1   ATGGACTTCA AACAAATTGA TTTTTCACAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCGG
101 CGCTGCTTAT TTTTGTGGTC GGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATGGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGGCGCGGG GTTGGCGGGT GCGGTGTGCC TTGAAAGACC AGCTGTCCAA
351 TTTTGGCGCC GCGCGCGCTG TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCGAGA GATTAAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCACA CTGCCGCTGT
551 GCCGCGCCCA AGTGATAGTC GCGTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCCG CCGCTACAT CACCGCCTTG GGCACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACCGCATC ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

```

a579-1.pep
1   M D F K Q F D F L H L I S A S G W E H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A
51  V M R A A M T R A Q V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I
101 G G A G L A V A L S L K D Q L S N F A A G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M
151 V Q T S L R T T D N E E V L P N S V V M G N S I V N R S T L P L C R A Q V I V G V D Y N C D L K V
201 A K E A V L K A A V E H P L S V Q N E E R Q A A Y I T A L G D N A I E I T L W A W A N E A D R W T
251 L Q C D L N E Q V V E N L R K V N I N I P F P Q R D I H I I N S *

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

a579-1.pep  10      20      30      40      50      60
             M D F K Q F D F L H L I S A S G W E H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A V M R A A M T R A Q
             |||||:

m579-1      M D F K Q F D F L H L I S V S G W E H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A V M R A A M T R A Q
             10      20      30      40      50      60

a579-1.pep  70      80      90      100     110     120
             V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I G G A G L A V A L S L K D Q L S N F A A
             |||||:

m579-1      V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I G G A G L A V A L S L K D Q L S N F A A
             70      80      90      100     110     120

a579-1.pep  130     140     150     160     170     180
             G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M V Q T S L R T T D N E E V L P N S V V M G N S I V N R S T
             |||||:

m579-1      G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M V Q T S L R T T D N E E V L P N S V V M G N S I V N R S T
             130     140     150     160     170     180

a579-1.pep  190     200     210     220     230     240
             L P L C R A Q V I V G V D Y N C D L K V A K E A V L K A A V E H P L S V Q N E E R Q A A Y I T A L G D N A I E I T L W
             |||||:

m579-1      L P L C R A Q V I V G V D Y N C D L K V A K E A V L K A A E H P L S V Q N E E R Q A A Y I T A L G D N A I E I T L W
             190     200     210     220     230     240

a579-1.pep  250     260     270     280
             A W A N E A D R W T L Q C D L N E Q V V E N L R K V N I N I P F P Q R D I H I I N S X

```

```

|||||
m579-1  AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

```

g580.seq
1  atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
51  cgcgtcgcag cccatttcga tggcaaggca gacttcgccg atcatgtcgc
101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc gggttcggca
151 tcgaaaatca gcttggtaaa gccgttgctg caaccgttgg caatcgcacg
201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg
251 ctttggcaga caattcgggt tcaccgaccc atgccacttc gggggaagtg
301 tag

```

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

```

g580.pep..
1  MDSPKVGCWG MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
101 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

```

m580.seq..
1  ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
101 CACCGTTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCGGCA
151 TCAAAAATCA GCTTGGTAAA GCCGTTGTCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCC GCCCAGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCGGA CAGTTCGGTT TCGCCACCC ACGCCACTTC GGGGGAAGTG
301 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

```

m580.pep..
1  MDSPKVGCWG MVLPMASASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
101 *

```

m580/g580 97.0% identity in 100 aa overlap

```

          10      20      30      40      50      60
m580.pep  MDSPKVGCWMMVLPMASASQPISMARQTSPISPPFGPTMPPPMRPVSASKISLVKPLS
          |||
g580       MDSPKVGCWMMVLPMASASQPISMARQTSPIMSPPFGPTMPPPMRPVSASKISLVKPLS
          10      20      30      40      50      60

          70      80      90      100
m580.pep  QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX
          |||
g580       QPLAIARPEAAHGKLALVILRPDALADNSVSPHATSGEVX
          70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

```

a580.seq
1  ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCTGC
101 CACCGTTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCAGCA
151 TCAAAAATCA GCTTGGTGAA ACCATTGTCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCAGA CAATTCGGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG
301 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

```

a580.pep
1  MDSPKVGCWG MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

```

902

101 \*

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPSAASQPISMARQTSPIISPPFGPTMPPPMRVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPSAASQPISMARQTSPIISPPFGPTMPPPMRVSASKISLVKPLS					
	10	20	30	40	50	60

  

	70	80	90	100
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSSEVX			
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSSEVX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1 atgcacttcg cccagcttgt gggcacaacc ggtatagaac aaaatacgtt
51 ctgtcgctcg gggttttacc gcacgatat gggcggaaat accgatgttg
101 cgggtacagg tgatcggggg cttacgagcc attttattag cctttcaaaa
151 ttagaaacgg aagtgagaga atgctttgtt ggcttcagcc atacggtgta
201 cttcttcacg ttttttcaac gcaccgccac ggcttcgga cgcataatc
251 aactcgctcg ccaaacgcag atccatggat ttctcaccac gtttcgggc
301 cgcgtcgcca acccaacgca ttgccaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LTSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLITTFAG
101 RVANPTHQCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51 CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CCGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCTTCGGA CGCATCAATC
251 AATTGCGCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGCGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1 MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTVQADRG LTSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFITTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGLTSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAQADRGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60

  

	70	80	90	100	110
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFITTFAGRIANPAHCQSQTAX				
g581	GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFITTFAGRVANPTHQCSQTAX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

903

```

a581.seq
1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATAG CCTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGCGGG
301 CGCATCGCGA ACCCAGCGCA TGCCAAAGC CAAACGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTVQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRG	LTSHFISLSKLETEVRECFV				
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTQADRG	LTSHFISLSKLETEVRECFV				
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLTFAGRIANPAHCQSQTAX					
a581	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLTFAGRIANPAHCQSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
1  atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
51  agagaccgcy ctgcaatgcy ccgcttttgac ggacaatggt acgcgtttgg
101 cgtgttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttggat aagggcgagg cggtcattgt tgttgaaaaa ggcgggggatg
251 cgcttcctgc cgacagtgcg gcggaacccg ccgatatcta tacgcctttg
301 agcctgatgt acgacttgga caaaaacgat ttgcgcgggc tgttgggcgt
351 acgcgaacac aatccgatgt accttatgcc gtttgggtat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttcggacagc agaaacgtgc ggaaaccaa ttgcaggttt cgttcaaaag
501 caaaattgcc gaaaatttgt ttaaaacccg cgcggatctg tggttcggct
551 acacccaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601 ccgttcgcga atacggatta caaacctgaa attttcctga cccagcctgt
651 gaagggcgat ttgcgcttcg gcggcaggct gcgtatgctc ggtgcggggt
701 ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttctggaac
751 aggtatttat ccatggcagg catggaatgg ggcaaatga cggtgattcc
801 gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851 ccgatatgac cgactatatg gggatatggc acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgttaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
1  MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
51  EQQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLVREH NPMYLMPPFY NNSPNYAPSS PTRGTTVQEK
151 FGQOKRAETK LQVSFKSKIA ENLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDRQNVYSV LRYNPKTYG AIEAAYTFPI KGKLGVVVR FHGYGESLID
351 YNHKQNGIGI GLMFNDWDGI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GCGGGGATG
251 CGCTTCTGCG CGACAGTGGG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAITCGC
401 CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAACCAAAA TTGCAGTTT CGTTCAAAG
501 CAAAAATTGCC GAAGATTGT TAAAAACCGC CCGGATCTG TGTTCCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CGGTTCCGCA ATACGGATTA CAAACCTGAA ATTTCTCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCGGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTATCG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTGCCT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATGCG CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAAATG GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQKKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTIVIPRVW VRAFDQSGDK NDNPDADYD GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKVVVR FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

```

      10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEQESKAVLN
          |||
g582      MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEQESKAVLN
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPSLMYDLKNDLRGLLGVREH
          |||
g582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPSLMYDLKNDLRGLLGVREH
          |||
      70      80      90     100     110     120

      130     140     150     160     170     180
m582.pep  NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKKRAETKLQVSFKSKIAEDLFKTRADL
          |||
g582      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKKRAETKLQVSFKSKIAENLFKTRADL
          |||
      130     140     150     160     170     180

      190     200     210     220     230     240
m582.pep  WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
          |||
g582      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
          |||
      190     200     210     220     230     240

      250     260     270     280     290     300
m582.pep  QSRPESRSWNRIYAMAGMEWGKLTIVIPRVVWRAFDQSGDKNDNPDADYDGYGDVKLQYR
          |||
g582      QSRPESRSWNRIYAMAGMEWGKLTIVIPRVVWRAFDQSGDKNDNPDADYDGYGDVKLQYR
          |||
      250     260     270     280     290     300

      310     320     330     340     350     360
```



905

```

m582 . pep      LNDQRNVYSVLRYPNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
                  |||
g582            LNDQRNVYSVLRYPNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
                  310      320      330      340      350      360

                  370
m582 . pep      GLMFNDLDGIX
                  |||
g582            GLMFNDWDGIX
                  370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1   ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTTT GCAGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAG CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCAATTGT TGTTGAAAAA GGCAGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGGG CAAAACGAT TTGCGCGGGC TGTGCGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGTG TTAACACCGG CCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTCG GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCGCTA TTGCGCTACA ATCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1   MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNG QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYD GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

m582/a582      100.0% identity in 370 aa overlap

                  10      20      30      40      50      60
m582 . pep      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
                  |||
a582            MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
                  10      20      30      40      50      60

                  70      80      90      100     110     120
m582 . pep      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVREH
                  |||
a582            LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVREH
                  70      80      90      100     110     120

                  130     140     150     160     170     180

```

906

```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQQKRAETKLQVSFKSKIAEDLFKTRADL
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582           NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQQKRAETKLQVSFKSKIAEDLFKTRADL
               130      140      150      160      170      180

               190      200      210      220      230      240
m582.pep      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSN
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582           WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSN
               190      200      210      220      230      240

               250      260      270      280      290      300
m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582           QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
               250      260      270      280      290      300

               310      320      330      340      350      360
m582.pep      LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582           LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
               310      320      330      340      350      360

               370
m582.pep      GLMFNDLDGIX
               ||||||||||
a582           GLMFNDLDGIX
               370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatttacc catcttgccct tctgtgcctt
51  ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgtaaccgat gccacgcgtt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg aaatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaacgca ctcaacgcat cgtcatcgc cgcccgccgt ttgtcggcgg
351 ttacgccggt tactgcgacc aaccgcgagg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcgcca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcc
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSQIFT HLAFCAPCGI GAVTAGNRLH NRMYNAAAAR GIGRGNQSQQ
51  QFGKSETVTD AQRFPSSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIAGR RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSRLRDP VYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGTTG ACCAAAGCCA AATATTACC CATCTGCCTT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCgcgc GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TCGATGGCA ATCAGCCAAA TCAACGGATT
301 GCGGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTGCGCGG
351 TTACGCCGCT TACTGCGACC AACCAGCAGG CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCGGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA

```

551 CCCAATTTCA TCATATTGAC CTCGGTAAAA AAGACCGTCC CGAAAAATCG  
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pcp..

```

1  MIVDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 QERTQRIahr RARFVGgYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 QQRPSLRLLDP VGYGQCQNGG AQYCGNGEGY RFETQFHID LRKDRPEKS
201 EK*

```

m583 / g583 98.5% identity in 202 aa overlap

		10	20	30	40	50	60
m583 . pep		MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAAARGIGRNGSQQQFGKSETVTD					
		:					
g583		MIIDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAAARGIGRNGSQQQFGKSETVTD					
		10	20	30	40	50	60
		70	80	90	100	110	120
m583 . pep		AQRFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRRARFVGGYAG					
g583		AQRFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRRARFVGGYAG					
		70	80	90	100	110	120
		130	140	150	160	170	180
m583 . pep		YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLPVGYGQCQNQGAQYCGNGEGY					
g583		YCDQPDGNNRQRAQRHNLADNGGNHTDKHSQQRPSLRLPVGYGQCQNQGAQYCGNGEGY					
		130	140	150	160	170	180
		190	200				
m583 . pep		RFETQFHHIDLRRKKDRPEKSEKX					
g583		RFETQFHHIDLRRKKDRPEKSEKX					
		190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1	ATGATAGTTG	ACCAAAGCCA	AATATTTACC	CATCTTGCCT	TCTGTGCCTT
51	TTGCGGGATT	GGAGCCGTAA	CTGCCGGCAA	TCGACTGCAT	AATCGGATGT
101	ATAATGCGCG	CGCCGCGCGC	GGTATTGGAA	GGGGTAACGG	GAGCCAGCAG
151	CAGTTTCGGAA	AGAGCGAGAC	GTTAACCGAT	GCCGACGTT	TTTCTTCCAA
201	AAACGGCGAT	AAACAAATAT	CCGATACGTA	TCCCCAGCCC	TTTTTTGAGC
251	AAACCGCGCG	AAATCATAAC	TGCGATGGCA	ATCAGCCAAA	TCAACGGATT
301	GGCGAACGCA	CTCAACGCAT	CGCTCATCGC	CGCACC CGGT	TTGTTCGGCG
351	TTACGCGCGT	TACTGCGACC	AACCCGACGG	CAATAATCGA	CAGCGCACCC
401	AACCGCATGG	CCTTCCCGAT	AATCGCGCGA	ATCACACCGA	TAAACATGGC
451	CAGCAGCGTC	CAAGCCTGAG	GCTTGACCCC	GTGCGGTACG	GGCAGTGCCA
501	AAACCAAGGC	GCACAATACT	GCGGCAATGG	CGAGGGGTAT	CGGTTTGAAA
551	CCCAATTTC A	TCATATTGAC	CTCCGTAAAA	AAGACCGTCC	CGAAAAATCG
601	GAAAAATAA				

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pap

1	MIVDQSQIFT	HLAFCACFCGI	GAVTAGNRLH	NRMYNAAAAA	GIGRGNQSQQ
51	QFGKSETVTD	AQRFSKNGD	KQISDTHPPQ	CFEQTARNHN	CDGNQPNQRI
101	GERTQRIAH	RTRFVGGYAG	YCDQPDGNNR	QRTQRHGLAD	NGGNHTDKHG
151	QQRPSRLRDP	VGYGQCQNQG	AQYCGNGEGY	RFETQFHHD	LKKDRPEKS
201	EK*				

m583/a583 99.0% identity in 202 aa overlap

m583.pep MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRNGSQQFGKSETVTD

908

```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNSSQQQFGKSETVTD
           10      20      30      40      50      60

           70      80      90      100     110     120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQNPNQRIGERTQRIAHRRARFVGGYAG
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQNPNQRIGERTQRIAHRRARFVGGYAG
           70      80      90      100     110     120

           130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
           130     140     150     160     170     180

           190     200
m583.pep  RFETQFHHDLRKKDRPEKSEKX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a583      RFETQFHHDLRKKDRPEKSEKX
           190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

g584.seq..

```

1  atgetgcgtt ctattttggc ggcttcctg ctggcggtat cttttcggc
51  ggcggtcag gcaattgaatt acaatattgt cgaattttcc gaatcggcgg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcgcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttgta aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattggat
251 cgcgcagtgc gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggaggcca gggattttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgccgtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcgttctg ggtgcgtccg gttataaaat cgtcaaatg aattttgggc
551 aaatcggcag ccatattgcg ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggt aagattcagc
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

g584.pep Length:..

```

1  MLRSILAASL LAVSFPAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNAVNA EFVKFNNFT RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK AEGRDFDALN RFIADVQTD SLEDTFPSVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAGVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDSAAPG VEBISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

m584.seq..

```

1  ATGTTGCGTC TTGTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAAATCAA
201 CAAGTTCATC AGAAAATCGA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTAAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTATTG CCGATATTCA AGCAGATGCC GCGTTGGMAT
401 ATACGGATTT CCATGTGTCG CGGAAACGCC GCAACGAGGT CATCATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATCCGC
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

909

m584.pep..

```

1 MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51 EGRDKNVNA EFVKKFNKFI RSKNGSFKT ELVSRSPMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep      MLRLVLAASLSAVSFPAAAEALNYNIVEFSAGVEVAQDTMSARFQVTAEGRDKNVNA
              ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g584           MLRSILAASLLAVSFPAAAEALNYNIVEFSAGIEVAQDTMSARFQVAAEGRDKNVNA
              10      20      30      40      50      60

              70      80      90     100     110     120
m584.pep      EFVKKFNKFI RSKNGSFKT ELVSRSPMPR YQYTNRRRIQ TGWEERAEFK VEGRDFDELN
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
g584           EFVKKFNKFI RSKNGSFKT ELVSRSPMPR YQYTNRRRIQ TGWEERAEFK AEGRDFDALN
              70      80      90     100     110     120

              130     140     150     160     170     180
m584.pep      RFIADIQADAALXYTDFHVS RERRNEVIXQVSKDAVLRFK ARAEKLAVLGASGYKIVKL
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g584           RFIADVQTDASLEDTFVS RERRNEVIDQVSKDAVLRFK ARAEKLAVLGASGYKIVKL
              130     140     150     160     170     180

              190     200     210     220     230
m584.pep      NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVEEISISVNGTVQFX
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g584           NFGQIGSHIAGDGAVRAKMLRAMPMAASVNMKGTD SAAPGVEEISISINGTVQFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

```

a584.seq
1 ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51 ..... ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG AAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAAATCAA
201 CAATTTCAAC AGAAAATCAA AAAATGGTAG CTTTAAAC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TCGGTTGAAC CGTTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGTTGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATCCGC
651 CGCGCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1802; ORF 584.a&gt;:

```

a584.pep
1 MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51 EGRDKNVNA EFVKKFNFT RSKNGSFKT ELVSRSPMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep      MLRLVLAASLSAVSFPAAAEALNYNIVEFSAGVEVAQDTMSARFQVTAEGRDKNVNA
              ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a584           MLRSILAASLL-----IVEFSAGVEAVQDTMSARFQVTAEGRDKNVNA
              10      20      30      40

```

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	70	80	90	100	110	120
m584.pep	EFVKKFNKFIRKSKNGSFKTELVSRSAMPYQYTNRRITQTGWEEAEFKVEGRDFDELN					
a584	EFVKKFNNFTRKSKNGSFKTELVSRSAMPYQYTNRRITQTGWEEAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADAALXYTDFHVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt  tccaacgcat  tttcgccaca  ttttgccggg  ttatcgctctg
51  cgcaatcttt  gtggcgagtt  tttctttttg  gctgggtgcag  aacacccttg
101  ccgaaaacca  attcaaccaa  cgccgcacca  tcgaaaccac  attgatgggc
151  agcattattt  ccgcattcaa  gacacggggc  gacaacggcg  cgcgcgaaat
201  cctgaccgaa  tggaaaaaca  gcccggtctc  atccgcggtt  tacgtcatac
251  agggcgacga  gaaaaaagac  atcttaaacc  gctatatcga  caattacacc
301  atagaacgcg  cccggctggt  tgccgccaac  aacccccatt  ccaacctgtg
351  ccgcacgaa  tacgaccgtt  tcggcgaa  atacctgttc  ttcattaaag
401  gctgggacaa  ccaccaggca  caacgcctgc  ccagcccgct  gtttatcccg
451  ggctgcccgc  ttgccccgat  ttggcacgaa  ttcatcatcc  tctccttcat
501  catcattgtc  ggactgctga  tggcatatat  ccttgccggc  aacattgcca
551  aacccatcag  aatcttaggc  aacggcatgg  acagggtggc  agaacgagaa
601  cttgaagacc  gcgtttgcca  acagggttcg  gaccgcgacg  acgaattggc
651  cgatgttgcc  atgaattcgc  acacaatggt  ggaaaaactg  gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFORIFAT  FCAVIVCAIF  VASFSFWLVQ  NTLAENQFNQ  RRTIETLMG
51  SIISAFKTRG  DNGAREILTE  WKNSPVSSAV  YVIQGEKKD  ILNRYIDNYT
101  IERARLFAAN  NPHSNLVRIE  YDRFGEEYLF  FIKGWDNHQA  QRLPSPLFIP
151  GLPLAPIWHE  FIILSFIIIV  GLLMAYILAG  NIAKPIRILG  NGMDRVAERE
201  LEDRVCCQVR  DRDELADVA  MQPDTMVEKL  E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAAACTGT  TCCAACGCAT  TTTGCCACA  TTTTGCGCGG  TTATCGTCTG
51  TGCAATCTTT  GTGGCGAGTT  TTTCTTTCTG  GCTGGTGCAG  AACACCCTTG
101  CCGAAAACCA  GTTCAACCAA  CGCCGCACCA  TCGAAACCAC  TTTGATGGGC
151  AGCATCATTT  CCGCATTCGG  GGCACGCGGG  GACGCGGGTG  CGCGCGAAAT
201  CCTGACGGAA  TGGAAAGACA  GCCCGGTCTC  ATCGGGCGTG  TACGTTATAC
251  AGGGCGACGA  GAAAAAGAT  ATCCTGAACC  GGTATATCGA  CAGCTATACC
301  ATCGAAGCGG  CCCGGCTTTT  CGCGCGCGGA  CACCCGCATT  CCAACCTCGT
351  CCATATCGAA  TACGACCGCT  TCGGCGAAGA  ATACCTGTTT  TTCACCAAG
401  ACTGGGACAA  ACTCCAAGCC  CGCGCGCTGC  CCAGCCCCCT  GTTGATCCCC
451  GGCCTGCCGC  TCGCCCCGAT  TTGGCACGAA  CTCATCATAT  TGTCTTCAT
501  CATCATCGTC  GGAATGCTGA  TGGCATATAT  CCTCGCGGCG  AACATTGCCA
551  AACCCATCAG  AATCTTAGGC  AACGGCATGG  ACAGGGTGGC  AAACGGAGAA
601  CTTGAAACCC  GTATCTCCCA  ACAGGTCGAC  GACCGCGACG  ACGAATTGTC
651  CCATCTTGCC  ATCCAATTGG  ACAAAATGGT  GGAAAAACTC  GAAAAACTCG
701  TTGCCAAGA  ACGCCACCTG  CTCCATCAGC  TCTCCCATGA  AATGCGTTCT
751  CCCCTTGCGC  GCATGCAGGC  AATTGTCCGA  CTGATTGAGG  CGCAGCCCCA
801  AAAACAGGAG  CAATATCTCA  AACGGCTGGA  AGGCGAACTG  ACCCGCATGG
851  ATACGCTGGC  CGGGGAACCT  TTAACCCGTG  CCCGTCTCGA  AACTTCCAAT
901  ATGGCTTTGG  AAAAAGAAAG  CCTGAAACTC  CTGCCCTTCC  TGGGCAACCT
951  GGTAAGAC  AATCAAAGCA  TTGCCAGAA  AAACGGACAA  ACGGTTACCC
1001  TGTCTGCCGA  CGGAAAAATC  CCCGAAACA  CAACCATCCT  TGCCAACGAA

```

```

1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCAGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAAACGGC CCGGCGTGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGAATGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

m585.pep..

```

1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKDD IILNRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDDELSHLA IQFDKMVEKL EKLVAKEHRL LHHVSHEMRS
251 PLARMQAIVG LIQAQPKQKE QYLKRLEGEL TRMDTLAGEL LTLSRLETSN
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTLSADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNYSPG GSTILINIGQ DHKHWIIDVT DNGPGVDEM Q
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585 / g585 88.3% identity in 231 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFRARG					
g585	MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFKTRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGDEKDD IILNRYIDSYT IERARLFAAG HPHSNLVHIE					
g585	DNGAREILTEWKNSPVSSAVYVIQGDEKDD IILNRYIDNYT IERARLFAANNPHSNLVRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHE LIILSFIIIVG LLMAYILAG					
g585	YDRFGEEYLF FIKGWDNHQAQRLPSPLFIPGLPLAPIWHEFIILSFIIIVG LLMAYILAG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAKPIRILGNMMDRVANGELETRISQQVDDRDDELSHLAIQFDKMVEKLEKLVAKERHL					
g585	NIAKPIRILGNMMDRVAERELEDVRCQQVDRDDELADVAMQFDTMVEKLEX					
	190	200	210	220	230	
	250	260	270	280	290	300
m585.pep	LHHVSHEMRSPLARMQAIVGLIQAQPKQKEQYLKRLEGELTRMDTLAGELLTLSRLETSN					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

```

1 ATGAAACTGT TCCAACGCAT CTTGCCACA TTTTGC GCGG TTATCGTCTG
51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCCTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAAGACA GCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC
301 ATCGAACGCG CCCGCTTTT CGCCGCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCTGC CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCG TCGCCCGCAT TTGGCAGAA CTCATCATAT TGTCTTCAT
501 CATCATCGTC GACTGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
551 AACCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCA ACAGGTGCAC GACCGGACG ACGAATTGTC

```

```

651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAGA ACGCCACCTG CTCCATCACG TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCTGA CTGATTCAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAACTG TTAACCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCGAAAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGCGGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACGCG TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

a585.pep

```

1 MKLFQRI FAT FCAVIVCAIF VASFSEWL VQ NTLAENQFNQ RRTIETTL MG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGD EKKD ILHRYIDS YT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWD KLQA RRLPSPL LIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIR ILG NGMDRVAN GE
201 LETRISQQVD DRDDEL SHLA IQFDKMVEKL EKLVAKE RHL LHHVSHEM RS
251 PLARMQAIVG LIQAQPQKQE QYLKRLE GEL TRMDTLA GEL LTLRLETS N
301 MALEKESLKL LPFLGNL VED NQSIAQKNGQ TVTLSAD GKI PENTTILAN E
351 SYLYRAFDNV IRNAVNY SPE GSTILINI GQ DHKHWID VT DNGPGVD EMO
401 LPHIFTAFYR ADSSANKPGT GLGLALTQ HI IEQHCGKI IA ENIKPNGL RM
451 RFILPKKKTG SKTEKSAN*

```

m585/a585 99.8% identity in 468 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQRI FATFCAVIVCAIFVASFSEWL VQNTLAENQFNQ RRTIETTL MGSIISAFRARG					
a585	MKLFQRI FATFCAVIVCAIFVASFSEWL VQNTLAENQFNQ RRTIETTL MGSIISAFRARG					
	10	20	30	40	50	60
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGD EKKDILNRYIDS YTIERARLFAAGHPH SNLVHIE					
a585	DAGAREILTEWKDSPVSSGVYVIQGD EKKDILHRYIDS YTIERARLFAAGHPH SNLVHIE					
	70	80	90	100	110	120
m585.pep	YDRFGEEYLF FTKDWD KLQARRLP SPLLPGLPLAPIWHE LIILSFIIIV GLLMAYILAG					
a585	YDRFGEEYLF FTKDWD KLQARRLP SPLLPGLPLAPIWHE LIILSFIIIV GLLMAYILAG					
	130	140	150	160	170	180
m585.pep	NIAKPIR ILGNMDRVANGELETRISQ QVDDRDEL SHLAIQFDKMVEKLEKLVAKERHL					
a585	NIAKPIR ILGNMDRVANGELETRISQ QVDDRDEL SHLAIQFDKMVEKLEKLVAKERHL					
	190	200	210	220	230	240
m585.pep	LHHVSHEMRS PLARMQAIVGLIQAQPQKQE QYLKRLE GELTRMDTLA GELLTLRLETSN					
a585	LHHVSHEMRS PLARMQAIVGLIQAQPQKQE QYLKRLE GELTRMDTLA GELLTLRLETSN					
	250	260	270	280	290	300
m585.pep	MALEKESLKL LPFLGNL VEDNQSIAQKNGQ TVTLSAD GKI PENTTILANESYLYRAFDNV					
a585	MALEKESLKL LPFLGNL VEDNQSIAQKNGQ TVTLSAD GKI PENTTILANESYLYRAFDNV					



913

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1  atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatatatt
51  ttggaaaacc acgggcaa at ggctgtttgc cctgctgatt ttggcggcac
101 tccggtactt gggatacacg gtttaccaaa accgtgcggc ttcccaaat
151 caggaagcgg cggcgggtgct ggcaaacatc gtggaaaagg cgcaaaacaa
201 agccccgcaa agcgaaatca atgccgaact gtccaaactc caacaaagct
251 acccccatct catttccgcc gcccaagcca cgtgatggc ggccggcaacc
301 gaatttgacg cgcagcgta c gatgttgcc gaaggtcatt tgaatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttggcg gcgcagcgctc
401 tggcggttgt gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451 ctcgacacgc cgggttgaggc ggacttcgcc cccctgctga tggaaactaa
501 aggcgatgtt tatgccgcac aggaaaaaag ccaggaagcc ttaaaaaact
551 acggacagcg tttgaaaaaa atgcctcaag attctgtcgg tcgcgaattg
601 cttcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1  MAAHLEEQQE LDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNRRAASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAElskl QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHlKWVLSN QKDSLlQALA AQLRGVVLlQ QKKYDAALAA
151 LDTpVEADFA PLLMETKGDV YAAQEKsQEA LKNYGQALEK MPQDSVGREL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1  ATGGCAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAAC TTAATATATT
51  TTGGA AAAACC ACGGGCAAAT GGCTGTTTGC CTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTAAAGT TTCCCAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAACATC GTAGAAAAGG CGCAAAGCAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GACCAAATC CAACAAAGCT
251 ACCCGCATTC CATTTCGCC GCCCAAGCCA CACTGATGGC GGCGGCAACC
301 GAATTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 GTTGTTCCAAC CAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAT ACATGCCCGC GCTTGCCGCG
451 CTCGATACGC CGGTTGAAGC GGACTCGCC CCCCTGCTGA TGGAAACCA
501 AGGCGATGTC TATGCCGCAC AGGGA AAAAG CCAGGAAGCC TTA AAAAAT
551 ACGGACAGGC TTAGAAAAA ATGCCTCAAG ATTCTGTCG TCGCAATTG
601 GTTCAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1  MAAHLEEQQE LDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNRKVSQN
51  QEAAAVLANI VEKAQSKAPQ SEINAEltkl QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHlKWVLSN QKDSLlQALA AQLRGVVLlQ QKKYDAALAA
151 LDTpVEADFA PLLMETKGDV YAAQKsQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAAHLEEQQELDNFKYFWKTGKWL Falli LAALGYLGYTVYQNRKVSQNQEAAAVLANI					

914

```

g586      MAAHLEEQQELDNFKYFWKTTGKWLFAALLILAALGYLGYTVYQNRAASQNQEAAVLANI
          10      20      30      40      50      60

          70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLVLN
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      VEKAQNKAPQSEINAELSKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLVLN
          70      80      90      100     110     120

          130     140     150     160     170     180
m586.pep  QKDSLIIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      QKDSLIIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQKSQEA
          130     140     150     160     170     180

          190     200     210
m586.pep  LKNYGQALEKMPQDSVGRELQMKLDSLKX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      LKNYGQALEKMPQDSVGRELLQMKLDSLKX
          190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1   ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTT
51  TTGGAAGAAC ACGGGCAAAT GGCTGTTTGC CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTACCAAAA ACCGTGCGGC TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAACATC GTGAAAAGG CGCAAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAAGCT
251 ACCCCCATTC CATTTCCGCC GCCCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 ATTGTCCAAC CAAAAGACA GCCTGATCCA GGCCTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTTCGAA CAAAAAAT ACATGCCGC GCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGAATTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAGAAC CCAGGAAGCC TTAAGAAACT
551 ACGGACAGGC TTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAATGA  AACTTGATTG GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1   MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAELAKL QQSYPHSISA AQATLMAAAAT
101 EFDAQRYDVA EGHKLKWLVLN QKDSLIIQALA AQLGVVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQGSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586/a586 97.6% identity in 209 aa overlap

```

          10      20      30      40      50      60
m586.pep  MAAHLEEQQELDNFKYFWKTTGKWLFAALLILAALGYLGYTVYQNRAASQNQEAAVLANI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      MAAHLEEQQELDNFKYFWKTTGKWLFAVLI LAALGYLGYTVYQNRAASQNQEAAVLANI
          10      20      30      40      50      60

          70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLVLN
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      VEKAQNKAPQSEINAELAKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLVLN
          70      80      90      100     110     120

          130     140     150     160     170     180
m586.pep  QKDSLIIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      QKDSLIIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
          130     140     150     160     170     180

```

915

	190	200	210
m586.pep	LKNYGQALEKMPQDSVGR	ELVQMKLDSLKX	
a586	LKNYGQALEKMPQDSVGR	ELVQMKLDSLKX	
	190	200	210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
1  atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 gccgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
201 ccccatcccg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251 ccggcacgct cggtttgcgc tacggactga ccggcaatac cgacatttac
301 ggcagcggca gctatctgtg gcacgaagaa cgcaaactcg acggcaacgg
351 caaaacccgc acaaaacgga tgtccgacat atccgccggc atcagccaca
401 ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501 gctttgcccc ttttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENSR
51  AALAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKD GK NPALISFLES
151 TVYEKSRNKA SLIKKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACTTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTCG ACGGCAACAG
351 CAAAACCCGC AAAAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGCGGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGCTGTC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACACGG CTTTAAACGC
801 ATCCGCACGT TCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTLDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60

916

```

m587.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587       MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENSRAELAAPVYIQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m587.pep  TGATSFIPITEIQENGSTNMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587       TGATSFIPITEIQENGSTNMLAGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
          70      80      90      100     110     120

          130     140     150     160     170     180
m587.pep  NKRMSDVSLSHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587       NKRMSDISAGISHTFLKDGKNPALISFLESTVYEKSRNKASLIKKRGLCPFFYNLRINYEY
          130     140     150     160     170     180

          190     200     210     220     230     240
m587.pep  LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK
g587      X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1819>:

```

a587.seq
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAAGTGG CCGCACCAGT TTACATCCAA ACCGGCGCAA CTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGC GC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTCG ACGGCAACGG
351 CAAAACCGGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCGTCGTC CTCTCATTTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCAATATAT CTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCT GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1820; ORF 587.a>:

```

a587.pep
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENN
51  AELAAPVYIQ TGATSFIPIP TEIQENGSTN DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVS LG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

m587/a587 95.2% identity in 289 aa overlap

```

          10      20      30      40      50      60
m587.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a587       MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m587.pep  TGATSFIPITEIQENGSTNMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a587       TGATSFIPITEIQENGSTNMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
          70      80      90      100     110     120

```

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHFTFX					
a587	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHFTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

g588.seq

```

1   atgcttaaac atctcgcat cctactgcc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacc
101 aaggcgggat cggaagagac gggcttcctt caggcaaagg catatggcgt
151 tgccgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgcggg ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaacaacg gcttggcaca cggcaggttc gccgcctcgc aaaacggcga
351 aacctctttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

g588.pep..

```

1   MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

m588.seq..

```

1   ATGCTTAAAC ATCTCGCATT CCTACTGCCG GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCCTGA CTTCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAGAC GGTAAACCCG CCGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTTC TTTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAGG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCTCTTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

m588.pep..

```

1   MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENMIK EVKLPHNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

918

```

m588.pep      MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVKGDKGKPGKGTWRCQDGRNYTGS
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g588          MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGLP SGKGIWRCRDGRGYTGS
               10      20      30      40      50      60

               70      80      90      100     110     120
m588.pep      FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g588          FKNGKFDGQGVYTVAAAGREVLEPFNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
               70      80      90      100     110     120

               130     139
m588.pep      IMKCENGMIKEVKLPKNKX
g588          YYEMRTRHDX
               130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1   ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CGCCGCGTCC GCCGTCTCTGA CTTCCCTATCA AGAACC CGGC TGCACCTACG
101 AAGGCGATGT CGGCAAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCCTACTA TACCGGTTTCG TTTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAACGG CATGATTAA GAAGTGAAGC
401 TGCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1   MLKHLAFLLP AMMFALPAAS AVLT SYQEPG CTYEGDVGKD GKPGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKLPKNK*

m588/a588    96.4% identity in 138 aa overlap

               10      20      30      40      50      60
m588.pep      MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVKGDKGKPGKGTWRCQDGRNYTGS
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a588          MLKHLAFLLPAMMFALPAASAVLT SYQEPGCTYEGDVGKD GKPGKGTWRCQDGRNYTGS
               10      20      30      40      50      60

               70      80      90      100     110     120
m588.pep      FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a588          FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
               70      80      90      100     110     120

               130     139
m588.pep      IMKCENGMIKEVKLPKNKX
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a588          IMKCENGMIKEVKLPKNKX
               130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq.
1   atgcaacaaa aaatccgttt ccaaatcgag gcgatgacct gtcaggcatg
51  tgcttcgcgc attgaaaaag tgttgaacaa aaaagatttt gtcgaatcgg
101 cgggagttaa ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgcgaggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251 atacggctg gcggtgtggt ctttctgtga ccatcaatat cccgttcctt

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919

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301 atcggatatgg tagggatgat gctaaaaggg ctgaattgga caccggcacga
351 ttggatgatt ccgcctgtat ggcagtttgt actggcaagc atagtgcAAC
401 tttggctggc aatcccgttt taaaaagcg cgtgggcaag cattaaggcg
451 gggctggcga atatggacgt actcgtttacc atcggcacgg tgtcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatgcg gcgcacggta
551 tggcgcattgt gtattttgaa gcgggcgtga tggtagtcgg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcaccaaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgcgaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttatc
751 cgcaccaacc acggcgaacg catcgtgccc gacggcatta tcgaaagcgg
801 cagcggttgg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggg gggcggcaaa gtgttgccg gcgcgctgat gaccgaaggc
901 agcgtggtgt accgcgccgc gcagctcggc agccaaaccc tgcctcggcg
951 catgatgaac gcgctctctg aagcacaagg cagtaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcatc
1051 gcgcttctga cttttatcgt tgcttggtcg attaagggcg attggacggt
1101 cgcactgatg caccgcgttg ccgcttttgg gattgcctgc ccgtgcgcg
1151 tcggtctggc gacccttgcg gcgattatgg tcggcatggg caaagcggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtatttg acaaaacccg tacgctgacc gaaggcaggc
1301 cgcaggttgc ccgcgtttat tacgttccc acagcggtt tgacgaagac
1351 gctttgtacc gcatcgccgc cgcgctcgag caaaacgccg cccaccgct
1401 cgcgcgcgcc atcgtctccg ccgcacaagc gcgcggtttg gagattcccg
1451 ctgcacaaaa tgcgcaaacg gttgtcggag caggcattac cgccgaagtg
1501 gaaggcgtgg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgcggaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacgg atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccgaagc cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtcc gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaaaccc tggcgtggtg
1851 cggcgacggc atcaacgacg cgcgcgcgct tgccgccgcc aacgtcagct
1901 tcgccatgaa aggcggtgcg gacgttgccc aacacaccgc ctccgccacg
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttctctaca
2051 atatattggg cattccgctc gccgcgctcg gctttttaa tcccgtcata
2101 gcaggcgcgg caatggcggc aagctcgggt tcggtatttg gcaatgccct
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

```

g589.pep.
1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIAKI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLTINIPFL
101 IGMVGMMLKG LNWTRHDWMI PPVWQFVLAS IVQLWLAIPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPQVAAYV YVPDSGFDED
451 ALYRIAABVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVVDG INDAPALAAA NVSFAMKGGG DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLEFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

```

m589.seq.
1  ATGCAACAAA AAATCCGTTT CCAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCGC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTCCCT

```

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301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTACAA AAGCGCGTGG GCGAGCATT AAGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCGTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGTCACTGGG TAAATTTTTG
601 GAACACCGTA CAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGCGGGGCG
851 GCAAAGTGTG GCGGGGCGCG TTAATGACCG AAGGCACTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AACCAGCTC GCGGACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TCGCGCGCTA GCCGATAAAG
1001 CGGCTGCGGT ATTCGTGCCT GCCGTGCTGG GCATTGCGGT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CGCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCGGT ATGGGCAAAG CGGTAAACA CGGTATTTGG
1201 TTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCCACGTCG ATGCCGTCGT
1251 GTTGGACAAA ACCGGTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCCG
1301 TTTATTGCGT TCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCGCCGCCG TCGAACAAAA CGCCGCCCAT CGGCTCGCCC GTGCCATCGT
1401 CTCCGCCGCC CAAGCGCGCG GTTGGACAT TCCCGCCGCA CAAAACGCAC
1451 AAACCGTTGT CGGCGCAGGC ATTACCGCCG AAGTGGAAAG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TCGGGTCTCA GTCGATAACA
1601 AACCATCGG CGCATTGCA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CGGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCCT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAACCTCAAAG CCGCCGGCAA AACCGTGGCG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCCGAACAT ACCGCATCCG CCACGCTGAT GCAGCATTCG
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTC
2051 CTCTCGCCGC GCTTGCTTTT TTAAATCCCG TCATCGCTGG CGCGGCAATG
2101 GCGGCAAGCT CGGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAACGGGT
2151 AAAATCGAT TAG

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This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

m589.pep..

```

1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIARI IEKTYGAKKE KTEDTLPOPE AEHHIGWRLW LLFTINVPEFL
101 IGMAGMMIGR HDWMIPPLWQ FALASVQLW LAIPFYKSAW ASIKGGLANM
151 DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVEFEVGMV IGFVSLGKFL
201 EHRTKKSSLN SLGLLLKLTP TQNVQNRGE WKQLPIDQVQ IGDILIRANH
251 ERIAADGIEE SGSGWADESH LTGESNPEEK KAGGKVLAGA LMTEGSVVYR
301 ATQLGSQTQL GDMNALSEA QGSKAPIARV ADKAAAVFVP AVVGIALLTF
351 IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401 FKDAAMEEA AHVDAVVLDK TGTLEGSPO VAAVYCVFDS GFDEDALYRI
451 AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVGAG ITAEVEGVGL
501 VKAGKAEFAE LALPKFLDGW WDIASIVAVS VDNKPIGAF A LADALKADTA
551 EAIGRLKHN IDVYIMSGDN QGTVEYVAKQ LGIAHAFGNM SPRDKAAEVQ
601 KLKAAGKTVA MVDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651 VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701 AASSVSVLSN ALRLKRVKID *

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Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

          10      20      30      40      50      60
m589.pep  MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIARI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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g589      MQQKIRFQIEAMTCQACASRIEKNLNKKDFVESAGLVNFASEEAQVTFDGSKTSVADIAKI
           10          20          30          40          50          60

m589.pep  IEKTGYGAKEKTEDTLQPQEAHHIGWRLWLLFTINVFLIGMAGMMIG-----RHDWMI
           70          80          90          100         1          110
           |||||:|||||:|||||:|||||:|||||:|||||:|||||

g589      IEKTGYGAKEKTEDTLQPQEAHHIGWRLWLLLTINIPFLIGMVGMMLKGLNWRHRDWMII
           70          80          90          100         110         120

m589.pep  PPLWQFALASVVQLWLAI PFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
           120         130         140         150         160         170
           ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

g589      PPVWQFVLASIVQLWLAI PFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA
           130         140         150         160         170         180

m589.pep  AYGMAHVYFEVGMVIGFVSLGKFLHRTKKSSLSLGLLLKLTPTQVNVQRNGEWKQLP
           180         190         200         210         220         230
           |:|||||:|||||:|||||:|||||:|||||:|||||:|||||

g589      AHGMAHVYFEAGVMVIGFVSLGKFLHRTKKSSLSLGLLLKLTPTQVNVQRNGEWKQLP
           190         200         210         220         230         240

m589.pep  IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           240         250         260         270         280         290
           |||||:|||||:|||||:|||||:|||||:|||||:|||||

g589      IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           250         260         270         280         290         300

m589.pep  SVVYRATQLGSGTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFTIVTWL
           300         310         320         330         340         350
           |||||:|||||:|||||:|||||:|||||:|||||:|||||

g589      SVVYRAAQLGSGTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVGIALLTFTIVAWL
           310         320         330         340         350         360

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922

	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTEGSPQVAAYVCVPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKTGTLTEGRPQVAAYVVPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAEEVGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	EIPAAQNAQTVVGAGITAEEVGVGLVKSAGKAEFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEAIIGRLKKNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSDALKADTAEAIIGRLKKNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALVLSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVLSNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVLGNALRLK					
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

a589.seq

1	ATGCAACAAA	AAGTCCGTTT	CCAAATCGAA	GGCATGACCT	GCCAGGCATG
51	TGCTTCGCGC	ATTGAAAAAG	TGTTGAACAA	AAAAGATTTT	GTGCAATCGG
101	CGGGGGTAAA	CTTCGCCAGC	GAAGAGGCTC	AGGTAGTGTT	TGACGACAGC
151	AAAACCTCAG	TAGCCGACAT	TGCCAAAATC	ATTGAGAAAA	CCGGTTACGG
201	CGCGAAGGAA	AAAACGGAAG	ATACATTGCC	GCAACCCGAA	GCAGAACACC
251	ATATCGGCTG	GAGGTTGTGG	CTTTTGCTGG	CCATCAATAT	CCCGTTCCTT
301	ATCGGTATGG	TAGGGATGAT	GCTAAAAGGG	CTGAATTGGA	CACGGCATGA
351	TTGGATGTTG	TCGCCCTTGT	TGCAGTTTGC	ATTGGCGAGT	GTGGTGACAGC
401	TTTGGCTGGC	GGTGCCATTT	TACAAAAGCG	CGTGGGCGAG	CATTAAAGGC
451	GGGCTGGCGA	ATATGGACGT	ACTCGTTACC	ATCGGCACGG	TCTCGATTTA
501	CCTGTATTCC	GTCTATATGC	TGTTTTTCAG	CCCGCACGCG	GCGTACGGTA
551	TGGCGCATGT	GTATTTTGAA	GTAGGCATAA	TGGTGATTGG	TTTGTGTGCA
601	CTGGGTAAAT	TTTTGGAACA	CCGCACCAA	AAATCCAGCC	TGAACAGCTT
651	GGGCTTGCTG	CTCAAACCTCA	CGCCAACCCA	AGTCAACGTG	CAACGCGATG
701	CGCAATGGCG	GCAGCTACCC	ATCGACCAAG	TGCAAAATCGG	CGACCTAATC
751	CGCGCAATC	ACGGCGAACG	CATTGCCGCC	GACGGCATCA	TAGAAAGCGG
801	CAGCGGCTGG	CGCGACGAAA	GCCATCTTAC	CGGCGAATCC	AATCCCAGAG
851	AGAAAAGGC	AGGCGGCAAA	GTATTGGCGG	GCGCGCTGAT	GACTGAAGGC
901	AGCGTGGTGT	ACCGCGCCGC	GCAGCTCGGC	AGCCAAACCC	TGCTCGGCGA
951	CATGATGAAC	GCGCTCTCCG	AAGCGCAAGG	CAGTAAAGCA	CCGATTGCGC
1001	GTGTGGCGGA	CAAGGCGGCG	GCGGTATTCT	TGCCTGCCGT	TGTGGGCATC
1051	GCACTTTTGA	CTTTTATCGC	TACTTGGCTG	ATTAAGGGCG	ATTGGACGCT
1101	CGCATTGATG	CACGCCGTCG	CCGTTTTGGT	GATTGCCTGC	CCGTGTGCAC

923

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1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAAACGCGC CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CGCCCGAGGC GCGCGGTTTG GAGATTCCCA
1451 CCGCACAAAA TGCCCAAACC ATTGTGCGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGCGCGG GTTTGGTAAA AGCAGGCAAA GCCGAATTTG CCGAACTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAG CGGCAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCCGCCGAAG TGCAGAACT CAAAGCCGCC GGCAAAACCG TGGCGATGGT
1851 CGGCGACGGC ATCAACGACG CGCCCGCGCT CGCCGCGGCC AACGTCAGCT
1901 TCGCCATGAA AGGCGGTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCCGCTC GCCGCGCTCG GCTTTTAAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCTGAAA CGGGTAAAAA TCGATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

a589.pep

```
1  MQQKVRFOIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIABI IEKTGYGAKE KTEDTLPOPE AEHHIGWRLW LLLAINIPFL
101 IGMVGMMMLKG LNWTRHDWML SPLAQFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201 LGKFLHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251 RANHGERIAA DGIIESGSGW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIA PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKPVAAVY CVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501 KGAGLVKAGK AEFAELTLPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGA DVAHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*
```

m589/a589 94.9% identity in 725 aa overlap

```
10 20 30 40 50 60
m589.pep MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIABI
|||||
a589 MQQKVRFOIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIABI
10 20 30 40 50 60

70 80 90 100 110
m589.pep IEKTGYGAKEKTEDTLPOPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
|||||
a589 IEKTGYGAKEKTEDTLPOPEAEHHIGWRLWLLAINIPFLIGMVGMMMLKGLNWTRHDWML
70 80 90 100 110 120

120 130 140 150 160 170
m589.pep PPLWQFALASVVQLWLAIFFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
||
a589 SPLAQFALASVVQLWLAVFFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
130 140 150 160 170 180

180 190 200 210 220 230
m589.pep AYGMHVYFEVGMVIGFVSLGKFLHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
|||||
a589 AYGMHVYFEVGIMVIGFVSLGKFLHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
190 200 210 220 230 240
```

924

	240	250	260	270	280	290
m589.pep	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
a589	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
	250	260	270	280	290	300
	300	310	320	330	340	350
m589.pep	SVVYRATQLGSQTQLGDMMNAL	SEAQGSKAPIARVADKAAAVF	VP	PAVVGIAL	LTFTVTWL	
a589	SVVYRAAQLGSQTLLGDMMNAL	SEAQGSKAPIARVADKAAAVF	VP	PAVVGIAL	LTFTIATWL	
	310	320	330	340	350	360
	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIA	CPALGLATPAAIMVGMGKAV	KHGIWFKDAAAMEEAAHVDA			
a589	IKGDWTLALMHAVAVLVIA	CPALGLATPAAIMVGMGKAV	KHGIWFKDAAAMEEAAHVDA			
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTEGSPQVA	AVYCV	PDSGF	DEDALYRIA	AAVEQNAAHPLARA	IVSAAQARGL
a589	VVLDKTGTLTEGKQVA	AVYCV	PDSGF	DEDALYRIA	AAVEQNAAHPLARA	IVSAAQARGL
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQT	VVGAGITA	VEGVGLVKAGKAEFAEL	ALPKFLD	GVWDIASIVAVSV	DNKP
a589	EIPTAQNAQT	IVGAGITA	EVKAGLVKAGKAEFAEL	LPKFS	DGVWEIASVAVSV	NGKP
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAE	AIGRLKKNIDVYIMSGDN	QGTVEYVAKQLGIAHAF	GNMSPRDK		
a589	IGAFALADALKADTAE	AIGRLKKNIDVYIMSGDN	QGTVEYVAKQLGIAHAF	GNMSPRDK		
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAM	VGDGINDAPALAAANVS	FAMKGGADVAEHTASAT	LMQHSVNQLA		
a589	AAEVQKLKAAGKTVAM	VGDGINDAPALAAANVS	FAMKGGADVAEHTASAT	LMQHSVNQLA		
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQN	LFFAFFYNILGIPLAAL	GFLNPVIAGAAMAASS	SVSVLSNALRLK		
a589	DALSVSRATLKNIKQN	LFFAFFYNILGIPLAAL	GFLNPVIAGAAMAASS	SVSVLSNALRLK		
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:  
g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcggca gtattgctcg gcgttgcttt
51  ggggtacacct tattatttgg gtgtcaaacg agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctggtttac ctctacggaa acgacggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtggttga acagccggtt acgctggtta accatatcac gcacggccct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgcctgaa acggaaaaag ttttgaacg ctttttggg aaacaagttc
401 cggtttccct tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtgttc cgcgttttca ttatgaagaa ctgtcgggca tcaggctgca

```

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501 ctgggaaggc ctgacggggg aaacgggtta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttggtca aaatcaagct ggcagacaaa
601 ggcgatgccc cgtttgaaaa agcgcatctc gattcggaaa cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatctt
701 cgctcgaatg gaaagagggg gtcgattaca acgtcaaatt gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccgggga atcggggcgg tttatcgaca gcaaggggcg gttccgtttc
901 gatacgttgg tgtacggcga tgaataatc ggcgcgtgg acatccatat
951 cgctgcccga cactcgcgt cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat cgcgaatgat
1051 ttgattgccc cagtcaaaag cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaatct tccgtttcac cctgcctcag ggaataattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaa
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tcctcaaaaa atgttggaag atttgccggt aagtcaggct ggaataatct
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgcct gatgggtggc agtacggtcc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 ccttataaaa caacgcctg aagttaaacg ggaataacgt gcaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttccggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGVKAES LTQQQKILQK TGFLTVESHQ
51 YDRGWFTSTE TTVIRLKPDL LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 FAGGFQTQAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNISIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMKKEDLN
401 QLGLMLKKTE ANIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEARASIA
451 INETLRIMVD STVQSMAREK YLTLDGNQID TVISLKNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

m590.seq (partial) ..

```

1 ..TGTTTTACCT CTATGGAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAAATACC TGCCGGATAA CCTGAAAACA GTGTTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACCGCCCTTT CGCCGGCGGA
151 TTCGGCAGCG AGCGGTACAT TGAACCGGAG TTCAAATACG CGCCTGAAAC
201 GGAATAAGTT CTGGAACGCT TTTTGGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AGCTGCACT GGGAAKGCCT
351 GACGGGAGAA ACAGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTGTGTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAAG TGCAATTCGA TTCGGAACCT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTTGTT
601 ACCGATTTGC AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTCGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAAAC
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATTT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTCAAC AACAATCCCG TATTGGACAT
951 TAAACTTTT CGATTACGC TGCCATCGGG AAAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTGGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCCAAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GCGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTCTT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGGT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

m590.pep.. (partial)

1	WFTSMETT	VLRLKPELL	NNARKYLPD	NKLVLEQPV	TLVNHITHG	PFFAGG
51	FGTQAYIE	TKFKYAPET	TEKVLERFFG	QKQVPSLAN	TVYFNH	SGSGKMS
101	AFDYEDLS	SGISLXHW	EXLTSVY	QNTFKS	YRNGYD	APLFLK
151	FEKVHFD	SETSDG	INPLALG	SNLKLE	FKSLEW	EGVDYN
201	TDLQIGAF	INPNSI	APSKIE	VEVGKL	APSTK	TGSGAF
251	YGDEKYG	GPLDNI	IAAEHL	DAFRTL	TVLKR	KKFAQIS
301	VKGASGL	FTNHIA	EDIKTF	SALT	PSGKID	VGGKIM
351	MLKKTEA	DIRMSI	PQKMLED	LAVSQAG	NIFFSV	NAEDEA
401	LRLMVD	STVSQ	SMAREKY	LTLNGD	QIDTAIS	LKNQNL
451	FDEGGM	SVSEP	OO			

m590 / g590 93.1% identity in 462 aa overlap

m590.pep  
g590

VKAESLSTQQQKILQKTGFLTVESHQYDRGWFTTSTETTVIRLKPELLHNAQKYLPDNLKI

30 40 50 60 70 80

m590.pep  
g590

VLEQPVTLVNHITHGPFAGGGFQTQAYIETFVKYAPETEKVLERFFGKQVPASLAN TVFYFN

90 100 110 120 130 140

m590.pep  
g590

GSGKM EVSVPAFDYEELSGIXLHWEXLTGETVYQKGFKSYRNGYDALPFIKLADKGDAA

150 160 170 180 190 200

m590.pep  
g590

FEKVHFDSSETSDGINPLALGSSNLTLEKFSLEWKEGV DYNVKLNELVN LVTDLQIGAFIN

210 220 230 240 250 260

m590.pep  
g590

PNGSIAPS KIEVGKLA FSTKTGESGAFINSEGRFRPD TTVYGDEKYGPLDIHIAAEHLDA

270 280 290 300 310 320

m590.pep  
g590

SALT V LKRKF AQISAK KMTEE Q IRNDLIAAVKGEA SGLFTNNPVLDIKTF RFTLP SGKID

330 340 350 360 370 380

m590.pep  
g590

VGGKIMFPKMKKEDLNQLGLMLKKTEADIRM SIPQMLED LAVSQAGNI FSVNAEDE AEG

390 400 410 420 430 440

m590.pep  
g590

RASLDDINETLR LMVDSTVQSMARE KYLT LNGD Q IDTA ISLKN NQL KL NGKT LQNEPE PD

450 460 470 480 490 500

m590.pep  
g590

FDEGGMVS-EPQQX  
FDEGDMVSGQPHX

510

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

a590.seq

```
1 ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51 GGGCACGCCT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGAT AACCTGAAAA
251 CAGTGTGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCTT
301 TTTGCCGCG GATTTCGGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GCGGATGCCG CGTTTGAAAA AGTGCATTTC GATTTCGAAA CTTCAGACGG
651 CATCAACCCG CTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACCTG
751 GTCATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTCAACCA
851 AGACCGGGGA ATCGGGGCGG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCCTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAATACTT TCCGATTCAC GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTGTAAC
1201 CAATTGGGTT TGATGCTGAA GAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGCGCGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAAAGTT GCAAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

a590.pep

```
1 MKKPLISVAA ALLGVALGTP YYLGVAEES LTQQQKILQE AGFLTVESHQ
51 YERGWTSTE TTVIRLKP EL LHNAQKYL PD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDVNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRETLPS GKIDVGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTLNGDQID TAISLKNQL KLNKTLQNE
501 PEPDFDEGGM VSEPPQ*
```

m590/a590 97.8% identity in 462 aa overlap

```

                                     10      20      30
m590.pep                               WFTSMETT VIRLKP ELLNNARK YLPDNLKT
a590      VKAEESLTQQQKILQEAGFLTVESHQYERGWFTSTETT VIRLKP ELLHNAQK YLPDNLKT
           30      40      50      60      70      80
m590.pep      VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
a590      VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
           90     100     110     120     130     140
m590.pep      GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPL FKIKLADKGDAA
a590      GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPL FKIKLADKGDAA
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928

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|||||
a590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
          150      160      170      180      190      200

          160      170      180      190      200      210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKNELVNLVTDLQIGAFIN
          |||||
a590      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKNELVNLVTDLQIGAFIN
          210      220      230      240      250      260

          220      230      240      250      260      270
m590.pep  PNGSIAPSKIEVGKLAfstktGESGAFINSEGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
          |||||
a590      PNGSIAPSKIEVGKLAfstktGESGAFIDSEGQFRFGTLVYGDEKYGPLDIHIAAEHLDA
          270      280      290      300      310      320

          280      290      300      310      320      330
m590.pep  SALTVLKRKFAQISAKKMTeeQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPsgKID
          |||||
a590      SALTVLKRKFARISAKKMTeeQIRNDLIAAVKGEASGLFTHNPVLDIKTFRFTLPsgKID
          330      340      350      360      370      380

          340      350      360      370      380      390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
          |||||
a590      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
          390      400      410      420      430      440

          400      410      420      430      440      450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLTlNGDQIDTAISLKNQLKLNGKTLQNEPEPD
          |||||
a590      RASLDDINETLRLMVDSTVQSMAREKYLTlNGDQIDTAISLKNQLKLNGKTLQNEPEPD
          450      460      470      480      490      500

          460
m590.pep  FDEGGMVSEPQQX
          |||||
a590      FDEGGMVSEPQQX
          510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTTGATTTC GGTTCGCGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGTCTGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGGCG GATTTCGGCA GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGGCCTCGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGCTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAATGGGAA
451 GTCAGTGTTT CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCAGATGCCG CGTTTGAAAA AGTGCATTTC GATTGGGAAA CTTGAGACGG
651 CATCAATCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAAAT GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACTG
751 GTCAAATCTG TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901 GATACATCGG TGTACGGCGA TGAATAATAC GGCCCGCTGG ACATCCATAT
951 CGTGCCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTTCA CCAACAATCC
1101 CGTATTGGAC ATTAATACTT TCCGATTAC GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTAAAGACA TGAAGAAGGA AGATTTTGAAT
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT

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1251 TCCCCAAAAA ATGCTGGAAG ACTTGCGCGT CAGTCAAGCA GGCAATATTT  
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC  
1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC  
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT  
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA  
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA  
1551 A

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

1 MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE TGFLTVESHO  
51 YERGWFSTME TTIVRLKPEL LNNARKYLPD NLKTVLEQPV TLVNHITHGP  
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME  
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK  
201 GDAAFEKVHF DSETSDGINP LALGSSNLTLEKFSLEWKEG VDYNVKLNEL  
251 VNLVTDLQIG AFINPNNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF  
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KKKFAQISAK KMTEEQIRND  
351 LIAAVKGEAS GLFTNNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN  
401 QLGLMLKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD  
451 INETLRLMVD STVQSMAREK YLTNGDQID TAISLKNQNL KLNKGTQLNE  
501 PEPDFDEGGM VSEPPQ\*

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	10	20	30	40	50	60
g590	10	20	30	40	50	60
m590-1.pep	70	80	90	100	110	120
g590	70	80	90	100	110	120
m590-1.pep	130	140	150	160	170	180
g590	130	140	150	160	170	180
m590-1.pep	190	200	210	220	230	240
g590	190	200	210	220	230	240
m590-1.pep	250	260	270	280	290	300
g590	250	260	270	280	290	300
m590-1.pep	310	320	330	340	350	360
g590	310	320	330	340	350	360
m590-1.pep	370	380	390	400	410	420
g590	370	380	390	400	410	420
m590-1.pep	430	440	450	460	470	480
g590	430	440	450	460	470	480
m590-1.pep	490	500	510			
g590	490	500	510			

g590	TVISLKNNAKLNKGLTQNEPDPDFDEGDMVSGQPHX	490	500	510	
a590/m590-1	98.3% identity in 516 aa overlap				
a590.pep	10 20 30 40 50 60				
m590-1	10 20 30 40 50 60				
a590.pep	70 80 90 100 110 120				
m590-1	70 80 90 100 110 120				
a590.pep	130 140 150 160 170 180				
m590-1	130 140 150 160 170 180				
a590.pep	190 200 210 220 230 240				
m590-1	190 200 210 220 230 240				
a590.pep	250 260 270 280 290 300				
m590-1	250 260 270 280 290 300				
a590.pep	310 320 330 340 350 360				
m590-1	310 320 330 340 350 360				
a590.pep	370 380 390 400 410 420				
m590-1	370 380 390 400 410 420				
a590.pep	430 440 450 460 470 480				
m590-1	430 440 450 460 470 480				
a590.pep	490 500 510				
m590-1	490 500 510				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1841>:

g591.seq

```
1   TTGCAAACCC TTCTAGCTTT TATCTTCGCC ATCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG GTTGTGCGGC GTCAAGGTTG
101 TCGGTTTTCG CGTCGGCTTC GGCAACCCG TTTTCACCGC AAGCGCGCG
151 GACACCGAAT GGTGCCTCGC CCCGATTCG TTTGGCGGCT ACCTCAAAAT
201 GGTGATACG CGCGAAGGCC AAGTATCAGA AGCGGATTTA CCCTACGCTT
251 TTGCAAAACA ACACCCCGCC AAGCGCATCG CCATCGTCTG CGCCGGTTCG
301 CTGACCAACC TCGCAActgc ggTTTGTGCT TACGGATCTGa cctTtctctt
351 cggcgtaaCC GAACTGCGGC CCTatgtcgg cacagtcgaA ccgcacaccc
```

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401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGA AAAAG GCAGCCCGC CGAAAAAGCA GGCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGc ctcaTGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCcg ggcAAAAAA Tcaccctgac
801 ctacgAaCGC GCcggacaaa ccaTAccgc CGACATCCGC CccgATactg
851 TCGAAcagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACC GTTCC CACTCGTGGA
1001 CAACCCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTACGC
1051 CATATTTCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAAATTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCCTT CTTCAACGAC GTTACCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591.pep..

```

1 LQTLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRKRG
51 DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDQWSSA QTEIVLNLEA GKAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSALGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFGALMM LMMAAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1 TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51 GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCGCG CGCCGGCTTC CAAAGCGGCG ACAAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGA AAAAG GCAGCCCGC CGAAAAAGCA GGCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACC GTTCC CACTCGTGGA
1001 CAACCCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTGAGC
1051 CATATTTCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAAATTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACCGGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..

```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRG
51 DTEWCLAPIP LGGYVKMVD REGEVSEADL PYAFDKQHFA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV PDIARAGF QSGDKIQSVN
151 GTPVADWGS QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPAeka GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLNYER AGQTHADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVR FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMAVAFFND VTRLIG*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSGFGKPFTRKRGDTEWCLAPIP					
g591	LQTLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSGFGKPFTRKRGDTEWCLAPIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m591.pep	LGGYVKMVDREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
g591	LGGYVKMVDREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m591.pep	ELRPYVGTVPEPDTIARAGFQSGDKIQSVNGTPVADWGSQAQTEIVLNLEAGKVAVGVQTA					
g591	ELRPYVGTVPEPDTVAARTGFQSGDKIQSVNGVSVQDWSSQAQTEIVLNLEAGKVAVGVQTA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m591.pep	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPAEGKAGLKPGRDLTA					
g591	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPAEGKAGLKPGRDLTA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQTHADIRPDTVEQSDHTLIGRVGLRPQ					
g591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQTHADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRFAFGMGEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
g591	PDRAWDAQIRRSYRPSVVRFAFGMGEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
g591	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTVIEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLIGX					
g591	GLRFGALMMLMAAAFFNDVTRLIGX					
	430	440				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:  
a591.seq

```
1 TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGTCAGCCT
51 GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TGCGTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGACACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCGGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAACC AAGGCTACAT CGGACTGATG CCTTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAGGAG GCAGCCCGC CGAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGCA AACCCATCGC CTGATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCATACCGC CGACATCCG CCCGATACG
851 TCGAACAGCC CGACCACACC CTGATCGGCG GCGTCGGCCT CCGTCCGCG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCGCTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCCTCA ATTTTTCGGC AACTAATCA GCGGCAACGC CTCCGTCAGC
1051 CATATTTCCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCGCA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTTT GGCATGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCGG TTTTGGACGG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTCGCGT TCGGGCTTGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G
```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```
a591.pep
1 LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRK
51 DTEWCLAPIP LGGYVKMVD TREGVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIAARAGF QSGDKIQSVN
151 GTPVADWGSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLYER AGQHTADIR PDTVEQPDHT LIGRVGLRPO
301 PDRAWDAQIR RSYRPSVVR FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLN PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFLALMM LMAVAFEND VTRLLG*
```

m591/a591 99.6% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRK	GDTEWCLAPIP
a591	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRK	GDTEWCLAPIP
	70	80	90	100	110	120
m591.pep	LGGYVKMVD	TREGVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
a591	LGGYVKMVD	TREGVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
	130	140	150	160	170	180
m591.pep	ELRPYVGTV	EPDTIAARAGF	QSGDKIQSVN	GTPVADWGSA	QTEIVLNLEA	GKVAVGVQTA
a591	ELRPYVGTV	EPDTIAARAGF	QSGDKIQSVN	GTPVADWGSA	QTEIVLNLEA	GKVAVGVQTA
	190	200	210	220	230	240
m591.pep	SGAQTVRTI	DAAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
a591	SGAQTVRTI	DAAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA

934

	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSISLGVNLNLPVPVLDGGHLVFTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVSISLGVNLNLPVPVLDGGHLVFTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGLALMMLMMAVAFFNDVTRLGX					
a591	GLRFGLALMMLMMAVAFFNDVTRLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg acgtgttcgg tcagattttt tcgggcgcgt tcaaattcga
51  cgcggcagca ggcggcttac tcggcggtct gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaacg aggcgggtat gggttccgcg
151 ccgaacgcgc cgcgcgcgcg cgaagtgaac caccctgttt cgcaaggatg
201 gattcaaatg ctgggcgtgt ttgtcgatac catcatcggt tgttcttgca
251 cgccttcatt catcttgatt taccaacagc cttatggcga tttgagcggt
301 gcgcgcgtga cgcaggcgcg gattgtcagc caagtggggc aatggggcgc
351 ggggtttcct gccgtcatcc tggttatggt tgccttttcc accgttatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttcgg tatgctggtt ttggcgtggg tctatttcgg
501 cgcggttgcc aatgtgcctt tggctcggga tatggcggat atggcgatgg
551 gcatcatggc gtggatcaac ctgcgcgcca tcctgctgct ctcgccattg
601 gcgtttatgc tgctgcgcga ttacaccgcc aagctgaaaa tgggcaaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcatacaat
701 ccgatgtttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFGQIF SGAFKFDAAA GLLGLLIQ TMMGIKRL YSNEAGMGS
51  PNAAAAIEVK HPVSQGMIMQ LGVFVDTIIV CSCTAFIILI YQPPYGDLSG
101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAB SNVQFIKSHW
151 LITAVFRMLV LAWVYFGAVA NVPLVDMAD MAMGIMAWIN LVAILLLSPL
201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG ACGTGTTCGG TCAGATTTTTC TCGGGCGCGT TCAAATTCGA
51  CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGATCAAA ACGCGGCTG TATTCCAACG AGGCGGGTAT GGGTTCGCGC
151 CCGAACGCGC CCGCGCGCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
251 CCGCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
301 CGCGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
351 GGGCTTCCTC GCCGTCATCC TGTATTATGT TGCCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCACTAA AAGCCATTGG
451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCGG
501 CGCGGTTGCG AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG

```

935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA  
 651 CCCGAGTTC AACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT  
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..  
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA  
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDIIIV CSCTAFIILI YQOPYGDL SG  
 101 AALTQAAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW  
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL  
 201 AFMLLRDYTA KLKMGKDPEF KLSHPGLKR RIKSDVW\*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSA PNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSA PNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDIIIVCSCTAFIILIYQOPYGDL SGAALTQAAIVSQVGQWAGFL					
g592	HPVSQGMQIMLGVFVDIIIVCSCTAFIILIYQOPYGDL SGAALTQAAIVSQVGQWAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEFKLSHPGLKRRIKSDVWX					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEFKLSHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq  
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTTT TCGGGCGCGT TCAAATTCGA  
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA  
 101 TGGGCATCAA ACGCGGCTG TATTCCAACG AGGCGGGTAT GGGTCCCGC  
 151 CCGAACGCCG CCGCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT  
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA  
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT  
 301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAACTGGGGC AATGGGGCGC  
 351 GGGCTTCCTC GCCGTCATCC TGTATTATGT TGCCTTTTCC ACCGTTATCG  
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG  
 451 CTGATTACCG CCGTTTCCG TATGCTGGTT TTGGCGTGGG TCTATTTCCG  
 501 CGCGGTTGCC AATGTGCCCT TGGTCTGGGA TATGGCGGAT ATGGCGATGG  
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG  
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA  
 651 CCCGAGTTC AACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT  
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep  
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA  
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDIIIV CSCTAFIILI YQOPYGDL SG  
 101 AALTQAAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW  
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL  
 201 AFMLLRDYTA KLKMGKDPEF KLSHPGLKR RIKSDVW\*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAGGLGGLISQTMGMGIKRGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAGGLGGLISQTMGMGIKRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLSPLAFMLLRDYTAKLKMKGKDEPKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLSPLAFMLLRDYTAKLKMKGKDEPKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1   atgcttgaac tgaacggact ctgcaaatgc ttcggcgcca aaacggctcgc
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101 ggcggtcggg ctgcgggcaa tccaccctgc tgaatatgat tgcggggcatc
151 gtccggccgg acggcgcgga aattcggtcg aacggggaaa acattacctg
201 tatgccgccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaaaagcga agccgaacgc ctgccttgt cggcacttgc
351 cgaagtcggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacggttg gcactggcgc gcgctttggt tgcgcgcct
451 tccctgctgt tgcctgatga atcgttttcc agtttggaac cgcatcttgc
501 cgaccggctg cgccgtatga ccgcccgaac catccgcaag ggcggcatcc
551 ctgccgtttt ggtaacgcat tcgcccgaag aggcctgcac ggcggcgga
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgag gtacgcccga
651 aaccttgatt caaacgcctg ccggcggtga ggtcgccgt ctgatggggc
701 gcccaatac cgacgatgac cgccatattc cgcaaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgctc gcctgcccga
801 ctgctccgg ctttccgccc tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacggta tttccgaaa cggtacggtc
901 cgcattccgg tcgatgaagg gcgtatcgct cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1   MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSLR LSAVHPEHGE LTLNLTVGQH TDGISGNQTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

```

1   ATGCTTGAAC TGAACGGACT CTGCAACGCG TTCGGCAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GGCGGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGAGAAA ACATTACCCG

```



```

201 TATGCCGCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCA TATGAGTGCG CTGGAAAATG CGGCATTCCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AAACCTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTCC AGTTGGACA CGCATTTGCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GGCAGCATCC
551 CTGCCGTTT GGTAAACGAT TCGCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTCGCCCGA CTGATGGGTT
701 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAAG CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
      1 MLELNLCKR FGKNTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
     51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAFLGLKM
    101 QKMPKAEAEER LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
    151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
    201 EIAVMHKGRI LQYGTPELTV KTPSCVQVAR LMGLPNTDDN RHIPQHAVRF
    251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWLNLMRHA GAVSGKDTV
    301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGKNTVADNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
g593	MLELNLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPEKRRISLMFQDYALFPHMSALENAAFGLKMOKMPKAEAEERLAMAALAEVG					
g593	NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMOKMPKAEAEERLALSALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEAHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
g593	LENEAHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIIVMHKGRI LQYGTPELTVKTPSCVQVARLMGLPNTDDN					
g593	GGIPAVLVTHSPEEACTTADEIIVMEHGKILQCGTPETLIQTPAGVQVARLMGLPNTDDD					
	190	200	210	220	230	240

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	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDDGMECRVLSRTCLPESFSLSVLHPEHGILWLNLDLDM-RHAGAVSGKDTV					
	:    :          :     :                  :     :     :					
g593	RHIPQNAVCLDNHGTECRLLSLVRLPDSLRLSAVHPEHGELTLNLTVGQHTDGISGNQTV					
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	:     :					
g593	RIRVDEGRIVRFRX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

```

a593.seq
1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCGGCA AAACGGTTGC
51  CGACGATATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGCGTCCGG CTGCGGCAAA TCCACCCTGC TGAATATGAT TCGGGGCATC
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AATGGGGAAA ACATTACCCG
201 TATGCCGCCC GAAAAACGCC GTATTTGCTG GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGCA CTGGAATGCG CGGCATTCCG TTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAATGCG AGGCGCACCG CAAGCCTGAN AAACCTTCCG
401 GAGGCGAAAA GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTTGGACGA ATCGTTTCC AGTTTGGACA CGCATTGCG
501 CGACCGGCTG CGCCGCATGA CTGCCGAACG TATCCGCAAG GGCGGCATCC
551 CTGCCGTTTT GGTAACGCAT TCGCCGAAG AGGCCTGCAC GGCGGCAGAC
601 GAAATCGCCG TCATGCACGA GGGGAAATC CTTCAATGCG GTACGCCCGA
651 AACCTTGTTT CAAACGCTG CCGGCGTGCA GGTGCGCCAT CTGATGGGGC
701 TGCCCAATAC CGACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTGCGCCGA
801 ATCGTTCAGC CTGTCCTGCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCCGCACGCC GGTGAAATAT CGGGAACAGA TACGGTACGC
901 ATCCATATCG AAGACAGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

```

a593.pep
1  MLELNLCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAES LAMAALAEVG LENEHRKPX KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLV QTPAGVQVAH LMGLPNTDD RHIPQHAVRF
251 DDGMECRVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
301 IHIEDREIVR FR*

```

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
a593	MLELNLCKRFGGKTVADDICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEERLAMAALAEVG					
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEESLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEAHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
a593	LENEAHRKPXKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTADEIAVMHKGRILQYGTPTLVKTPSCVQVARLMGLPNTDDN					

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```

|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a593  GGIPAVLVTHSPEEACTAADEIAVMHEGKILQCGTPETLVQTPAGVQVAHLMGLPNTDDD
      190      200      210      220      230      240
      250      260      270      280      290      300
m593.pep RHIPQHAVRFDQDGMCECVLSRTCLPESFSLSVLHPEHGILWLNLDMRHAGAVSGKDTVR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a593  RHIPQHAVRFDQDGMCECVLSRTCLPESFSLSVLHPEHGILWLNLDMPHAGEISGNDTVR
      250      260      270      280      290      300
      310
m593.pep IHIEEREIVRFRX
|||||:|||||:
a593  IHIEDREIVRFRX
      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

```

g594.seq..
1  atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51  tctcgTTTT agcatactcc ggctgctgtt ccgcacgga attgggatcg
101 gtaagttcgc cgttcaggcc tttcaggtct ttaagctgct gatctgtacg
151 gttgagcacc caaatcgggt tgccttgcca ctcggcggtc agcagctgac
201 ccgcttcgat tttactgaca tccacctcga cggcagcacc ggaggccttg
251 gctttttccg aagggaAAAA actggccaca aacggcgttg ccacacccaa
301 tgctgccact ccgcccgcgc cgcaggtcgc aagtgtcagg aaacggcggc
351 ggccgttggt gatttcttga ttatccatta ttcagtcgtc ctaatatTTT
401 gggaatgccg agccattaaa cattgcaatt ttaccagtt tgcagtgata
451 ctcaaagcat tatttaaaat aaggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

```

g594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR KCQETAAAVV DFLIIHYSV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

```

m594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAGCTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGGCGCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCgcgc CGCAGGTGCG GAGTGTcAGG AAACGGCGGC
351 GGCCGTtGTT GATTtCTTGA TTATCCATTA TTCAGTcGTC CTAATATTTT
401 GGGAATACCG AGCCATTAaA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTtAAAAA AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

```

m594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECOETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRCQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```
a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAACACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GGCGGCCTTG
251 GCTTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTGCG GAGTGTGAGG AAACGGCGGC
351 GGCCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGAATACCG AGCCATTAAG CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```
a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLGST GGLGFFREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*
```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```
g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttgggttt
51  gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgtccg
101 gtgagacca atccgccaac gaaggcgtt cggtcggtat cgccgtcaac
```

```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgtgat ggtggtggac gaacgcgaaa atatcgccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgaaa aactgcccc accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgc gtccattacg aacgcacga accgattgcc
601 gagcttttca gcgaactcga ccccgtcac gatgcgtgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggcttcac cgtatcgaac
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcgaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg caaaaaaca agccttggtg gaaaaaaccg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcacaaa
```

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1051 gacggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt  
 1101 acaggctcct attaacgcgc ttgccgaaga cttgccccaa cttcgcgga  
 1151 tactcggtt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..  
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGI AVN  
 51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGMVVD ERENIAPGLS  
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA  
 151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA  
 201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA  
 251 KLMTDVEALQ KEIDALAFPP GKVVGGADEL IEEAAGSKIS GEEDRYSHTD  
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDNTFKQV NEILAKYRTK  
 351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRGILGLK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq  
 1 ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT  
 51 GACCGCGTGC CAGCCGCCGG AGCGCGAGAA AGCTGCGCCG GCAGCGTCCG  
 101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCACTAT CGCCGTCAC  
 151 GACAATGCCT GCGAACCAGT GGAAGTACC GTGCCGAGCG GACAGGTTGT  
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA  
 251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC  
 301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG  
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA  
 401 AAGACACCGC CAACGAAGCG GATTGGGAAA AACTGTCCCA ACCGCTCGCC  
 451 GACTATAAAG CCTACGTTC AAGCGAGGTT AAAGAGCTGG TGGCGAAAAC  
 501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAT  
 551 CCTGTTTGC CGACACCGCG GTCCATTACG AACGCATCGA ACCGATTGCC  
 601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT  
 651 CAAAGACGGC GCGAAGATG CCGGATTTAC CGGCTTTTAC CGTATCGAAT  
 701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG  
 751 AAAGTATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTTGG  
 801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACCT ATTGAAGAAG  
 851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT  
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT  
 951 GTTCCGTCCG CTGATCGAGG CAAAAACAA AGCCTTGTG GAAAAACCG  
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA  
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT  
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA  
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep  
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSI AVN  
 51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVD ERENIAPGLS  
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA  
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA  
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA  
 251 KLMTDVEALQ KEIDALAFPP GKVVGGADEL IEEVAGSKIS GEEDRYSHTD  
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDNTFKQV NEILAKYRTK  
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK\*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSI	AVNDNACEPMELT
g595	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGI	AVNDNACEPMNLT
	10	20	30	40	50	60
	70	80	90	100	110	120

943

m595.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
g595	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMNRLNLLPGEYEMTCGLLT
	70 80 90 100 110 120
m595.pep	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
g595	NPRGKLVVADSGFKDTANEADLEKLPQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE
	130 140 150 160 170 180
m595.pep	KAKSLFADTRVHYERIEPIAELEFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
g595	KAKSLFAATRVHYERIEPIAELEFSELDPVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK
	190 200 210 220 230 240
m595.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD
g595	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEAAGSKISGEEDRYSHTD
	250 260 270 280 290 300
m595.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG
g595	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLS
	310 320 330 340 350 360
m595.pep	EADRKALQASINALAEDLAQLRGILGLKX
g595	EADRKALQAPINALAEDLAQLRGILGLKX
	370 380 389

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

a595.seq

1	ATGAGAAAAT	TCAATTTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCGCGTGC	CAGCCGCCCG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGGCGGTT	CGGTCAGTAT	CGCCGTCAAC
151	GACAATGCCT	GCGAACCGAT	GGAACGTACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AAGGCGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAAATGA	CCGTCACCCCT	GTTGCCGGGC	GAATACGAAA	TGACTTGCGG
351	TCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTGGAAA	AACTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTATGTTCA	AGGCGAAGTC	AAAGAGCTGG	TGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGCGGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACGGC	GCGAAAGATG	CCGGATTTAC	CGGCTTCCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	GCGTGAAGGA	AATTGCAGCG
751	AAACTGATGA	CCGATGTCTGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCCTCCG	GGCAAGGTGG	TCGGCGGCGC	GTCCGAAGTG	ATTGAAGAAG
851	TGGCGGGCAG	TAAAATCAGC	GGCGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGACT	TCCAAGCCAA	TGTGGACGGA	TCGAAAAAAA	TCGTCGATTT
951	GTTCCGTCGG	TTGATCGAGA	CCAAAAACAA	AGCCTTGTTG	GAAAAAACCG
1001	ATACCAACTT	CAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGGACTAAA
1051	GACGGTTTGG	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAGCGGTT
1101	ACAGGCCTCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAAATAA			

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

a595.pep

1	MRKFNLTALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTN	EGGSVSIAVN
51	DNACEPMELT	VPSGQVVFNI	KNSGRKLEW	EILKGMVVVD	ERENIAPGLS

944

101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA  
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA  
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA  
 251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD  
 301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK  
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK\*

m595/a595 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLTALSVMALGLTACQPPEAEKAAPASGEAQTANEGGSVSIIVNDNACEPMELT					
a595	MRKFNLTALSVMALGLTACQPPEAEKAAPASGEAQTANEGGSVSIIVNDNACEPMELT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m595.pep	VPSGQVVFNIKNNSGRKLEWEILKGVMMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
a595	VPSGQVVFNIKNNSGRKLEWEILKGVMMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m595.pep	NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
a595	NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m595.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
a595	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m595.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
a595	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m595.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFEYTDKLG					
a595	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFEYTDKLG					
	310	320	330	340	350	360
	370	380	389			
m595.pep	EADRKALQASINALAEDLAQLRGILGLKX					
a595	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

1 ..atgctgctct tggacgagcc gaccaaccac ttggatgctg aatcggtgga  
 51 atggtctggag caattcctcg tgcgttccc cggcacagtg gtcgcggttaa  
 101 cgcacgaccg ctacttcctc gacaacgccg ccgaatgatg tttggaactc  
 151 gaccgcggac acggcattcc gtggaaaggc aattactcgt cttggctgga  
 201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg  
 251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc  
 301 cgccaagcca agccaaagc gcgtttggcg cgttttgaag aaatgagcaa  
 351 ctacgaatac caaaaacgca acgaaactca ggaaatcttt atccctgttg  
 401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg



945

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451   ttcggcgata aagtgtgat tgacggtttg agcttcaaag tgccggcggg
501   cgcgattgtc ggcatcatcg gcccgaaacg cgcgggtaaa tcgacgctgt
551   tcaaaatgat tcggggcaaa gagcagcccg attcgggcga agtgaaaatc
601   gggcaaaccg tgaaaatgag cttgattgac caaagccgcg aaggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggctcg gatattttgc
701   aggtcggaca gtttgaaatc cccgccccgc aatatttggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgca
801   acgcggccgt ctgcacttgg caaaaacctt gttgggcgcg ggcaatgtgt
851   tgctgtctga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgcg
901   ttggaagacg cattgttgga atttgccggc agcgtgatgg tgatttcgca
951   cgaccgctgg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1001  gcgactcaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcatcaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   .MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKG NYSSWLEQKE KRLENEAKSE AARVKAMKQE LEWVRQNAKG
101 ROAKPKARLA RFEEMSNEYE QKRNETQEIF IPVAERLGNE VIEFVNVSKS
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGFQEI PARQYLGRFN
251 FKGSQSKIA RQLSGGERGR LHLAKTLLGG GNVLLDEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351 DKRRLGKEG AKPKRIKYK VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCTAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTG AAGATATTTT CCTTTCTTTC TTCCCGGGCG
101 CGAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CCGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 CCGCAGGTTT GTCCACGGGC GGCGGTGCGG AACACGAATT GGAAATCGCC
451 GCCGACGCGC TCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTGTGTC
501 CCGCGGTGAA AAACGCCGCG TTGCCTGTGT CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCGGCA CAGTCGTTCG
651 GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCGGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAGAA GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGCCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTGTG AATGTTTCCA
1001 AATCGTTCGG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCC
1051 CCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTCGG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
1151 AAATCGGACA AACCCTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAAACCGT GTTCGACAAC ATTGCCGAAG GCCGCGACAT
1251 TTTGACGTTT GGTCAAGTTT AAATCCCGC CCGCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGCTGGC
1351 GGCGAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTTGA GCGGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCTGTC
1451 GCGCGTTGGA AGACGCATTG TTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GTTGGTTCCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGCGCAC TCTAAATGGG TGTCTTCGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAATACA AACCAGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

```

1 MSQQYVYSML RVSKVVPPOK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51 RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAAVRK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGLHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYEADEKRR LGEEGAKPKR
551 IKYKPVTR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m596 g596 98.4% identity in 373 aa overlap

	160	170	180	190	200	210
m596.pep	LPEWDAKIDNLSGGEKRRVALCKLLLSKPDMLLDDEPTNHLDAESVEWLEQFLVRFPQTV					
g596				MLLDDEPTNHLDAESVEWLEQFLVRFPQTV		
				10	20	30
	220	230	240	250	260	270
m596.pep	VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAAVRKAMKQE					
g596	VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAAVRKAMKQE					
	40	50	60	70	80	90
	280	290	300	310	320	330
m596.pep	LEWVRQNAKGRQAKSKARLARFEEMSNEYEQKRNETQEIFIPVAERLNEVIEFVNVSKS					
g596	LEWVRQNAKGRQAKPKARLARFEEMSNEYEQKRNETQEIFIPVAERLNEVIEFVNVSKS					
	100	110	120	130	140	150
	340	350	360	370	380	390
m596.pep	FGDKVLIDDLSEKVPAGAIIVGIIGPNGAGKSTLFKMSGKEQPDGGEVKIGQTVKMSLID					
g596	FGDKVLIDGLSEKVPAGAIIVGIIGPNGAGKSTLFKMIAGKEQPDGGEVKIGQTVKMSLID					
	160	170	180	190	200	210
	400	410	420	430	440	450
m596.pep	QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR					
g596	QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIARQLSGGERGR					
	220	230	240	250	260	270

947

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLD	DEPSNDLDVETL	RALEDALLEFAGSVMVISHDRWFLDRIATHIL			
g596	LHLAKTLLGGGNVLLLD	DEPSNDLDVETL	RALEDALLEFAGSVMVISHDRWFLDRIATHIL			
	280	290	300	310	320	330

  

	520	530	540	550	559
m596.pep	ACEGDSKWVFFDGN	QYEYADKKRRLG	EAGAKPKRIKYKPVTRX		
g596	ACEGDSKWVFFDGN	QYEYADKKRRLG	EAGAKPKRIKYKPVTRX		
	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTA AAGATATTTT CCTTCTTTTC TTCCCGGGCG
101 CGAAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGG TAAAGAATTG GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGAAAGCG GTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTGGAGGA AGTGATGCC GAGTACGCCA ATCCCGATGC
351 GATTTTTGAC GCGTTGGCGG AAGAGCAGGG GCGTTTGGA GCGATTATTG
401 CGGCGGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCT
451 GCCGACGCGC TGGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CGGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCGGTA CAGTCGTTGC
651 CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA CTCGTCTTGG
751 TTGGAGCAGA AAGAAAAACG TTTGAAAAAC GAGGCGAAAT CCGAAGCCGC
801 GCGCGTGAAA GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGTCA AGCCAAGTCC AAAGCGCGTT TGGCGCGTTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTTCG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GTCGCGATAT
1251 TTTACAGTGC GGGCAGTTTG AAATCCCGC CCGCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCCGCG
1351 GGCGAACGCG GACGTTTGCA CTGGCAAAA ACCTTGTGG GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCCTGC
1451 GCGCGTTGGA AGACGCATTG CTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GCTGGTTCCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGGCGAC TCAAATGGG TGTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.pep
1  MSQQYVYSML RVSKVVPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAAVRK AMKQELWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNIEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSQ QSKITGQLSG
451 GERGLHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGN YQEYADKKRR LGEEGTEPKR
551 IKYKPVTR*

```

m596/a596 99.3% identity in 558 aa overlap

948

m596.pep	10	20	30	40	50	60
	MSQQYVYSMLRVSKVVPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
m596.pep	70	80	90	100	110	120
	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
	70	80	90	100	110	120
m596.pep	130	140	150	160	170	180
	ALAEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
m596.pep	190	200	210	220	230	240
	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
	190	200	210	220	230	240
m596.pep	250	260	270	280	290	300
	IPWKGNYSWLEQKEKRLNEAKSEAA RVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAA RVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
m596.pep	310	320	330	340	350	360
	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
	310	320	330	340	350	360
m596.pep	370	380	390	400	410	420
	NGAGKSTLFKMIAGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFKMIAGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
m596.pep	430	440	450	460	470	480
	GQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGRHLAKTLLGGNVLLLDEPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSDQSKITGQLSGGERGRHLAKTLLGGNVLLLDEPSNDLDV					
	430	440	450	460	470	480
m596.pep	490	500	510	520	530	540
	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYQY EADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYQY EADKKRR					
	490	500	510	520	530	540
m596.pep	550	559				
	LGEEGAKPKRIKYKPVTRX					
a596	LGEEGTPKPKRIKYKPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

```
1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAA CAGCGGAGG CTGGGACAA ATTCCAAAAA
```

```

151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCG CGTTTCGTAT CGGGGAACCTA TAAAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGAAGAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGCGCGGAA CAGACGGAAG GCCGCAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaAAAaagcc
601 gaacaccgCA TtcaggAtgc ggAagcaaaa agaAAATTGG CTGAagcCaa
651 actGcgcgca gccgAAAAAG CCAGAAAAGA AGCGCGCAG CAGAAGGCTG
701 AAGCGCGACG TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACggtT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcgC GATGTTTGA AAGCGGTGT TATTCCACT
901 GCGCTGCAAA CGGTTGAAAG CATTGCGCg gGAACggtaa GCTATGCGGA
951 cgaGTTGAC GGCTACGGCA AAGTGGTCGT GATCGATCAC GGCAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGCCGG CAAGGGTTAT
1051 ACGGTTCGGG CAGGAAGCAA AATCGGCACG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTCCGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

g597.pep

```

1 MLLHVSNSLK QLQEEIRIQE RIRQERIROA RGNLASVNRK QREAWDKFKQ
51 LNTLNLRLKT EVAATKAQIS RFVSGNYKNS RPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKQNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ QKAEARRAEM SNLTAEARNI
251 QAPVSMGTGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISIIYAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLRIRYRQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

m597.seq

```

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAACAGCG CGAGGCTTGG GACAAAGTCC AAAAACTCAA TACCGAGCTG
151 AACCGTTTGA AAACGGAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTCC
251 TGA AAAACGCG CGAACCGGGT CAGAAAAACC GCTTTTGGC TTATACGCGT
301 TATGTAACCG CCTCCAATCG GGAAGTTGTC AAGGATTGG AAAAAACGCA
351 GAAGGCTTTG GCGGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAAGAAAAT TCAGGCAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAAGCCGC AGACAGAAATG CCAAAATCGC
501 CAAAGATGCC CGAAAATGCG TGAACAGAAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTG GAGAAGAAAA AGGCCGAACA CCGCATTAG
601 GATCGCGAAG CAAAAAGAAA ATTGGCTGAA GCCAGACTGG GCGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCCGGCAG AACCGGAGCG
851 GCGGCGATAT TTGGAAAGGC GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAAGCTAT CGGACGAGT TGGACGGCTA
951 CGGCAAAGTG GTCGTGGTCG ATCACGGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGAG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GCTCGAGCGG GTCGCTGCCG GACGGGGAAG AGGGGCTTTA
1101 CCTGCAATAA CGTTATCAAG GTCAGGTATT GAACCCCTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.pep

```

1 MLLHVSNSLK QLQEEIRIQE RIRQARGNLA SVNKRQREAW DKFQKLNTL
51 NRLKTEVAAT KAQISRFSVG NYKNSQPNV ALFLKNAEPG QKNRFLRYTR
101 YVNASNREV KLEKQKQKAL AVQEQKINNE LARLKKIQAN VQSLLKKQGV
151 TDAAEQTESR RQNAKIAKDA RKLLEQKQNE QQLNKLKLSNL EKKKAEHRIQ
201 DAEAKRKLAE ARLAAAARAR KEAAQQAQAE RRAEMSNLTA EDNRNIQAPSV
251 MGGSADGFS RMQGRLLKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADELDSYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEEGLYLQI RYQGQVLNPS SWIR*

```

950

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLQQLQEERIRQERIRQERIRQARGNLSVNRKQREAWDKFQKLNTLNLRLKT					
m597	MLLHVSNSLQQLQEERIRQERIRQ-----ARGNLSVNRKQREAWDKFQKLNTLNLRLKT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFVSGNYKNSRPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QQKALAVQEQQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QQKALAVQEQQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLKLSNLEKKKAHRIQDAEAKRKLAEAKLAAAEKARKEAAQQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAHRIQDAEAKRKLAEAKLAAAEKARKEAAQQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRKKPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRKKPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELDGYGKVVVDHGENYISYIYAGLSEISAGKGYTVAAGSKIGT					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISYIYAGLSEISVKGKGYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX					
m597	SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCTCAAG CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTTGGGACAA GTTCCAAAAA
151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCG CGTTTCGTAT CGGGGAACTA TAAAAACAGC CAGCCGAATG
251 CGGTTGCCCT GTTCTTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGAAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAAG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGGCGGAA CAGACGGAAG GCCGCAGACA
501 GAATGCCAAA ATCGCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGGAGAA GAAAAAGGCC
601 GAACACCGCA TTCAGGATGC GGAAGCAAAA AGAAAATTGG CTGAAGCCAG
651 ACTGGCGGCA GCCGAAAAAG CCAGAAAAAG AGCGGCGCAG CAGAAGGCTG
701 AAGCACGACG TCGGGAATG TCCAACCTGA CCGCGGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGGTT TCAGCCGCAT
801 GCAAGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGACTTTTCG
851 GGCAGAACCG GAGCGCGGCG GATGTTTGA AAGCGGTGTT CTATTCCACT
901 GCACCGGCAA CGGTTGAAAG CATTGCGCCG GGAACGGTAA GCTATCGCGA

```

951

```

951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTGATCAC GCGGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTCGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

```

a597.pep
  1 MLLHVSNSLK QLQEEIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
  51 LNTLNRLKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEFGQKNRF
 101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
 151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
 201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
 251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
 301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISIIYAG LSEISVGKGY
 351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQQG VLNPSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

```

m597/a597 98.5% identity in 389 aa overlap

      10      20      30      40      50      60
a597.pep MLLHVSNSLKQLQEEIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTLNRLKT
          |||||
m597      MLLHVSNSLKQLQEEIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTLNRLKT
          10      20      30      40      50

      70      80      90      100     110     120
a597.pep EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
          |||||
m597      EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
          60      70      80      90      100     110

      130     140     150     160     170     180
a597.pep QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
          |||||
m597      QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
          120     130     140     150     160     170

      190     200     210     220     230     240
a597.pep QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
          |||||
m597      QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
          180     190     200     210     220     230

      250     260     270     280     290     300
a597.pep SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDVWKGVFYST
          |||||
m597      SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDIWKGVFYST
          240     250     260     270     280     290

      310     320     330     340     350     360
a597.pep APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS
          |||||
m597      APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS
          300     310     320     330     340     350

      370     380     390
a597.pep SGSLPDGEEGLYLQIRYQQGVLPSSWIRX
          |||||
m597      SGSLPDGEEGLYLQIRYQQGVLPSSWIRX
          360     370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

```
g601.seq
  1  ATGTTCCCAA CCGGCAATTT GGTCGACGAA ATTGATGTGC CGAATATAGG
 51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCTTGA
101  ACGCCGCCGA CTGGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151  AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
201  GCTGAAAAATG GGTTTGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251  GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301  AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTGCCGG TACGCGCCCT
351  GAGCATGGGC AAAGTGCACC ACGCTATGAT GGGCATCGCC TCGGTGCGCA
401  TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451  ACGCGTAAAG AAGTGCCTT CGGGCATCCG TCAGGTACGC TCGGTGTCGG
501  TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGGCCGCG aaagcggtca
551  tgaGCCGCAG CGCACgcgtg attatggaaa gttgGGTGCg cgttcccgat
601  gattGTTTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

```
g601.pep
  1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
 51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101  SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151  TRKEVRFGHP SGTLRVGAAA ECQDQGWTA KAVMSRSARV IMESWVRVPD
201  DCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

```
m601.seq
  1  ATGTTCCCAA CCGGCAATTT GGTCGATGAA ATTGATGTGC CGAATATAGG
 51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCTTGA
101  ATGCCGCCGA CTGGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151  AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201  GCTGAAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251  ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301  AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTTGCTGG TACGCGCCCT
351  GAGCATGGGC AAAGTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401  TTGCGACCGC CGCCGCCGTA CCGGTACGC TGGTCAACCT TGCCGAGGC
451  GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTCCG GCACATGCG
501  CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551  CCGTCATGAG CCGTAGCGCA CGCGTGATGA TGAAGGTTG GGTCAAGGTG
601  CCTGAGGATT GTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

```
m601.pep
  1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
 51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101  SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151  GGTRKEVRFG HPSGTLRVGA AAECQDQWT ATKAVMSRSA RVMMEGWVRV
201  PEDCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

```

          10      20      30      40      50      60
m601.pep  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          |||||
g601       MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          10      20      30      40      50      60

          70      80      90     100     110     120
m601.pep  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
```



[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1887>:

a601.seq

```
1 ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51 CCGTTTGAAG GCCACGCTCA TCAACGCGGG CATTCGACG GTTTTCCTGA
101 ATGCCGCGAA CTGGGCTAC ACGGGCAAAG AGTTGCAAGA GCACATCAAC
151 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAATGG GGTCGTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251 ACACGCCGAA AGTCGCTTC GTCCGCGCCG CGCCCGATTA CACCGCTCTC
301 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTGTGCTG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC ACGGCATGAT GGGTACCGCC TCTGTGCCA
401 TTGCGACCCG CGCCGCCGTG CCGGATACGC TGGTCAACCT TGCCGCGAGG
451 GCGGGAACGC GTAAAGAAGT CGCGTTCGGG CATCCTTCGG GCACATTGCG
501 CGTGGTGACA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGAAGGTTG GGTGAGGTTG
601 CCGGAAGATT GTTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1888: ORF 601.a>:

a601.pep

1	MFPPTGNLVDE	IDVPNIGRLK	ATLINAGIPT	VFLNAADLGY	TGKELQDDIN
51	NQAAALEKFE	KIRAYGALKM	GLISDVSEAA	ARAHTPKVAF	VAPAADYTAG
101	SGKTVNAADI	DLLVRLSMG	KLHHAMMGTA	<u>SVAIATAAAV</u>	<u>PGTLVNLNLAG</u>
151	GGTRKEVRFG	HPSGTLRVGA	AAECQDGQWT	ATKAVMSRSA	RVMMEGWVRV
201	PEDCF*				

m601/a601 100.0% identity in 205 aa overlap

		10	20	30	40	50	60																																																						
m601.pep		M	F	P	T	G	N	L	V	D	E	I	D	V	P	N	I	G	R	L	K	A	T	L	I	N	A	G	I	P	T	V	F	L	N	A	A	D	L	G	Y	T	G	K	E	L	Q	D	D	I	N	N	D	A	A	A	L	E	K	F	E
a601		M	F	P	T	G	N	L	V	D	E	I	D	V	P	N	I	G	R	L	K	A	T	L	I	N	A	G	I	P	T	V	F	L	N	A	A	D	L	G	Y	T	G	K	E	L	Q	D	D	I	N	N	D	A	A	A	L	E	K	F	E
		10	20	30	40	50	60																																																						
		70	80	90	100	110	120																																																						
m601.pep		K	I	R	A	Y	G	A	L	K	M	G	L	I	S	D	V	S	E	A	A	A	R	A	H	T	P	K	V	A	F	V	A	P	A	A	D	Y	T	A	S	S	G	K	T	V	N	A	A	D	I	D	L	L	V	R	A	L	S	M	G
a601		K	I	R	A	Y	G	A	L	K	M	G	L	I	S	D	V	S	E	A	A	A	R	A	H	T	P	K	V	A	F	V	A	P	A	A	D	Y	T	A	S	S	G	K	T	V	N	A	A	D	I	D	L	L	V	R	A	L	S	M	G
		70	80	90	100	110	120																																																						
		130	140	150	160	170	180																																																						
m601.pep		K	L	H	H	A	M	M	G	T	A	S	V	A	I	A	T	A	A	A	V	P	G	T	L	V	N	L	A	A	G	G	T	R	K	E	V	R	F	G	H	P	S	G	T	L	R	V	G	A	A	E	C	Q	D	G	Q	W	T		
a601		K	L	H	H	A	M	M	G	T	A	S	V	A	I	A	T	A	A	A	V	P	G	T	L	V	N	L	A	A	G	G	T	R	K	E	V	R	F	G	H	P	S	G	T	L	R	V	G	A	A	E	C	Q	D	G	Q	W	T		
		130	140	150	160	170	180																																																						
		190	200																																																										
m601.pep		A	T	K	A	V	M	S	R	S	A	R	V	M	M	E	G	W	V	R	V	P	E	D	C	F	X																																		
a601		A	T	K	A	V	M	S	R	S	A	R	V	M	M	E	G	W	V	R	V	P	E	D	C	F	X																																		
		190	200																																																										

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTTCTGCT
51  CGGCGGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTTG TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCCTGCAAA TgcgagattA TATCACTTGC TTTtggcgGC TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
1  MLLHQCDKAR HMRPFLGGQ INRHRQASNR GLCSFGGFQG NREAQVFNAD
51  LIDRQVAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLCAA
101 CLQMRDYITC FWRLLH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
1  ATGTTGCTCC ATCAATGCGA CAAACGCGA CATATGCGTC CCCTTCTGCT
51  CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTAT GAGTTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
1  MLLHQCDKTR HMRPLLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHIVI VEMCAWYGVS AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	:     : :   ::      :  :   :     :     :					
g602	MLLHQCDKARHMRPFLGGQINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVS-GEYTVN---LQMRDYITRF*QLHX					
	:       :: :    :   :  :					
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGRMPSEKTLAAQLQMRDYITCFWRLLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
51  CGGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTAT GAGTTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
1  MLLHQCDKAR HMRTLLLRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHIVI VEMCAWYGVS TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

955

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
a602	MLLHQCDKARHMRLLLGROVNRHGQTGNCGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVVSAGEYTVNLQMRDYITRFQQLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQQLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603.seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTTT
101 CAGACGGCCC CGCACCAAAA AAACAACCAC AAATACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCTGAAC TGCCTCAGTT CATCGCTCAA
201 AGGCGCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCTTA AGCTGCCTCG
251 GGGAAACGCT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCTCT GAGCGGCCGC AACTGCCACG CCGGCGCGGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCAGCGCG GCGAAAAATA TCACGAGTCC
451 GTCTCATCG ACCAAGACGT CTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTTCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCGC GCGAATTGCG
651 CAAAAAATAC GCCTTCGCCC GCTACGGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaagACATC
751 CGCTGATTA TTGCCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCG ATCGAAGGTT
851 TGGTAATGGG TACACGTTGC GCGACACCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTTCCCGG GTATTTCcgA actTCCCAAC GACTGCCGCA
1001 CCCTCGAAAT CGCCGCCGAC GAAGCCCGCG AAGGCGCGCG CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTCAC CGGCGGTATC GGCGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCCT ATCTTGATT CTGGGTCTG
1201 CACATCGACA CCAAAGCCAA TATGGAAAAA CGTACGGCA ATTCCGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCCTG GACACTGCCG AACTTGCCGG CATCTTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603.pep

```

1  MDSRLRGNDA RKYGIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTTRRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTTP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPANISGIL AAQEHFPGLP NVGVMDTSFH
201 QTMPERAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISLPN DCRTLEIAAD EGREGARLAL
351 EVMTCLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDPLGL
401 HIDTKANMEK RYGNSGIISP TDSSPAVLVV PTNEELMIAC DTAEALAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603.seq

```

1  CTGTCCTCGC GTAGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TGCGCCTGAT GTCTGC.CTT
101 TTTCAGACGA CCCACACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAmAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCAG CCCGAAGCCG TCATTACGTT CAACAAAGAC

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956

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301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGAAATTGCC ACGCCGGCGC
351 GGTGGGTATG CTTTGAACG AACTGGAAAA ACACGGTCTG CACGACCGCA
401 TCAAAGCCAT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTTGCCGCAC
551 AGGAACATTT CCCCCTGCTG CCCAATGTCG GCGTGATGGA TACTTCGTTC
601 CACCAAAACCA TGCCGGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTGTC CCCTGAAGCC GCACGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACACGT TGCGGCGACA TCGATCCGGG CGTATACAGC
901 TATCTGACTT CCCACGCCGG GATGGATGTT GCCCAAGTGG ATGAAATGCT
951 GAACAAAAAA TCAGGTTTGC TCGGTATTTC CGAATTTC AACGACTGCC
1001 GCACCCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTCA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGGTTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 CATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTTGGTT GTCCCGACCA
1301 ATGAAGAAGT GATGATTGCC TCGGACACTG CCGAACTTGC CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1898; ORF 603>:

m603.pep

```

1  LSSRRRGRNN DRKCGIRFAQ RGRCLKHLAPD VCXFSDDPTL KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRXSGSVV LSCLGERLTT PEAVITFNKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHGL HDRIKAIGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHNPNANISGI LAAQEHFPGP PNVGVMDTSF
201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ARILGKPLED
251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
301 YLTSHAGMDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA
351 LEVMTYRLAK YIASMAVCGC GVDALVFTGG IGENSERNIRA KTVSYLDFLG
401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELAGIL
451 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

m603/g603

```

              10      20      30      40      50      60
m603.pep  LSSRRRGRNNDRKCGIRFAQRGRCLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL
          ::|| || |: || ||||| ||||| ||:: ||| |: ||||| ||||| |||||
g603      MDSRLRG-NDARKYGIRFAQRGRCLKHTPPNAHPFSDGPAPKKQPQTTRRNIMSDQLILVL
              10      20      30      40      50

              70      80      90      100     110     120
m603.pep  NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGKNKRQVPLSGRNCHAGAVGM
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g603      NCVSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGKNKRQVPLSGRNCHAGAVGM
          60      70      80      90      100     110

              130     140     150     160     170     180
m603.pep  LLNELEKHGLHDRIKAIGHRIAHGGEKYESVLIQAVMDLACIPLAPLHNPANISGI
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g603      LLNELEKHGLHDRIKAIGRIAHGGEKYHESVLIQDVLDLAKCIPFAPLHNPANISGI
          120     130     140     150     160     170

              190     200     210     220     230     240
m603.pep  LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSMRYVAPEA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

g603      LAAQEHFPGLPNVGMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLGNGASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISELPNDCRTLEIAADEGREGARLALEVMTCRLAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVCGGVDALVFTGGIGENSRNIRAKTVSYLDLGLHIDTKANMEKRYGNSGIIS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          |||||:|||||:|||||:|||||:|||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1   CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
101 TTTGAGACGA CCCACACC. AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAAGC CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAAGTCC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGAAAA ACACGAACTG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCGC CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCGTCTG CCAATGTCG GCGTGATGGA TACTTCGTTC
601 CACCAACCA TGCCGGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTCC GCCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAAAC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGTAAT GGGTACGCGC TCGGCGGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTC CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGTTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TCGGACACTG CCGAACTTGT GGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1   LSSRRRGRNN DRKCGIRFAQ RGRLKHTPPN AHPFSDPTX KKQPQTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHNPNANISGI LAAQEHFPGLP NVGVMDDTSF

```

201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED  
 251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS  
 301 YLTSHAGLDV AQVDEMLNKK SLLGISSELS NDCRTLEIAA DEGHEGARLA  
 351 LEVMTYRLAK YIASMAVGCG GVDALVFTGG IGNSRNIRA KTVSYLDFLG  
 401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL  
 451 \*

## m603/a603 96.7% identity in 450 aa overlap

m603.pep	10	20	30	40	50	60
	LSSRRRGRNDRKCGIRFAQRGLKHLAPDVCXFSDDEPTLKKQPQTRRNIMSDQLILVL					
a603	LSSRRRGRNDRKCGIRFAQRGLKHTPPNAHPFSDDEPTXKKQPQTRRNIMSDQLILVL					
	10	20	30	40	50	60
m603.pep	70	80	90	100	110	120
	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGKNKQVPLSGRNCHAGAVGM					
a603	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFSKDGKNKQVPLSGRNCHAGAVGM					
	70	80	90	100	110	120
m603.pep	130	140	150	160	170	180
	LLNELEKHGLHDRIKAIGHRIAHGGEKYESVLIQAVMDELNACIPLAPLHN PANISGI					
a603	LLNELEKHGLHDRIQAVGHRIAHGGEKYESVLIQAVMDELNACIPLAPLHN PANISGI					
	130	140	150	160	170	180
m603.pep	190	200	210	220	230	240
	LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHG TSMRYVAPEA					
a603	LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHG TSMRYVAPEA					
	190	200	210	220	230	240
m603.pep	250	260	270	280	290	300
	ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
a603	ACILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
	250	260	270	280	290	300
m603.pep	310	320	330	340	350	360
	YLTSHAGMDVAQVDEMLNKKSGLLGISSELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
a603	YLTSHAGLDVAQVDEMLNKKSGLLGISSELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
	310	320	330	340	350	360
m603.pep	370	380	390	400	410	420
	YIASMAVGCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
a603	YIASMAVGCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
	370	380	390	400	410	420
m603.pep	430	440	450			
	PTDSSPAVLVVPTNEELMIACDTAELAGILX					
a603	PTDSSPAVLVVPTNEELMIACDTAELVGILX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:  
 g604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA  
 51 CCAGCGTACC GAGCACGCG GCGGCGATGG CGACCGAGGC GATGCCCATC  
 101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT  
 151 GTCGGCGGCG TTTACGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG  
 201 GCGCGACGAA GGCGGGTTTC GGCGTGCGCG CGCGGCGGC GGCTTCGGAT

959

251 ACGTCGCTGA TCAAACCCAT TTTCAGCGCG CCATATGCGC GGATGGTTTC  
 301 AAATTTTCC AGCGCGGCGG CATCGTTGTT GATGTCGTCC TGCAACTCTT  
 351 TGCCCGTGTA GCCCAAGTCG GCGGCGTTCA GGAACACGGT CGGAATGCCC  
 401 GCGTTGATGA GCGTGGCTTT CAGACGACCT ATATTCGGCA CATCAATTTC  
 451 GTCGACCAAA TTGCCGGTTG GGAACATACT GCCTTcgCG TCGGCTGGAT  
 501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1902; ORF 604.ng>:

g604.pep

1 MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVQFA HAQGAYRQID  
 51 VGGVYGFAAG GGVIGGGRDE GGFRRARAGG GFGYVADQTH FQRAICADGF  
 101 KFFQRGIVV DVVLQLFARV AQVGGVQENG RNARVDERGF QTTYIRHINF  
 151 VDQIAGWEHT AFAVGWI\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1903>:

m604.seq

1 ATGCCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA  
 51 CCAGCGTACC GGGTACGGCG GCGGCGGTCC CAATGGCAAC AGAGGCGGTA  
 101 CCCATCATCG CGTGGTGCAAG TTGCCCCATG CTCAGGGCGC GTACCAGCAA  
 151 ATCGATGTCG GCGGCGTTCA CGGTTTTGCC ACTGGAGGCG GTGTAATCGG  
 201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG AGCGGCAGCT  
 251 TCGGATACGT CGCTGATCAG ACCATTTC AGCGCACCGT AAGCGCGGAT  
 301 TTTCTCGAAT TTTTCCAAAG CCGCGGCATC GTTGTGTATG TCGTCTTGCA  
 351 ACTCTTTGCC TGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA  
 401 ATGCCCCGCGT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC  
 451 AATTTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG  
 501 CTGGATC

This corresponds to the amino acid sequence <SEQ ID 1904; ORF 604>:

m604.pep

1 MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVQ FAHAQAYQQ  
 51 IDVGVHGF A TGGVIGGGR DEGDFRRVRA SGSFGYVADQ THFORTVSAD  
 101 FLEFFQSRGI VVDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTYAIRHI  
 151 NFIDQIAGWE HTAFAVGWI

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng) from *N. gonorrhoeae*:

m604/g604

	10	20	30	40	50	60
m604 . pep	MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQAYQQIDVGGVHGF					
	:     :     :     :     :     :					
g604	MPEAHFFTRSAACGKVDQRTGHEGGG--DGDGRDAHHSVVQFAHAQAYRQIDVGGVYGFA					
	10	20	30	40	50	
	70	80	90	100	110	120
m604 . pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFORTVSADFLEFFQSRGIVVDVVLQLFA					
	:     :     :     :     :     :     :					
g604	AGGGVIGGGRDEGDFRRARAGGGFGYVADQTHFQRAICADGFKFFQRGIVVDVVLQLFA					
	60	70	80	90	100	110
	130	140	150	160	169	
m604 . pep	CVAQVGGIQENGRNARVDERGFQTYAIRHINFIDQIAGWEHTAFAVGWI					
	:     :     :     :     :     :					
g604	RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFAVGWIX					
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1905>:

a604.seq

1 ATGCCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA  
 51 CCAGCGTACC GGGCACGGCG GCGGCGGTCC CAATGGCAAC AGAGGCGGTA  
 101 CCCATCATCG CGTGGTGCAA TTGCCCCATG CTCAGGGCGC GTACCAGCAA  
 151 ATCGATGTCG GCGGCATTCA CGGTTTTGCC ACTGGAGGCG GTGTAATCGG

960

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201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GGCGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGAT TCGTCTTGCA
351 ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTACAGGAA AACGGTCGGA
401 ATGCCCGCGT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
451 AATTTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551 TCGAGCTCAA AATCGCCTGT TTCCAAAACT GCGCCGTTT GCATCGGTAC
601 ATGGGCAATA ATGGTTTTGC CGATGTTTTT CTGCCAGATT TTGACTGTGC
651 AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
1  MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51  IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101 FLEFFQSCGI VVDVVLQLFA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWIK KFDLYFGCRE RYAVELKIAC FQNCVHLHRY
201 MGNNGFADVF LPDFDCADAV *

```

m604/a604 97.0% identity in 169 aa overlap

```

m604.pep      10      20      30      40      50      60
MPEAHFFTRSAAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA
|||||
a604          10      20      30      40      50      60
MPEAHFFTRSAAACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA

m604.pep      70      80      90      100     110     120
TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGIVVDVVLQLFA
|||||
a604          70      80      90      100     110     120
TGGGVIGGGRDEGDFRRVRAGSFGYVADQTHFQRTVSADFLEFFQSCGIVVDVVLQLFA

m604.pep      130     140     150     160     169
CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI
|||||
a604          130     140     150     160     170     180
RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWIKKFDLYFGCRE

a604          190     200     210     220
RYAVELKIACFQNCVHLHRYMGNNGFADVFLPDFDCADAVX

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
1  ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51  AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGTTTA TCAGCGAAAA CTTACCCGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGGACAG
201 CATCATCACG CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATCtacCc cgGCCAGCTT TTTTgcaata ttgccgccga agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA atCTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTAcccgT CCGAACAAGG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCCGTCTT TAAAGGCGTG GCGGAACTCG ATTTTCGGCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCAATA CGCcgCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGCGAGGA
651 GAAAGTCAAC AAAATCTACG ACCCCGCCTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATCCA CATCGAATTG GGCGACACGC
851 TGACCAACCC CAAACTCAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgat

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951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCGGGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATc CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTKLKE IFTAIESSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLOAKKQF DEHIEEGFF
251 GQEINHHTYN LARMNMF LHN VNYNKFHIEL GDTLTNPKLK DSKPFDVAVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPPI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTICIAVNI
401 LVLSKHKDNT DIQFIDASGF FKKETNNNV L TEEHIAEIVK LFADKADVPH
451 IAQNAAQQT V KNGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACC GATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACTCG ATTTCGGCAA
501 TTTTGAAAAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGTGCCAAAC GCAGGCAAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GGCGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCGGGCATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

```

101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN  
 151 KRLA AVLKGV AELDFGNFEN HHIDLFGDAY EYLISNYAAN AGKSGGEFFT  
 201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLQAKKQF DEHIEEGFF  
 251 GQEINHHTYN LARMNMF LHN VNYNQFHIEL GDTLTNP K LK DSKPFDAIVS  
 301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG  
 351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI  
 401 LVLSKHKDNT DIQFIDASGF FKKETNNNV L IEEHIAEIVK LFADKADVP H  
 451 IAQNAAQQT V KONGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER  
 501 LRREIDEVIA EIEA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng)  
from *N. gonorrhoeae*:

m605/g605

	10	20	30	40	50	60
m605.pep	MMTEMQRAQLHRQIWKIADAVRGAVDGDWDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
g605	MMTEMQRAQLHRQIWKIADAVRGAVDGDWDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVGKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	YAAMPDSIITPEIKDDAVKVGKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFENHHIDLFGDAY					
g605	GYPSEQGIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFEDHRIDLFGDAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m605.pep	EYLISNYAANAGKSGGEFFT PQSVSKLIAR LAVHGQEKVN KIYDPACGSGSLLQAKKQF					
g605	EYLISNYAANAGKSGGEFFT PQSVSKLIAR LAVHGQEKVN KIYDPACGSGSLLQAKKQF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m605.pep	DEHIEEGFFGQEINHHTYN LARMNMF LHN VNYNQFHIEL GDTLTNP K LK DSKPFDAIVS					
g605	DEHIEEGFFGQEINHHTYN LARMNMF LHN VNYNQFHIEL GDTLTNP K LK DSKPFDAIVS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFIL HALNYLSGRGRAAIVSFPGI					
g605	NPPYSIDWIGSDDPTLINDDRFAPAGVLAPKSKADFAFIL HALNYLSGRGRAAIVSFPGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m605.pep	FKKETNNNV L IEEHIAEIVK LFADKADVP HIAQNAAQQT VKONGYNLAVSSYVEAEDTRE					
g605	FKKETNNNV L IEEHIAEIVK LFADKADVP HIAQNAAQQT VKONGYNLAVSSYVEAEDTRE					

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		430	440	450	460	470	480
		490	500	510			
m605.pep		IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX					
		:    :     :     :     :     :					
g605		VIDIRQLNAEISETVAKIERLRREIDEVIAEITX					
		490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1911>:

```

a605.seq
1  ATGATGACCG  AAATACAACA  ACGCGCCCAA  CTGCACCGCC  AAATTTGGAA
51  AATTGCCGAC  GAAGTACGCG  GCGCGGTGGA  TGGCTGGGAC  TTCAAACAAT
101 ACGTTCTCGG  CACACTTTTC  TACCGCTTTA  TCACGCAAAA  CTTATCCGAC
151 TATATGCAGG  CAGGCGACAG  CAGTATTGAT  TACGCCGCTA  TGCCGGACAG
201 CATCATCACG  CCCGAAATCA  AAGACGATGC  CGTCAAAGTC  AAAGGCTATT
251 TCATCTACCC  CGGCCAGCTT  TTTTGCAATA  TTGCCGCCGA  AGCCCATCAA
301 AACGAAGAGC  TCAACACCAA  GCTGAAAGAA  ATTTTACCG  GATTGCAAG
351 CTCCGCCTCC  GGCTATCCGT  CCGAACAAAG  CATTAAAGGC  CTGTTTGACG
401 ACTTCGACAC  CACCGACGAG  CGGCTCGGCA  GCACCGTTGC  GCACAAGAAC
451 AAACGCCTTG  CCGCCGTCTT  AAAAGCGGTG  CGGGAATCTG  ATTTCCGGCA
501 TTTTGAAGAC  CACCATCATG  ACCTTTTCGG  GCATGCTTAC  GAATACCTGA
551 TTTCCAATA  CGCTGCCAAC  GCAGGCAAA  CCGGCGGCGA  ATTTTTACC
601 CCGCAAAGCG  TATCCAAGCT  GATTGCGCGG  CTGGCGGTGC  ACGGGCAGGA
651 GAAAGTAAAC  AAAATCTACG  ACCAGCTTTC  CGGCTCGGGC  AGCCTGCTCT
701 TCGAGCGGAA  AAAACAGTTT  GCAGAGCACA  TCATCGAAGA  AGCCTTCTTC
751 GGGCAGGAAA  TCAACCACAC  CACCTACAAC  CTCGCCCGCA  TGAATATGTT
801 TCTGCACAAC  GTAATTACA  ACAAATTTCA  CATCGAATTG  GGGCAGACAC
851 TGACCAATCC  CAAACTCAA  GACAGCAAA  CCTTTGATCG  CGTCGTTTTC
901 AATCCGCCCT  ATTCATCAA  CTGTGATAGC  AGCGGCGACC  CACCTTAAT
951 CAACGACGAC  CGCTTTGCC  CTGCAGGCGT  ACTCGCCCCG  AAATCCAAAG
1001 CCGATTTTGC  CTTCTATTCT  CACGCACTTA  ACTACCTTTC  CGGCAGAGGC
1051 CGCGCGGCCA  TCGTCTCAT  CCCCGCATT  TTCTATCGCG  GCGGCGCAGA
1101 GCAGAAAATC  GCCCAATATC  TGGTGGAGGG  CAACTACGTG  GAAACCGTCA
1151 TCGCCCTTGC  GCCCAATCTC  TTTTACGGCA  CCGGCATCGC  CGTCAATATA
1201 CTGTTTGTG  CCAAACAAA  AGACAATACC  GACATCCAA  TCTCGACGCG
1251 AGCGGCTTTC  TTTAAAGAA  AAACCAACA  CAACGTCTTA  ACCAGAAGAC
1301 ACATTGCCGA  AATCGTCAAA  CTCTTCGCCG  ATTAAGCCGA  TGTGCCGCAT
1351 ATCGCCCAA  ACGCGGCCA  GCAAACCGTC  AAAGACAACG  GCTACAACCT
1401 CGCGGTCACT  AGCTATGTTG  AACCCGAAGA  CACCCGCGAA  ATTATCGACA
1451 TCAAACAGCT  TAACGCCGAA  ATCAGCGAAA  CCGTTGCCAA  AATCGAACGG
1501 CTGCGGCGTG  AAATTGACGA  AGTGATTGCA  GAGATTGAAG  CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

```
a605.pep
1 MMTEIQQRAQ LHRQIWKIAD EVRGAVDGDWDFKQYVLGTLFYRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDFTSS RLGSTVADKN
151 KSLAAVLKGV AELDFGSFED HHIDLFGDAY EYLISNYAAN AGKSGGEEFTT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLOAKKQF DEHIEEGFF
251 GQEINHTTYN LARMNMFLHN VNYNKFHIEL GDTLTNPCLK DSKPFDVAVS
301 NPPYSINWIG SGDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGVNY ETVIALAPNL FYGTGIAVNI
401 LVLSKHKDNT DIQFIDAGGF FKKETNNNVL TEEHIAETVK LPADKADVPH
451 IAQNAAQQTV KDNQYNLAVS SYVEPEDTRE IIDIKQLNAE ISETVAKIER
501 LRREIDEVIA EIEA*
```

**m605/a605 98.1% identity in 514 aa overlap**

	10	20	30	40	50	60
m605.pep	MMTEMQ	RAQLHRQIWK	IADEV	RGAVD	GWDFKQYVL	GLFYRF
	:					
a605	MMTEIQ	RAQLHRQIWK	IADEV	RGAVD	GWDFKQYVL	GLFYRF
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDS	IITPEIKDDA	VKVGYFI	YPGQLFCN	IAAEAHQNEE	LNTKLKEIFTA
						IESSAS

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|||||
a605  YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS
      70      80      90     100     110     120

      130     140     150     160     170     180
m605.pep GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAELDFGNFENHHIDLFGDAY
|||||
a605  GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAELDFGSFEDHHIDLFGDAY
      130     140     150     160     170     180

      190     200     210     220     230     240
m605.pep EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF
|||||
a605  EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF
      190     200     210     220     230     240

      250     260     270     280     290     300
m605.pep DEHIIIEGFFGQEIINHHTYNLARMNMF LHNVNYNQFHIELGDTLTNPKLKDSKPFDAIVS
|||||
a605  DEHIIIEGFFGQEIINHHTYNLARMNMF LHNVNYNKFHIELGDTLTNPKLKDSKPFDAVVS
      250     260     270     280     290     300

      310     320     330     340     350     360
m605.pep NPPYSINWIGSDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI
|||||
a605  NPPYSINWIGSDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI
      310     320     330     340     350     360

      370     380     390     400     410     420
m605.pep FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGI AVNVLVLSKHKDNTDIQFIDASGF
|||||
a605  FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGI AVNVLVLSKHKDNTDIQFIDAGGF
      370     380     390     400     410     420

      430     440     450     460     470     480
m605.pep FKKETNNNVLIEEHIAEIVKLFADKADVPHIAQNAAQTVKDNGYNLAVSSYVEAEDTRE
|||||
a605  FKKETNNNVLTEEHIAEIVKLFADKADVPHIAQNAAQTVKDNGYNLAVSSYVEPEDTRE
      430     440     450     460     470     480

      490     500     510
m605.pep IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX
|||||
a605  IIDIKQLNAEISETVAKIERLRREIDEVIAEIEAX
      490     500     510

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1913>:

g606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGTGCGGAAG TCATCGACAC
51  GCCGcgCACC GAAGAAGAAG CCTGGCTTCT GAACACTGTC GAAGCCCAAg
101 cgcGGCAATG GAATCTGAAA ACGCCAGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCacc ggtttgctcg accaTatgaC GCGCGACgaa gtggaagccg
251 tgTTGCGGCA CGAAATGGCG CACGTCGGCA ACGGCGACAT GGTACGCTG
301 ACGCTGAtTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCCT AGTCAGCATG GTATTCCAAA TCCTGTTCCG CTTCCTTGCC
451 AGCCTGATTG TCATGTGGTT CAGCCGCCAA CGGAATACC GCGCCGAcgc
501 gggCGcggCA AAACCTGGTC GCGCACCGAA AATGATTTC GCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTGCCCC AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep

```

1 MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51 EPNFATGAS RNSSLIAVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRRIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSL STHPSLDNRI ARLKSL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1 ATGTCCAAAT TTATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51 GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GTTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCGGAA AATGATTTC GCCCTGCAAA
551 GGCTCAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGTATC GCCCGCTCA AATCGTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1 MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51 EPNFATGAS RNSSLIAVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRRIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSL STHPSLDNRI ARLKSL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

	10	20	30	40	50	60
m606.pep	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNFATGAS					
g606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNFATGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRRIAN					
g606	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRRIAN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1 ATGTCCAAAT TCATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51 GCGCGCACC GAAGAAGAA CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CTTTGGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTGCTCTG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCATAT GTTACGCTG
301 ACGCTGATT CAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCC GAAACAACGA CGGCAGCCAG TCCAGGGAA
401 CTTATTCTT GGTGAGCAT GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGT CAGCCGACAA CGCAATACC GCGCCGACGC
501 GGGCGCGGCA AAAGTGGTC GCGCGCGGAA AATGATTTC GCCCTGAAA
551 GGCTTAAAG CAACCGGTC GATTGCCCC AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCA CTCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCCCGCTCA AATCGCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1 MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51 EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAVALHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

	10	20	30	40	50	60
m606.pep	MSKFIAKQSVGAEVIDTPRT EEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
a606	MSKFIAKQSVGAEVIDTPRT EEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
a606	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSQGTFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
a606	LIARNNDGSQSQGTFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
a606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1 ATGCTGCTCG accTgaCCG CTTTTCCTt tccGTCTTCC TGAAAGAAAT
51 CCGCCTGCTG ACGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGATTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCAGC
251 TTTACGGCGC GGGTAAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTCG GGCTGATTTT GGGGATTTT GGCATGATTT TGATGTGGGC
351 GCGGATTACG CCGTTCGCA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAatggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGCGGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCCGTA TGCCCGCTTT GGGTGGCGCA

```

```

601  GGTTCGCGCG  TGGCGACAAT  GGCGGTGTTT  TGGTTCAGCG  CGCTGGCATT
651  GTGGATTATAT  ATCGCCAAGG  AAAAATTCTT  CCGCCCCTTC  GGACTGACAG
701  CGAAATTCGg   caaACCGGat  tGGgcGGTGT  TCAAACAGAT  TtGGAAAATC
751  gGcgcgCCCA  TCGGGCTGTC  TTATTTTGTG  GAAGccaGcg  cGTTTTCGTT
801  TATCGTGTTT  TTGATTGCGC  CTttcggCGA  GGATTATGTG  GCGGCGCAGC
851  AGGTCGGCAT  CAGTTTGTCT  GGGATTCTCT  ATATGATTCC  GCAAAGCGTC
901  GGCTCGGCAG  GGACGGTGCG  CATCGGCTTT  TCGCTTGGGC  GGCGCGAATT
951  TTCGCGGGCG  CGTTATATTT  CAGGAGTGTC  GCTGGTGTCG  GGCTGGGTGC
1001 TCGCCGTGAT  TACCGTGCTT  TCCTTGGTAT  TATTCGGTTC  GCCGCTGGCA
1051 AGCATGTACA  ACGATGaTCC  GGCAGTTTTA  AGCATCGCCT  CCACCGTCCT
1101 GCTGTTTCGCC  GGCCTGTtcc  aACCGGCAGA  CTTACCCCAA  TGTATCGCGT
1151 CCTATGCCCT  GCGCGGCTAC  AAAGTCACCA  AGGTGCCGAT  GTTCATCCAC
1201 GCCGCCGCCT  TCTGGGGCTG  CGGCCTGCTG  CCGGGCTATC  TGCTCGCCTA
1251 CCGTTTCGAT  ATGGGCATT  ACGGCTTCTG  GACGGCATTG  ATTGCCTCGC
1301 TCACCATCGC  AGCCGTGCGC  TTGGTGTGGT  GCTTGAAAA  ATACAGTATG
1351 GAGTTGGTCA  AATCACACAA  GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1  MLLDLDRFSF  SVFLKEIRLL  TALALPMLLA  QVAQVGIGFV  DTVMAGGAGK
51  EDLAAVALGS  SAFATVYITF  MGIMAALNPM  IAQLYGAGKT  GEAGETGRQG
101 IWFGILIGIF  GMILMWAAIT  PFRNWLTLSD  YVEGTMAQYM  LFTSLAMPAA
151 MVHREALHAYA  SSLNRPRLLM  LVSFAAFVLN  VPLNYIFVYG  KFGMPALGGA
201 GCGVATMAVF  WFSALALWIY  IAKEKFRPF  GLTAKFGKPD  WAVFKQIWKI
251 GAPIGLSYFL  EASAFSFIVF  LIAPFGEDYV  AAQQVGISLS  GILYMIPQSV
301 GSAGTVRIGF  SLGRREFSRA  RYISGVSLVS  GWVLAVITVL  SLVLFRRSPLA
351 SMYNDPDAVL  SIASVTLLFA  GLFQPADFTQ  CIASYALRGY  KVTKVPMPFIH
401 AAAPFWCGLL  PGYLLAYRFD  MGIYGFWTAL  IASLTIAAVA  LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1  ATGTCGCTCG  ACCTCAACCG  CTTTTCCTTT  CCCGTCTTCC  TGAAAGAAGT
51  CCGCCTGCTG  ACCACTCTTG  CCCTGCCCAT  GCTGTGGCG  CAGGTGCGGC
101 AGGTGGGCAT  CGGTTTTGTC  GATACTGTGA  TGGCGGGCGG  TGCGGGCAAG
151 GAAGACTTGG  CGGCGGTGGC  TTTGGGCAGC  AGCGCGTTTG  CCACGGTTTA
201 TATTACCTTT  ATGGGCATTA  TGGCGGCGCT  GAACCCGATG  ATTGCCCAGC
251 TTTACGGCGC  GGGTAAAACC  GACGAAGTGG  GCGAAACGGG  GCGGCAGGGG
301 ATTTGGTTTC  GGCTGTTTTT  GGGCGTGTTT  GGCATGGTCT  TGATGTGGGC
351 GCGGATTACG  CCGTTCGCCA  ACTGGCTGAC  CTTGAGCGAT  TATGTGGAAG
401 GCACGATGGC  GCAGTATATG  TTGTTACCA  GCTTGGCGAT  GCCGGCGGCA
451 ATGGTACACC  GCGCGCTGCA  CGCCTACACT  TCCAGCCTGA  ACCGCCCGCG
501 CCGTATTATG  TTGGTCAGCT  TTGCGGCGTT  TGTGTTGAAC  GTGCCGCTGA
551 ACTATATTTT  CGTTTACGGC  AAATTCGGTA  TGCCCGCTTT  GGGCGGCGCA
601 GGCTGCGGAC  TGGCGACGAT  GCGGTGTTT  TGGTTCAGCG  CGCTGGCATT
651 GTGGATTATAT  ATCGCCAAGG  AAAATTCTT  CCGCCCATT  GGACTGACGG
701 CGAAATTCGG  CAAACCGGAT  TGGCGGTGT  TCAAACAGAT  TTGGAAAATC
751 GCGCACCCCA  TCGGGCTGTC  TTATTTTGTG  GAAGCCAGCG  CGTTTTCGTT
801 TATCGTGTTT  TTGATTGCGC  CTTTCGGCGA  GGATTATGTG  GCGGCGCAGC
851 AGGTCGGCAT  CAGTTTGTCT  GGGATTCTCT  ATATGATTCC  GCAAAGCGTC
901 GGCTCGGCGG  GGACGGTGCG  CATCGGCTTT  TCGCTTGGGC  GGCGCGAATT
951 TTCGCGGGCG  CGTTATATTT  CGGGCGTGTC  ACTGGTGTTA  GGATGGATGC
1001 TCGCCGTGAT  TACCGTGCTT  TCCTTGGTAT  TATTCGGTTC  GCCGCTGGTA
1051 AGTATGTACA  ACAATGATCC  GCGGTTTTTA  AGCATCGCCG  CCACCGTCTT
1101 ACTGTTTCGCC  GGCTTGTTCC  AACCAGCAGA  CTTACCCCAA  TGTATCGCCT
1151 CCTACGCCCT  GCGCGGCTAC  AAAGTACAA  AGGTGCCGAT  GTTCATCCAC
1201 GCCGCCGCCT  TTTGGGGCTG  CGGCCTGCTG  CCGGGCTATC  TGCTCGCCTA
1251 CCGTTTCAAT  ATGGGCATT  ACGGCTTCTG  GACGGCATTG  ATTGCCTCGC
1301 TCACCATCGC  CGCCATCGCC  TTGGTGTGGT  GCTTGGAATT  GTGCAGTAGG
1351 GAGATGGTCA  GATCGCATAA  GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1  MLLDLNRFSF  PVFLKEVRLL  TTLALPMLLA  QVAQVGIGFV  DTVMAGGAGK
51  EDLAAVALGS  SAFATVYITF  MGIMAALNPM  IAQLYGAGKT  DEVGETGRQG

```

101 IWFGFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA  
 151 MVHRALHAYT SSLNRPRLIM LVSFPAFVLN VPLNYIFVYG KFGMPALGGA  
 201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI  
 251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIQSV  
 301 GSAGTVRIGF SLGRREFSRA RYISGVSLVL GWMLAVITVL SLVLFPSPLV  
 351 SMYNNDDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFIFH  
 401 AAAPWGCGLL PGYLLAYRFN MGIYGFWTAL IASLTIAAIA LVWCLELCSR  
 451 EMVRSHKAV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng)  
from *N. gonorrhoeae*:

m607/g607

m607.pep	10	20	30	40	50	60
	MLLDLNRFSFPVFLKEVRLLTTTLALPMLLAQVAQVGIGFVDVTVMAGGAGKEDLAAVALGS					
g607	MLLDLDRFSFSVFLKEIRLLTALALPMLLAQVAQVGIGFVDVTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	70	80	90	100	110	120
	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
g607	SAFATVYITFMGIMAALNPMIAQLYGAGKTGEAGETGRQGIWFGILGIFGMILMWAAIT					
	70	80	90	100	110	120
m607.pep	130	140	150	160	170	180
	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVMHRALHAYTSSLNRPRLIMLVSFPAFVLN					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVMHRALHAYASSLNRPRLIMLVSFPAFVLN					
	130	140	150	160	170	180
m607.pep	190	200	210	220	230	240
	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD					
g607	VPLNYIFVYGKFGMPALGGAGCGVATMAVFWFSALALWIYIAKEKFFRPFGLTAKFGKPD					
	190	200	210	220	230	240
m607.pep	250	260	270	280	290	300
	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIQSV					
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIQSV					
	250	260	270	280	290	300
m607.pep	310	320	330	340	350	360
	GSAGTVRIGFSLGRREFSRRARYISGVSLVLGWMLAVITVLSLVLFPSPLVSMYNNDDPAVL					
g607	GSAGTVRIGFSLGRREFSRRARYISGVSLVSGWMLAVITVLSLVLFPSPLASMYNNDDPAVL					
	310	320	330	340	350	360
m607.pep	370	380	390	400	410	420
	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPFIFHAAAFWGCGLLPGYLLAYRFN					
g607	SIASTVLLFAGLFQPADFTQCIASYALRGYKVTKVPFIFHAAAFWGCGLLPGYLLAYRFD					
	370	380	390	400	410	420
m607.pep	430	440	450	460		
	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSKAVX					
g607	MGIYGFWTALIASLTIAAVALVWCLEKYSMELVKSHKAVX					
	430	440	450	460		



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTGGGCGAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACCC GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCC TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGACTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAATAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTGTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTCGCC GGCTTGTTCC AACCGGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1  MLLDLNRFSF SVFLKEVRLT TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFGFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRALHAYA SSLNRPR LIMLVSF AAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMPIQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFPSPLV
351 SMYNNDPAYL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFMFIH
401 AAAPWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCSR
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLTTTALPMLLAQVAQVGIGFVDTVMAAGGAGKEDLAAVALGS					
a607	MLLDLNRFSFVSFLKEVRLTALALPMLLAQVAQVGIGFVDTVMAAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
	70	80	90	100	110	120
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRALHAYTSSLNRPR LIMLVSF AAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRALHAYASSLNRPR LIMLVSF AAFVLN					
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRALHAYTSSLNRPR LIMLVSF AAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRALHAYASSLNRPR LIMLVSF AAFVLN					
	190	200	210	220	230	240

970

```

m607.pep      VPLNYIFVYGKFGMPALGGAGCGLATMAVWFWSALALWIYIAKENFFRPFGLTAKFGKPD
a607           VPLNYIFVYGKFGMPALGGAGCGLATMAVWFWSALALWIYIAKENFFRPFGLTAKFGKPD
                190      200      210      220      230      240

                250      260      270      280      290      300
m607.pep      WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMPIQSV
a607           WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMPIQSV
                250      260      270      280      290      300

                310      320      330      340      350      360
m607.pep      GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFRSPLVSMYNNDPAVL
a607           GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFRSPLVSMYNNDPAVL
                310      320      330      340      350      360

                370      380      390      400      410      420
m607.pep      SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPMTFIHAAAFWGCGLLPGYLLAYRFN
a607           SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPMTFIHAAAFWGCGLLPGYLLAYRFD
                370      380      390      400      410      420

                430      440      450      460
m607.pep      MGIYGFWTALIASLTIAAIALVWCLELCSREMRVSHKAVX
a607           MGIYGFWTALIASLTIAAIALVWCLELCSREMRVSHKAVX
                430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

```

g608.seq
1   ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTCAGG CAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAAT ACCTTCGCA ACAGCGCGAT
201 ACGGAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCTCGGC ATGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTCCCGCG CATCGGacgA ATTGGCACGG ATTTTCGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCaTCaaa CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTGGAACGCG
551 ACATTTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

```

g608.pep
1   MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGGEPGAGD IRLEGLILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRRLDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

```

m608.seq
1   ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGGCG CCTTTCAGG CAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAAT ACCTTCGCA ACAGCGCGGT
201 ACAGAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCTCGGC ATGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCG ACATCGGACA CGGCATCAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

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971

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACCGC  
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS  
51 AGNGFADTEI TFRNSAVQKI LQGGEFGAGD IGLEGLLIG IAVLSLLGSL  
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA  
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	:					
g608	MSALLPIINRLILQSPDSRSELTSFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEFGAGDIGLEGLLIGIAVLSLLGSLRSRASDELARIFGTQADIGS					
	:					
g608	TFRNSAIRKILQGGEFGAGDIRLEGLLIGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
	:					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq

1 ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA  
51 CAGCCGCTCG GAACTTGGCG CCTTCGCAGG CAAAACACTG ACCCTGAACA  
101 TTGCCGGGTT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG  
151 GCGGGAACG GCTTTGCAGA CACCGAAATC ACCTCCGCA ACAGCGCGGT  
201 ACAGAAAATC CTCCAAGCG GCGAACCCGG GCGGGCGAC ATCGGGCTCG  
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCTGCT CGGCAGCCTG  
301 CGTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA  
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAA CAAATCGGCA  
401 GGAACATCGC CGAACAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA  
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT  
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACCGC  
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS  
51 AGNGFADTEI TFRNSAVQKI LQGGEFGAGD IGLEGLLIG IAVLSLLGSL  
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA  
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID\*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

```

m608.pep  MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
a 608      MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
           10      20      30      40      50      60

           70      80      90      100     110     120
m608.pep  TFRNSAVQKILQGGEPGAGDIGLEGLLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
a 608      TFRNSAVQKILQGGEPGAGDIGLEGLLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
           70      80      90      100     110     120

           130     140     150     160     170     180
m608.pep  RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR
a 608      RAADIGHGIKQIGRNIAEQIGRFSREPESANIGNEALADCLDEISRLRDGVERLNERLDR
           130     140     150     160     170     180

           189
m608.pep  LERDIWIDX
a 608      LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAACTTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGCGCCATAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTCTG TGGCCGTATG
351 CCCCGTCTTT CATTTACCCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pap
1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRVVFV GLFGNVFFIG
51 AFEQAVELAA RLRFHIIIDNF LDTDFGIGSQ ADGNVRTLM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGCGCCGTAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTCTG TGGCCGTATG
351 CCCCGTCTTT GATTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pap
1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRVVFV GFEGNVFFIG
51 AFEQAVELAA RLRHLIIDDF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFARETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

           10      20      30      40      50      60
m609.pap  MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVVFVGFEGNVFFIGAFEQAVELAA
           10      20      30      40      50      60
g609       MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVVFVGLFGNVFFIGAFEQAVELAA
           10      20      30      40      50      60

           70      80      90      100     110     120
m609.pap  RLRHLIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTAKRGYGNHDLHTVAVCPVF
           70      80      90      100     110     120

```

g609 RLRFHIIIDNFDLDTDFGIGSQADGNVRTLIMRAILGNFFGTRAKRGYGNHDLHTVAVCPVF  
70 80 90 100 110 120

m609.pep DFARETDIIIQX  
|:|:|:|:|:|:|  
g609 HFTREADIIIIQX  
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1935>:

```
a609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTTGA
51  TGCGTTTGTG GGCAATCAGC GAAGTACGCA CATCGCGCAC CATATCTTCC
101 ACGAATTTCG GGTTTTCGTA GGCTTTTTCG GTACAGTATT TTTCATCTGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGCGCCATAT TGGGAAATTT CTTTGGAAAC
301 CGGGCAAAGC GAGTTTACGG GAATCATGAC CTTCACTACT TGGCCGTATG
351 CACCGTCTTT CATTTCGCCC GTGAGGCTGA CATCATAATC CAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1936; ORF 609.a>:

```
a609.pep
      1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRVFEV GFFGNVFFIG
     51  AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAILGNFFGT
    101  RAKRGYGNHD LHTVAVCTVF HFAREADIII Q*
```

m609/a609 96.9% identity in 131 aa overlap

		10	20	30	40	50	60
m609.pep		MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFEVGGFFGNVFFIGAFEQAVELAA					
a609		MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFEVGGFFGNVFFIGAFEQAVELAA					
		10	20	30	40	50	60
		70	80	90	100	110	120
m609.pep		RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF					
a609		RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAILGNFFGTRAKRGYGNHDLHTVAVCTVF					
		70	80	90	100	110	120
		130					
m609.pep		DFARETDIIIQX					
		:					
a609		HFAREADIIIQX					
		130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1937>:

```

g610.seq
1  ATGATTGGAG  GGCTTATGCA  ATTTCCCTTAC  CGCAATGTTC  CGGCTTCGCG
51  TATGCGCCGT  ATGCGCAGGG  ATGATTTTTC  ACGCGCGCTG  ATGCGCGAGC
101 ATATGCTGAC  CGCGCATGAT  TTGATTTATC  CGGTGTTCGT  ATTGGAGGGG
151 CGCGGCGCGC  AGGAGGATGT  GCCTTCTATG  CCGGCGCGTA  AGCGTCFAGG
201 TTTGGACAGG  TCTGCTTTTA  CGCCGGAAGA  GCGCGTGAAG  TCCGTTATTC
251 CGATGTTGGC  ACTCTTTCCC  GTGGTTACGG  CAAACAAAC  CGGGCGTCCG
301 CAGGAGCGCT  ACAATCCCCA  AGGACTCGTG  CCGTCAACTG  tccgagctcc
351 GCGCGAGAGG  TttcCggaac  tggggattat  gacggatgtc  gctgcgatac
401 ctatacgggt  gcaacGGTCG  GACGACGATGA  CGGACgaaaa  cggtataCGTG
451 ATGAatcGAtg  aaacCCGTAGA  AGTCTTGGTG  CAACAGGCTT  TATGTCATGC
501 AGAGGCGGGC  ACGCAGGTCG  TTGCTCCTTC  CGCATGATG  GACGGGCGTA
551 TCGGCGCCAT  CCGCGAGGCT  TTGGAGGATG  CGGCACATAT  CCATACGGCG
601 ATTATGGCAT  ATTCCGCGAA  ATATGCTTCT  GCATTCTACG  GCATCTTCCG
651 TGATGCGGTA  GGCACGTTCC  GCAATTTGGG  AAAGGCAGAT  AAAAAAGACCT
701 ATCAGATGGA  TCTTGCAAAT  ACCGATGAGG  CGTGTCATGA  AGTGGCGCTA
751 GATATTACAG  AAGGTGCGGA  TATGGTGATG  GTGAAGCCCG  GTTGTCGGTA

```

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```
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
851 CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
951 ACGTGC GGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

g610.pep

```
1 MIGGLMQFPY RNVFASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51 AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG TQVVAPSDMM DGRIGAIRES LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KPTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSSE YAMLOAAVAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYAI EAAKMLKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

m610.seq

```
1 ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CCGCTTCGCG
51 TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCTGT ATGCGCGAAC
101 ACACGCTGAC CGCGATGAT TTGATTATC CGGTGTTCTG ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCG GTGGTTACGG CAAACAAAAC CGAGCGTGGC
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT TCACGGTCAG GACGGGCTGA CCGACGAAA CCGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGCCACGC
501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTC CGATATGATG GACGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTGCACGA AGTGGCGTTG
751 GACATTACAG AAGGTGCGGA TATGTAATG GTCAAGCCCG GTTGGCGTA
801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCAGC GATTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
951 ACGTGC GGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
1001 AGATGTTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

m610.pep

```
1 MIGGLMQFPY RNVFASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51 SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIRES LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KPTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSSE YAMLOAAIAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYAI EAAKMLKR*
```

m610/g610 98.5% identity in 338 aa overlap

m610.pep	10	20	30	40	50	60
	MIGGLMQFPYRNVFASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM					
g610	10	20	30	40	50	60
	MIGGLMQFPYRNVFASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM					
m610.pep	70	80	90	100	110	120
	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	70	80	90	100	110	120
	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTGRAEAYNPEGLVPSTVRALRER					
m610.pep	130	140	150	160	170	180
	FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVVAPSDMM					
g610	130	140	150	160	170	180
	FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGTQVVAPSDMM					
m610.pep	190	200	210	220	230	240
	DGRIGAIRESLEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKPTYQMDPAN					

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```

g610      DGRIGAIREALDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240
           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFQVPTIAYQVSGEYAMLQAAIAN
           |||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFQVPTIAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300
           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           |||
g610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTATC CGGTGTTCGT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTCCCC GTGGTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAA CGGTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTGGG CAAGGCAGAT AAAAGACCT
701 ACCAGATGGA TCCGCCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTGATG GTCAGGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGG TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1  MIGGLMQFPY RNVASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFQV PTIAYQVSGE YAMLQAAVAN
301 GWLDGGKVVV LESLLAFKRAG ADGILTYAI EAAKMLKR*

m610/a610  99.4% identity in 338 aa overlap

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVFASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           |||
a610      MIGGLMQFPYRNVASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60
           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120
           130     140     150     160     170     180

```

976

```

m610.pep    FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
|||||
a610        FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
              130      140      150      160      170      180

              190      200      210      220      230      240
m610.pep    DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
|||||
a610        DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
              190      200      210      220      230      240

              250      260      270      280      290      300
m610.pep    TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
|||||
a610        TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
              250      260      270      280      290      300

              310      320      330      339
m610.pep    GWLDGGKVVLLESLLAFKRAGADGILTYAIEAAKMLKRX
|||||
a610        GWLDGGKVVLLESLLAFKRAGADGILTYAIEAAKMLKRX
              310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGC GG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCGAG
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGctgt
201 tatectTGGG CGGGCTGggt tgtttgcccg ccataaTTtc cagtacctgA
251 TcgcgGTCTa tggtttCCa ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTa ggcaacCTGA TACTgctcgt
351 ccaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTCTCGGAA
401 ATGTTTTGCG AACGGgttac gctGCCCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc gCTCATgcCG TAGCGCGTTA
501 CCATTTCCGC TGCCATTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51 RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIIVYGFP FHQGFARHNF
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGC GG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGggt TGTTCGCCC CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTCGCGG TTTTCATCGA GGATTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTC GCGTCGATGT CCGTCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTtac GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc GCTCATGCCG TAGCGCGTTA
501 CCATTTCCGC CGCCATTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51 RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIIVDGFP FHQGFARHNF
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60



977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
g611          MPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIAVDGFPPHQGFAHRFHLVAVFIEDFVGNLILLVQNP
g611          LAQVVAVILGRAGLFARHNFQYLIAVYGFPPHQGFAHRFHLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAFVAHAVARYHFARHLGCAFKVV
g611          ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAFVAHAVARYHFACHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X
g611          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1   ATGCCGTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTGCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTT CAGTACCTGA
251 TCGCGGTCGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTCGCGG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAAATCCG GCGGATTTCG GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCGC AACGGGTTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GCTCATGCCG TAGCGCGTTA
501 CCATTTGCGG CGCCATTGCG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1   MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIAVDGF F HQGFAHRFH
101 LVAVFIEDFV GNLILLVQNP ADFRIDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAFV AHAVARYHFA RHLGCAFKVV *

m611/a611    98.9% identity in 180 aa overlap

              10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
a611          MPSENRMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIAVDGFPPHQGFAHRFHLVAVFIEDFVGNLILLVQNP
a611          LAQVVAVIFGRAGLFARHDFQYLIAVDGFPPHQGFAHRFHLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAFVAHAVARYHFARHLGCAFKVV
a611          ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAFVAHAVARYHFARHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X

```

a611

X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

g612.seq

```

1 ATGGGcttcg gcgcaatat tgcAAAAAAG CTGGCcgGg taGATGAAAT
51 AGCCTttgac ttgacggcA TCGTCTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CCGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCATTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGCATTCAA ATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

g612.pep

```

1 MGFGGNIACK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NAAVAGLHIV
51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRFFY GHSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

m612.seq

```

1 ATGGGCTTCG GCGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51 AGCCTTTAAC TTTGACGGCA TCGTCTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CCGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCATTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGCATTCAA ATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

m612.pep

```

1 MGFGGNIACK LAGVDEIAFN FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLNKSK SPDIFRFFY GHSN*

```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIACKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
g612	MGFGGNIACKLAGVDEIAFDGIVDFDGRDDAVRHSGVINAAGVAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m612.pep	KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRFFY					
g612	KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

a612.seq

```

1 ATGGGCTTCG GCGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51 AGCCTTTGAC TTTGACGGCA TCGTCTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CCGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTT.AC GGCATTCAA ATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVFDFGR DDAVRHSGVI NTAVACLHIV
  51  GKVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
 101  NPYXKLNSK SPDIFRRFFX GHSN*

m612/a612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep      MGFGGNIAKKLAGVDEIAFNFDGIVFDFGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a612           MGFGGNIAKKLAGVDEIAFDGIVFDFGRDDAVRHSGVINTAVACLHIVGKVFADKAVE
              10      20      30      40      50      60

              70      80      90     100     110     120
m612.pep      KCAENVLFKVPAlHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNSKSPDIFRRFFY
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a612           KCAENVLFKVPAlHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNSKSPDIFRRFFX
              70      80      90     100     110     120

m612.pep      GHSNX
              ||||
a612           GHSNX
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
  51  GCGCAGTCTG CTTATTTCGT CGaggcagtc ggcaagggct tcgttgccgg
 101  tgtttGcgGA CTCGGGTTCG CGGGAATATC CGCCGATTG TTCGGCGATG
 151  TTCCTGCCGA TTTgtttGAt GCCGTGTCG ATGTCGGTGG CACGgctgcc
 201  gatgcCTGCC TGCGTGCCGA AAATCCGTGC CAATTegtCC GATGCGCGGG
 251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCC
 301  CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCCTT GGAGGATTTT
 351  CCGTATCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
 401  CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCC
 451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
 501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGCGCG
 551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT
 601  ATTTTACAGG CTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
  51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERLPSR DSTAMPRMRS
 101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFPAESKPS SVMRPASFSP
 151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
 201  ILQA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

.m613.seq
  1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
  51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
 101  TGTTTGCGGA CTCGATTTCG CGGGAATATC CGCCGATTG TTCGGCGATG
 151  TTCCTGCCGA TTTGTTTgAT GCCGTGTCG ATGTCGGCGG CACGGCTGCC
 201  GATGCTGCC TGCGTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
 251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCC
 301  CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
 351  CTGTACCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
 401  CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCC
 451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
 501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGCGCG
 551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT
  
```

980

601 ATTTTACAGG CTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

```
m613.pep
  1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSDS RENPPICSAM
 51  FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201  ILQA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
g613	MSRSSLSRRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRIFCTA					
	:					
g613	MSVARLPMPACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSLMSPAPGSPPWRIFRIA					
	70	80	90	100	110	120

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSVMPASFSFAMFRVSVLPKAASSERLSGLCRIRRLMMG					
	:					
g613	LLRKVISVSAKPFPAESKPSVMPASFSFAMFRVSVLPKAKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101 TGTTCGCGGA CTCGGGTTTC GGGGAAATC TGCCGATTG TTCGGCGATG
151 TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201 GATGTCTGCC TGCCTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301 CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCGCCTT GGAGGATTTT
351 CTGTACCGCG CTGTTGCGGA AGGTGATTTC GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAACCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCG AAGGCGGCAA GTTCCGAGCG
501 GCTGTCCGGG CTTTGACAGT TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551 ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTGTGCT GTTGACGCTT
601 ATTTTACAGG CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

a613.pep	1	MSRSSRSRRS	LRRSTPSRSL	LISSRQSARA	SLPMFADSGS	RENLPICSAM
	51	FLPICLMPCP	MSAARLPMSA	CVPKIRANSS	DARERRLPSR	DSTAMPRMRS
	101	PSSPMSAPAG	SPPWRIFCTA	LLRKVISVSA	KFFPAESKPS	SVMRPAFNP
	151	AMFRVSVLPA	KAASSERLSG	LCRIRRLMMG	RRADIFSDRG	GECLLLLLTL
	201	ILQA*				

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
a613	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSGSRENLPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSPMSPAPGSPPWRICTA					
a613	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSPMSPAPGSPPWRICTA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSVMPASFSFAMFRVSVLPKAASSERLSGLCRIRRLMMG					
	:					
a613	LLRKVISVSAKPFPAESKPSVMPASFSFAMFRVSVLPKAASSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLTLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

g614.seq

```

1   AtggcTgcgt tcAacgcttt ggacggcaaa aaagaagaca acgggcaaat
51  cgaaTATTCT CAGTTCATCC GACAGGTCAG CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGTT ACCTGATTAA AGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTGGATG ACAACCTGAT
201 TCAAACCTTT TTGAACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCGAGCGC GCTGACTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGGCGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCCT TCGGCAAAAG CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCAC CGAACCCTa
501 tcaAAGcctc ggcggccgtg ttcCGCGCGG CATCctgCtg gcgGgcagcc
551 CGGGAaccgg taaAACACTC TTGGCGAAAG CCATTGCAGG CGAGGCGGCG
601 GTGCCGTTCT TCAGCATTTT CCGTTCCGAT TTTGTGAAA TGTTCTGTCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCA AAGAAAACG
701 CCCCATGCAT TATCTTTATC GACGAGATTG ACGCGGTAGG CCGCCAACGC
751 GCGCAGgTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTATTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACGCCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGCTTCG ACCGCCAAGT CGTCGTCCCC CTGCCGACA TCCGGGGGCG
951 CGAACAGatn ttGAACGTCC ATTCTaaaAA AGTGCcttTG gacgaATCTg
1001 tggatTTATT GTCCCTCGCG CGCGGCACGC ccggtttTtc cggcgcggtat
1051 tTggcgaaac tgggtcaacga agccccctg tttgccggcc gccgcaacaa
1101 agtgaagtc gatcaaagcg atttGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep

```

1   MAAFNALD GK KEDNGQIEYS QFIRQVNNGE VSGVNIIEGSV VSGYLIKGER
51  TDKSTFFTNA PLDDNLIQTL LKNKNVRVKVT PEEKPSALTA LFYSLLPVLL
101 LIGAWFYFMR MQAGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQX LNVHSHKVPL DESVDLLSLA RGTGPGFSGAD
351 LAKLVNEAPL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq

```

1   ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
51  CGAATACTCT CAGTTCATCC AACAGGTCAG CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151 ACCGACAAAA GCACTTTCTT CACCAACGCG CCTTTGGACG ACAACCTAAT
201 TAAACACTG CTCGACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCGAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGGTTCTA CTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGTAAAAG CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTGACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TACAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCCTa
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCGGCG
601 GTGCCGTTCT TCAGCATTTT AGGTTCGAC TTTGTGAAA TGTTCTGTCG
651 TGTCGGTGCG AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAACG
701 CCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GCGCAGGTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACGCCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTTCG ACCGCCAAGT GGTGTCCCC CTGCCGACA TCCGAGGGCG
951 CGAACAGATT TTGAACGTCC ATTCTAAAAA AGTGCCTTTG GACGAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

m614.pep  
 1 MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER  
 51 TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL  
 101 LIGAWFYFMR MQTGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA  
 151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEAG  
 201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR  
 251 GAGLGGGND REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP  
 301 GRFDRQVVV PLDIRGREQI LNVHKKVPL DESVDLLSLA RGTPGFSGAD  
 351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

m614.pep	10	20	30	40	50	60
	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFTNA					
g614	MAAFNALDGKKEDNGQIEYSQFIRQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFTNA					
	10	20	30	40	50	60
m614.pep	70	80	90	100	110	120
	PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG					
g614	PLDDNLIQTLLNKNVRVKVT PEEKPSALTALFYSLPVLL LIGAWFYFMR MQAGGGKGG					
	70	80	90	100	110	120
m614.pep	130	140	150	160	170	180
	AFSFGKSRARLLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
g614	AFSFGKSRARLLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
	130	140	150	160	170	180
m614.pep	190	200	210	220	230	240
	AGSPGTGKTL LAKAIAEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
g614	AGSPGTGKTL LAKAIAEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
m614.pep	250	260	270	280	290	300
	DEIDAVGRQR GAGLGGGNDEREQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
g614	DEIDAVGRQR GAGLGGGNDEREQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
m614.pep	310	320	330	340	350	360
	GRFDRQVVV PLDIRGREQI LNVHKKVPL DESVDLLSLARGTPGFSGAD LANLVNEAAL					
g614	GRFDRQVVV PLDIRGREQX LNVHKKVPL DESVDLLSLARGTPGFSGAD LAKLVNEAPL					
	310	320	330	340	350	360
m614.pep	370	380	390			
	FAGRRNKVKVDQSDLKTPKTSIWVRNAAVWX					
g614	FAGRRNKVKVDQSDLKTPKTSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

a614.seq  
 1 ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT  
 51 CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG  
 101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC  
 151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTGGACG ACAACCTGAT  
 201 TAAACACTG CTCGACAAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA  
 251 AACCAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG

```

301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGGGCGCG TGGCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTCTC TCAGCATTTT AGGTTCCGAC TTTGTCGAAA TGTTCTGTCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GGCGCAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCCGTTTC ACCGCCAAGT GGTGTCTCCC CTGCCGGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 GRFCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```

a614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER
51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGGKGG AFSFGKSRR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAAGEA
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGND EQLTNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHSHKVP LDKSVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

m614/a614 99.7% identity in 391 aa overlap

	10	20	30	40	50	60
m614.pep	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKERTDKSTFFTNA					
a614	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKERTDKSTFFTNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m614.pep	PLDDNLIKTL LDKNVRVKVTPPEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGGKGG					
a614	PLDDNLIKTL LDKNVRVKVTPPEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGGKGG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m614.pep	AFSFGKSRR LLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
a614	AFSFGKSRR LLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m614.pep	AGSPGTGKTL LAKAIAAGEAVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
a614	AGSPGTGKTL LAKAIAAGEAVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m614.pep	DEIDAVGRQR GAGLGGGNDEREQLTNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
a614	DEIDAVGRQR GAGLGGGNDEREQLTNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m614.pep	GRFDRQVVVPLPDIRGREQILNVHSHKVP LDKSVDLLSLARGT PGTGPGFSGAD LANLVNEAAL					
a614	GRFDRQVVVPLPDIRGREQILNVHSHKVP LDKSVDLLSLARGT PGTGPGFSGAD LANLVNEAAL					



985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAC  GCGGCGGCG  CGGTGtcggC  AGCTTtgaag  agcagcGaAT
51  agatgCCGCC  GGCAAACCAC  AATGCCGAAa  gcaggCtgaa  gcGGTTgcgC
101 GGCagcTTca  tGCCGCCTCC  TcGTCCaGCC  ACGtttGgca  gattttggac
151 aggcgcAGga  ATTTGCcgCc  gcgtgcggCA  agtatgtcgc  gcCAttgtgc
201 cacttcttcg  gcggaacggTG  ctctgtcgat  gctgCATTCG  TACagcagga
251 aatcgagggt  ttcttcgatg  acggGgatgg  AttccgTTTG  GataAgCTgc
301 ttgagttcgt  tcatgactGt  TCgGATAcgg  aaatcgggaa  aatgccgtct
351 gAaagggctt  CAGACGGCat  tggATTATTT  GCTGTGCAGG  AAgcgcgttg
401 cctcttccca  tttgcCGGAA  AtgATGTCGg  gtacggcctg  cAGGGATttg
451 gCGACGGcat  cgtcgatttg  ccgGcggtgc  ttCcgcgctc  ggtttGTTca
501 agacgtagcc  gaCGACGagg  ttgcggtcGC  CGGGTggtcC  GATGCCGAGG
551 CGCAGGCGGt  aatagtctgC  CGTGCCGAGT  TTTGCctgAA  TGTCTTTCAA
601 GCCGTGTGTG  CgcCGttgc  cgcCGCCGAG  TTTGAATTTg  ATCCGTCCGC
651 AAGGGATGTC  GAGTTCGTGC  TGGACGACGA  GGATTCTTTC  GGGTTTGATT
701 TTGTAGAACT  GTCAAGCGC  GGCAACCGCC  TGTCCGGAAC  GGTTCATGAA
751 CGTGGCCGGT  TTGAGCAGCC  AAACATCGCC  GTCGGGCAGG  GCGGCGCGGG
801 CAACTTCGCC  GAAGAATTTT  TTTCTTCTT  TAAACGAAGC  CTTCCATTTC
851 CACGCCAGTT  CGTCGAGGAA  CCAAAAGCCC  GCATTGTGGC  GGGTCTGTTC
901 GTATTCTTTG  CCCGGGTTGC  CCAAGCCGAC  AACCATTTTG  ATTGTGttcg
951 acatgataTT  TtccgtgTTT  CTgTCGaatg  cggTCtgAG  GCTTCAGacg
1001 gcatggTtaT  TCTTCTTgaT  TTtgaACgcg  tgtgcggCGC  GCTTCTTTGG
1051 GGTCTGATCA  CAGCGGCGCG  TACACTTCGA  TCGGTCGCC  GTCGCGCAGC
1101 GCGTGTCTGT  CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG  SFEEQRIDAA  GKPQCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCAATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101 LSSFMTVIR  KSGKCRLLKGL  QTALDYLLCR  KRVASSHLPE  MMSGTACRDL
151 ATASSICRR  FRARFVQDVA  DDEVAVAGVA  DAEAQAVIVC  RAEFCLNVFQ
201 AVVSAVAAAE  FEFDPSARDV  EFVVDDEDF  GFDFVELCKR  GNRLSGTVHE
251 RGRFEQPNIA  VGQGGAGNFA  EEEFFFKRS  LPFPRQFVEE  PKARIVAGLF
301 VFFARVAQAD  NHFDCVRHDI  FRVSVECLG  ASDGMVILL  D  FERVCGALLW
351 GRSTAGGTLR  CGRRRAAACR  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq  Length: 1116
1  ATGCGGAAAA  GCGGTGGCG  CGGTTTCGGC  AGCTTTGAAA  AGCAGTGAGT
51  AAATGCTGCC  TGCAAACCAC  AATGCCGAGA  GCAGGATAAA  GCGGTTGCGT
101 GGCAGATTCA  TGCTTGTTCC  TCTTCAAGCC  ATGTCTGGCA  TAGTTTGGAT
151 AGGCGCAGGA  ATTTCCGCC  GCGTGCAGCC  AGCATATCGC  GCCAAACGGC
201 AATTTCTTCG  GCGGAGGGGG  CATCGTCTAT  GCTGCATTCT  TAGAGCAGGA
251 AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTCCGTTTG  GATAAGCTGC
301 TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351 GAAAGGGCTT  CAGACGGCAT  CGGGTCAATT  GCTGTGCAGG  AAGCGGGTTG
401 CTTCTTCCCA  TTTGCCGGCA  AGGATGTCGG  GTATGGCTTG  CAGGGATTTG
451 GCGACGGCAT  CGTCAATCTG  TCGGCGGTGT  .TCCGTAAGT  GGTTTGTTCa
501 GGACATAGCC  GACGACGAGG  TTGCGGTGCG  CCGGGTGGCC  GATGCCGAGG
551 CGCAGGCGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCCTGAA  TGTCTTTCAA
601 GCCGTGTGTG  CCGCGGTTGC  CGCCGCCGAG  TTTGAATTTG  ATCCGTCCGC
651 AGGGAATGTC  GAGTTCGTGC  TGGACGACGA  GGATTCTTTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACTGCC  TGTCCGGAAC  GGTTCATGAA
751 CGTGGCAGGT  TTGAGCAGCC  AAACGTCGCC  GTCGGGCAGG  GCGGCACGGG

```

```

801 CGACTTCGCC GAAGAATTTT TTTCTTCTT TAAATGAAGC CTTCCATTTT
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTT
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTCGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTGCGGCGC GCTTCTTTGG
1051 GGTCGATCAA CAGCGGGCGG TACACTTCGA TCGGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFEKQXVNA CKPQCREQDK AVAWQIHACS SSSHVWHS LD
51 RRRNFP PRAA SISRTA ISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAVAAAE FEFDP SAGNV EFVVDDEDF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTG DFA EEEEEFFKXS LPFRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVX HDI FRVSVECC LK ASDGMVILL DFERVCGALLW
351 GRSTAGT LRGRRRAAAC RL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNA	CKPQCREQDKAVAWQIHACS	SSSHVWHS	LD	RRRNFP	PRAA
g615	MWKRRRRRGVGSFEEQRIDA	AGKPGCKQAEAVARQLHA	ASSSHVWQILD	RRRNLP	PRAA	
	10	20	30	40	50	60
	70	80	90	100	110	120
m615.pep	SISRTA ISS AEGASSMLHS	XSRKSRVSSMTGMDSVWIS	CLSSVMTVRIWKSGTCRLKGL			
	:					
g615	SMSRHCATSSADGASSMLHS	YSRKS RVSSMTGMDSVWIS	CLSSFM TVRIKSGKRLKGL			
	:					
	70	80	90	100	110	120
	130	140	150	160	170	180
m615.pep	QTASGHLLCRKRVASSHL	PARMSGMACRDLATASSICRRC	XRTGFVQDIADDEVAVARVA			
g615	QTALDYLLCRKRVASSHL	PEMMSGTACRDLATASSICRRC	FRARFVQDVADDEVAVAGVA			
	130	140	150	160	170	180
	190	200	210	220	230	240
m615.pep	DAEAQAVIVCRAEFCLNVFQ	AVVSAVAAAEFEFDP SAGNV	EFVVDDEDFG	GFDFVELCKR		
g615	DAEAQAVIVCRAEFCLNVFQ	AVVSAVAAAEFEFDP SARDV	EFVVDDEDFG	GFDFVELCKR		
	190	200	210	220	230	240
	250	260	270	280	290	300
m615.pep	GNCLSGTVHERGRFEQPNV	AVGQGGTGDFAE	EEEEFFKXSLPFRQFVEE	PKTRIVACLF		
g615	GNRLSGTVHERGRFEQPN	IAVGQGGAGNFAE	EEEEFFKXSLPFRQFVEE	PKARIVAGLF		
	250	260	270	280	290	300
	310	320	330	340	350	360
m615.pep	VFFARVAQADNHFDCVX	HDI FRVSVECC LKASDGMVILL	DFERVCGALLWGR	STAGGTLR		
g615	VFFARVAQADNHFDCV	RHDI FRVSVECC LKASDGMVILL	DFERVCGALLWGR	STAGGTLR		
	310	320	330	340	350	360
	370					
m615.pep	CGRRRAAACRLX					
g615	CGRRRAAACRLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1  ATGCGGAAAC  GCGCGCGGCG  CGGTGTCGGC  AGCTTTGAAG  AGCAGCGAAT
51  AGATGCCGCC  GGCAAACCAC  AATGCGGAAA  GCAGGCTGAA  GCGGTTGCGC
101 GGCAGCTTCA  TGCCGCCTCC  TCGTCCAGCC  ACGTTTGGA  GATTTTGGAC
151 AGGCGCAGGA  ATTTGCCGCC  GCGTGGCGCA  AGTATGTCGC  GCCATTGTGC
201 CACTTCTTCG  GCGGATGGTG  CGTCGTCGAT  GCTGCATTGC  TACAGCAGGA
251 AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTGGGTTTG  GATAAGCTGC
301 TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351 GAAAGGGCTT  CAGACGGCAT  CGGGTCATTT  GCTGTGCAGG  AAGCGGGTTG
401 CCTCTTCACA  TTTGCCGGCA  AGGATGTCGG  GTATGGCTTG  CAGGGATTTG
451 GCGACGGCAT  CGTCAATCTG  TCGGCGGTG  TTCCGTA CTG  GGTTTGTTCA
501 GGACATAGCC  GACGACGAGG  TTGCGGTCGC  CCGGTGGGCC  GATGCCGAGG
551 CGCAGGCGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCGTGA  TGTCTTTCAA
601 GCCGTTGTGT  CCACCGTTGC  CGCCGCCGAG  TTTGAATTG  ATCCGTCCGC
651 AGGGAATGTC  GAGTTCGTCG  TGGACGACGA  GGATTTCTTC  GGGTTTGATT
701 TTATAAACT  GCGCAAGGGC  GGCAACTGCC  TGTCGGAAC  GGTTCATGAA
751 CTGGTTCGCG  TTGAGCAGCC  AGACATCGCC  GTCGGGCAGG  GTAGCACGGG
801 CGACTTCGCC  GAAGAATTTT  TTTCTTCTT  TAAATGAAGC  CTTCCATTTT
851 CACGCCAGTT  CGTCGAGGAA  CCAAAAACCC  GCATTGTGGC  GTGTCTGTTT
901 GTATTCTTTG  CCCGGGTTGC  CCAAGCCGAC  AACCATTTTG  ATTGTGTTTG
951 ACATGATATT  TTCCGTGTTT  CTGCCGAATG  CCGTCTGAAG  GCTTCAGACG
1001 GCATGGTTAT  TCTTCTTGAT  TTTGAACGCG  TTTGCGGCGC  GCTTCTTTGG
1051 GGTCGATCAA  CAGCGGGCGG  TACACTTCGA  TCGGTCGCC  GTCGCGCAGC
1101 GCGGTGTCGT  CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1  MRKRRRRGVG  SFEEQRIDAA  GKPQCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101 LSSVMTVRIW  KSGTCRLKGL  QTASGHLLCR  KRVASSHLPA  RMSGMACRDL
151 ATASSICRRX  FRTFGVQDIA  DDEVAVARVA  DAEAQAVIVC  RAEFCLNVFQ
201 AVVSTVAAAE  FEFDPAGNV  EFVDDDEFF  GFDIFIKLRG  GNCLSGTVHE
251 RGRLEQPDIA  VQGSGTGDF  EEEEEFFK*S  LPFRQFVEE  PKTRIVACLF
301 VFFARVAQAD  NHFDCV*HDI  FRVSAECLRK  ASDGMVILL  FERVCGALLW
351 GRSTAGGTLR  CGRRRAACR  L*
```

m615/a615 90.3% identity in 371 aa overlap

m615.pep	10	20	30	40	50	60
a615	10	20	30	40	50	60
m615.pep	70	80	90	100	110	120
a615	70	80	90	100	110	120
m615.pep	130	140	150	160	170	180
a615	130	140	150	160	170	180
m615.pep	190	200	210	220	230	240
a615	190	200	210	220	230	240
	250	260	270	280	290	300

988

```

m615.pép  GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFFFFFKXSLPFPRQFVEEPKTRIVACLF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a615      GNCLSGTVHERGRLEQPDIAVGQGGTGDFAEFFFFFFFKXSLPFPRQFVEEPKTRIVACLF
          250      260      270      280      290      300

          310      320      330      340      350      360
m615.pép  VFFARVAQADNHFDVCVXHDIFRVSVECLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a615      VFFARVAQADNHFDVCVXHDIFRVSACRLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          310      320      330      340      350      360

          370
m615.pép  CGRRRAAACRLX
          |||:|||||:
a615      CGRRRAAACRLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACTGG
101 CGTGGAATG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CGCCCTGCC CGACGCGCAT GTTGGCTGC TCAAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGGCGGAC GGATCAAATT CAAACTCGGC GcgggcaacG gcgGACACAA
351 CGGCTTGAAG GACATTcagG CAAACTCGG CACGGcagac tattaCCGCC
401 TGCGCCTCGG CATCGgccac CCCGGCgacc gcaacctCGT CGtcggctac
451 gtctttgAACa aaccgagcgc gGaagcaccg Ccggaatc gacgatgCCG
501 TCGccaaATC CCTgcaggcc gtaccCGACA TcaTTTCGGg caaatgggaa
551 gaggcaacgc gcTTCTTGCA CAGCAAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgg cattttcccg atttccgTAT CcGaaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaaTccatcC ccgtcatcga agaaaccctc
701 gatttctgc tGTACGAATG cagcAtcgac gaagCAccgt ccgccgaaga
751 agtggcaca TGgcgcgaca tactTGccgc acgcgGcgGC AAATtcCTgc
801 gcctgtccaa aatctgcCaa aCGTGGCtGG ACgAGGAGGC GGCatgAAgc
851 tGCCGcgcaA CCgcttcaGc ctgctTTCCG CATGTGGTt TGCCGCGGc
901 atctAtTCgc tgctettcaA AGCTGccgaC ACCGCGCCGC CGCCGTTTCC
951 ACATTTcgac AAAGCAGCAC ACCTTGCCCT GTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAAA ACCGGAAC TTCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGGCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTGCCG CGCGTTCTGC CTGCCGcccg
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pép
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEKKFFGE
51  VARAALPDGD VWLLKPATFM NRSQAVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTD YYRLRLGIGH PGDRNLVVG
151 VLNKPSAEAP PANRRCRRI PAGRTRHFR QMGRGNALPA QQIIQCRLKP
201 FQTAFSRFPY PNSHRTQAA YPNGIHPRHR RNPRFPAVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPRNRF LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QILEFLAKAFK TGKLPYR
351 LIAFAFCFAV GSECAQAWFT ATRTGS LGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101 CGTGGAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCGTG CGCCCTGCC CGACGCGGAC GTTGGCTGC TCAAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGAT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTTGGCGGAC GGATCAAATT CAAACTCGGC GCGGCAACG GCGGACACAA
351 CGGCTTGAAG GACATTcagG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCCG CAAATGGGAA

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989

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551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCTC
701 GATTTCTGCT TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGCGCGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCATCCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

```

m616.pep
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSQQAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGGHNLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGY
151 VLNKPSTEXP PTDXRRCRQI PASHTRHPCR QMGRSNPLPA QQMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPALRM QHRRCLPLRR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPFPFHD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGSGLDV LADLTGAALA LFTARAACRF
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

m616.pep	10	20	30	40	50	60
	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
m616.pep	70	80	90	100	110	120
	VWLLKPATFMNRSQQAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNLK					
g616	VWLLKPATFMNRSQQAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNLK					
m616.pep	130	140	150	160	170	180
	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYVLNKPSTEXPPTDXRRCRQIPASHTRHPCR					
g616	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYVLNKPSTEXPPTDXRRCRQIPASHTRHPCR					
m616.pep	190	200	210	220	230	240
	QMGRSNPLPAQQMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRNRNPRFPALRM					
g616	QMGRSNPLPAQQIQCRLKPFQTAFSRFPYPNSHRTQAAAYPNRIHPRHRNRNPRFPALRM					
m616.pep	250	260	270	280	290	300
	QHRRCLPLRRNRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS					
g616	QHRRCLPLRRNRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS					
m616.pep	310	320	330	340	350	360
	IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
g616	IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
m616.pep	370	380	390	400		
	FSECAQAWFTATRGSGLDVLADLTGAALALFTARAACRPDX					
g616	FSECAQAWFTATRGSGLDVLADLTGAALALFAARSACRPDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq

```
1 ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51 ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAAGTGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTCGGCGAA
151 GTCGCCCGTG CTACCTGCGC CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCCG GACAGGCAGT TGCCGCCCTT GCGCAGTTT
251 ATAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTGCGGAC GGATCAAATT CAAACTCGGC GGCGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTGAGG CAAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCCGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTGAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCTC
701 GATTTCTGTC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAAGA
751 AGTGGCACA TGGCGCGACA TACTTGCCGC ACGCGGCGGC AAATTCTGTC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCCGCGCAA CCGCTTCAGC CTGCTTCCG CATTGTGCTT TGCCGGCGGC
901 ATCTATTGCG TGCTCTTCAA AGCTGCCGAC ACCGCGCCGC CGCCGTTTCC
951 GCATTTGCGA AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAA ACCGGAACAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTACC GCAACGAGAA CCGGCAGTT GGGCGATGTT CTGCGCGATA
1151 TGGCAGGTAC GGTTCCTGCA CTCTTTGCCG CCCGCGCCGC CGACCGCCCG
1201 GACTGA
```

This corresponds to the amino acid sequence &lt;SEQ ID 1978; ORF 616.a&gt;:

a616.pep

```
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARATLPDGD VLLKPTTFM NRSGQAAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QQMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPVRM QHRRRTTRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMKLPNRNFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPHFD KAAHLALFFA QIWLTLKAFK TGLPLPIYRS
351 LMVFALCFAL FSECAQA*FT ATRTGSIGDV LADMAGTVLA LFAARAADRP
401 D*
```

m616/a616 90.0% identity in 401 aa overlap

```
10 20 30 40 50 60
m616.pep MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
|||||:|||||
a616 MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARATLPDGD
10 20 30 40 50 60

70 80 90 100 110 120
m616.pep VLLKPATFMNRSGQAAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK
|||||:|||||
a616 VLLKPTTFMNRSGQAAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK
70 80 90 100 110 120

130 140 150 160 170 180
m616.pep DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR
|||||:|||||
a616 DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR
130 140 150 160 170 180

190 200 210 220 230 240
m616.pep QMGRSNPLPAQQMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRRNPRFPALRM
||:|||||
a616 QMXRGNPLPAQQMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRRNPRFPVRM
190 200 210 220 230 240

250 260 270 280 290 300
```

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1979>:

**g619.seq**

1	ATGCCGCTCTG	AAAAAAATAT	CGGTTTTATG	GCAGGAAGCA	GCCGTCGGTT
51	CGGGGTCGCC	TTTGGCGTGT	TGCTGGTTTC	CTGCATCTGT	TTTATGACGC
101	TCAACGTCAA	AGGAGATTGG	ACTTTGTGCT	TGCACCTCGC	CTCTGACCAA
151	CTTGCCGCGC	TGCTGATGGT	CGCCTATCGG	GTCGGCGTGT	CCACTCAACT
201	CTTCCAAACG	CTGACCAACA	ATCCGAGACT	GACCCCTTCG	ATTTTGGGTT
251	TCGATTGCGT	GTATGTGTTT	TCCGAGACCT	TGCTGgtGTT	TACGTTcgGC
301	GGCGTGGGCT	ATAcatccct	gccggttgacg	gGCAAAATGCT	GCGTTTGAAC
351	GGTTGTTATG	ATGGGCGGGT	CGCTGCTGCT	GTTTACACG	CTCATCCGTC
401	AGGGCGGGCG	CGAATTGGCC	CACATGATTT	TAATCGGCGT	GATTTTCCGG
451	ATTTTGTTCG	CGACGCTTTC	CTCGCTGCTT	TCGCGCATGA	TAGACCCGGA
501	AGAATTATACC	GCCGCGCAGG	CGAATATGTT	TGCCGGATTG	AATACCGTCC
551	GCAGCGAGCT	TTTAGGCATA	CGGCGCGCTGG	TCTTGCTCGT	CAGCGCGGCG
601	GTCTGTTTGGC	ACGAACGCTA	CGCCTCGGAG	GTACACCTTT	TGGGGCGCGA
651	CCAAGCCGTC	AATTTGGGCA	TCAGCTACAC	GCGCAACACC	TTATGGATAC
701	TGCTTTTGGAT	TGCGCGATTG	GTGGCGACGG	CGACCGCCGT	TGTCGGGCCG
751	GTGAGCTTTT	TCGGGCTTCT	CGCCGCTCTG	CTTGCCAACC	ACTTTTCCCC
801	gtCCGTGCGC	CATTCCGTCC	GCTTCGcgat	gacggtttGc	gtcgGcgGCA
851	TCTCTTGGt	cggCggaaca	ACCGATATCG	AACACTTCTT	GGGCATGAag
901	gCggTATTAA	CGCTGGTGGT	cgAAATTGCG	ggcggactcG	TTTTTCTCTA
951	TCTCGTTTTA	AGCAACAAA	AATGA		

This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>:

g619.pap

1	MPSEKNIGFM	AGSSRLPLRA	FALLVSCIL	FMTLNVKGDW	DFVLHLRLTK
51	LAALLMVAYA	VGSTQLFQT	LTTNPILTPS	ILGDFSLLXVF	LQTLLVFTFG
101	GVGYTSLPLT	GKPGFELVVM	MGGSLLLEYT	LIRQSGELDI	HMILIGVIFG
151	ILFRSLSSLL	SRMIDPEEFT	AAQANMFAG	NTVRSELLGI	GALVLLVSA
201	VVWHERYRSD	VHLLGRDQAV	NLGISYTRTN	LWILLWIAAL	VATATAVUGP
251	VSFVFGLLAAS	LANHFSPSR	HKVRPLMPTV	VGGILLVGGQ	TVFEHFLGMK
301	AVLSVVVEFA	GGLVFLYLVL	KHKK*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1981>:

```

m619.seq
1  ATGCCGTCGTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGCCCGTT
51  GTGGGTCGCC TTTGCGCTGT TGCTGGTTTC TCGCGTCTGT TTTATGACGC
101 TCAACGTCAA AGCGATTTGG GATTTTGGTT TGCAACTCGC GCTGACCAAA
151 CTTGCCGCGC TGCTGATGGT CGCCTATTGC GTCGGCGTGT CCACGCAACT
201 CTTCCAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
251 TCGATTCGCT GTATGTGTTT TGCAGACCTT TGCTGGTGTG TACGTTCCGC
301 GGCCTGGGCT ATGCTTCCCT GCCGTGACG GGCAAAATCG GCTTTGAAC
351 GGTCGTCATG ATGGGCGGCT CGCTCGTGCT GTTCTACACG CTCATCAAAC
401 AGGGCGGACG CGATTTGTGC CGCATGATT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTC CGACCTGTC GTGCTGCTT TCGCGCATGA TCGATCCGGA
501 AGAATTTACC GCGCGCGAG CGCAATATGT TGCCGGATT AATACCGTTC
551 ACAGCGAGCT TTTGGGCATA GGCCTCGTGA TTTGCTCGT CAGCGCGGCC
601 GTCGTTTGGC GCGAACGCTA CCGCTTGAC GTTACCTTT TGGGGCGTGA
651 CCAAGCCGCT AATTTGGGCA TCAGCTACAC CGCGCAACCC TTATGGTATC
701 TGCCTTGGAT TCGCCGATTG GTGGCGACGG CGACCGCCGT GGTCCGCCCC
751 GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCGCTTC GCCTGCGTGA GACGGTTTGT ATCGCGGACA
851 TCCTCTTGGT CCGCGGACAG ACCGTGGTTC AACACCTGCT CGGTATGACG

```

901 GCAGTGTGTA GCGTAGTAGT AGAATTTGCC GCGGACTCG TTTTCCTCTA  
951 TCTCGTTTTA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep  
1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNKGDW DFVLQRLTK  
51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVFTFG  
101 GVGYSASPLT GKFGFELVVM MGGSLLLFYT LIKQGGRLDS RMILIGVIFG  
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA  
201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG  
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMQ  
301 AVLSVVVEFA GGLVFLYLVL KHKK\*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNKGDWDFVLQRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
m619.pep	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASPLTGKFGFELVVM					
g619	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYTSPLTGKFGFELVVM					
	70	80	90	100	110	120
m619.pep	130	140	150	160	170	180
	MGGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGGSLLLFYTLIRQGGRLPHMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVHSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
m619.pep	250	260	270	280	290	300
	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
g619	VATATAVVGVPVSFFGLLAASLANHFSPSVRHSVRLPMTVCVGGILLVGGQTVFEHLLGMK					
	250	260	270	280	290	300
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYLVLKHKKX					
g619	AVLSVVVEFAGGLVFLYLVLKHKKX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq  
1 ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT  
51 GTGGGTGACC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC  
101 TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCACCTGCG CCTGACCAAG  
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTTT CGACCCAGCT  
201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTTGGGTT  
251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCCGC  
301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT  
351 GGTCTGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC  
401 AGGGCGGGCG CGATTGCGG CGTATGATTT TAATCGGCGT GATTTTCGGG  
451 ATTTTGTTCC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCGA  
501 AGAATTTACG GCGGCGCAGG CGAATATGTT TGCCGGATTG AATACCGTCC  
551 ACAGCGAGCT TTTAGGCATA GCGCGCTGTA TTCTGCTCGT CAGCGCGGCG  
601 GTCGTTTGGC GCGAACGCTA CCGCTTGAC GTACACCTTT TGGGGCGCGA  
651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC  
701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTCGGCCCG



```

751 GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCTGCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851 TCCTCTTGGT CGCGGACAG ACCGTATTCG AACACTTCTT GGGCATGAAG
901 GCGGTATTA GCGTGGTGGT CGAATTGCG GCGGACTCG TTTTCCTCTA
951 TCTCGTTTA AGACACAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

a619.pep

```

1  MPSEKNIGFM AGSSRPLWVA FALLVSCIL FMTLNVKGDW DFLHLRLTK
51  LAALLMVAYA VGVSTQLFOT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
101 GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGGDLRPMILIGVIFG
151 ILFRSLSSL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLV L RHHK*

```

m619/a619 97.2% identity in 324 aa overlap

	10	20	30	40	50	60
m619.pep	MPSEKNIGFMAGSSRPLWVAFALLVSCVLFMTLNVKGDWDFVLQRLRLTKLAALLMVAYA					
a619	MPSEKNIGFMAGSSRPLWVAFALLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m619.pep	VGVSTQLFOTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM					
a619	VGVSTQLFOTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m619.pep	MGSLLLFYTLIKQGGDLRPMILIGVIFGILFRSLSSLSRMIDPEEFTAAQANMFAGF					
a619	MGSLLLFYTLIKQGGDLRPMILIGVIFGILFRSLSSLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m619.pep	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
a619	NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m619.pep	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
a619	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
	250	260	270	280	290	300
	310	320				
m619.pep	AVLSVVVEFAGGLVFLYLVLRHHKX					
a619	AVLSVVVEFAGGLVFLYLVLRHHKX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

g620.seq

```

1  ATGAAGAAAA CCCTGTTGGc AATTGTTGCC gTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgcgcCTTT ACCCCGGCAG AtTAGCGacc
101 gttcgggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCCT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

```
g620.pep
1  MKKTLAIVA VFALSACRQA EEAPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

```
m620.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGTC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTC GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

```
m620.pep
1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	MKKTLAIVAVFALSACRQAEAPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFGYTKLPEEPKIRVIYVTDGNVTDWTPNADTEWMDAKKAFYVIDS					
g620	DQPVWFSTVKQMFGYTKLPEEPKIRVIYVTDGNVTDWTPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
g620	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

```
a620.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGTC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTC GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

```
a620.pep
1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

m620/a620 100.0% identity in 164 aa overlap

```

      10      20      30      40      50      60
m620.pep MKKTLIAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
|||||
a620      MKKTLIAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
      10      20      30      40      50      60

      70      80      90     100     110     120
m620.pep DQPVWFSTIKQMFQYTKLPEEPKGIIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS
|||||
a620      DQPVWFSTIKQMFQYTKLPEEPKGIIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS
      70      80      90     100     110     120

      130     140     150     160
m620.pep GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX
|||||
a620      GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta cgcgtgtcgg ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAaag ctggCGTTTG CCGCCGCCGC CCTGCCAGAA gccgTccgCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGCGAT TCGGAaGaaa TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACACGCTGGA TATGCAGGAA ACCGTGCGCC ACGCCTTCCG CGTTGCCTGC
301 GGCTTGGATT CGATGGTTT GGGCGAGCCG CAGATTTTGG GGCAGATTAA
351 AGATGCGGTG CGTGCGGCTC AAGAACAGGA AAGTATGGGG GCAAAACTCA
401 ATGCCCTGTT CCRAAAAACC TTTTCCGTTG CTAAAGAAGT CCGTACCGAT
451 ACCGCTGTCT GCGAAAATTC GGTTCGATG GCTTCCGCGT CCGTCAAGTT
501 GCGGGAACAG ATTTTTCCTG ACATCGGCGA TTTGAACGTA TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAAT
601 CCGCGGTGTA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTTA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTGGTGG TTTCTTCAAC GCGAGCCAG
751 CTTCGGATAG TCGGCAAAGG CATGGTCGAA CGCGCATTGA AACAGCGTCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGC GATATTGAAG
851 CGGAAGTCGG CGATTGAAAC GATGCGTATC TTTATACGGT GGACGATATG
901 GTCAACATCG TCCAAAGCGg caaggaggca aggcagaaag ccgccgcCgc
951 cgcgaaacg ctggTGTCGG AAAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GagggttcCG CTGATTAAAG CCTTGCGGGA CGAGGGCGAG
1051 AAGCGCGCGA AGCAGGTGTT GGAAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGcaacGGCG GAAGaggttt TGgaacggct gtcggtcCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCAACT CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGatttGG TTCATGCCgt cGCGCAGAtt tatcatttGG ACAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYTLDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RAAQEQUESMG AKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEO IFPDIGDLNV LFIGAGEMIE LVATYFAAKN
201 PRMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMF LFMLDLAVPR DIEAEVGLN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV LKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAQAQI YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA CCGCTGTCTG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAaag CTGGCGTTTG CCGCCGCCGC CCTGCCTAAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGTGAT TCGGAAGAAA TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACGCGCTGGA TATGCAGGAG ACTGTGCGCC ATGCTTCCG CGTCGCCTGC

```

```

301 GGGCTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCATG GCTTCCGCTT CCGTCAAATT
501 GGCAGAACAG ATTTTCCCG ACATCGGCGA TTGAATGTC TTGTTTATCG
551 CGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTGC CGCCAAAAGT
601 CCCCCTGTA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTC ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTTG TCGGCAAAGG CATGGTGGAG CGTGCAATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATG TTGATTTGGC AGTGCCGCGT GACATTGAAG
851 CGGAAGTCGG CGATTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCG AGAAAGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGCAGGCA GAGTGTCCCC TTGATTAAGG CGTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AACAGGTGTT GGAATGTC ATGAACAGC TTGCCAAAGG
1101 CGCAACGCGA GAAGAGGTTT TGAACGGCT GTCCGTCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGCGGGG GGAAGAAAGT
1201 AAAGATTTGG TTCATGCCGT CGCGCAGATT TATCATTTGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

#### m622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SLDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMPL FMLDLAVPR DIEAEVGLND DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPLI KALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

m622/g622 98.8% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHQTAPLSIREKLAFAAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m622.pep	SEEIIRWLADYHSLPIEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEIRPYLYTLDQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m622.pep	RVAQEESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEESMGAKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	LFIGAGEMIELVATYFAAKNPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
g622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370                    380                    390                    400                    410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```

a622.seq
1  ATGCAACTTA  CCGCTGTCGG  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAAAAA  CTGGCGTTTG  CGCGGGCCTG  CCGTCCCGAA  GCGCTCCGCA
101 ATCTTGGCCG  AAGCAATGCG  CCAAGCAGAG  CGGTAATCCT  TTCTACCTGC
151 AACCGTACCG  AGCTTTACTG  TGTAGGTGAT  TCGGAAGAAA  TCATCCGTTG
201 GCTCGCAGAC  TATCAGAGCC  TTCCCATAGA  AGAAATCAGC  CCCTACCTTT
251 ATACTTTGGG  GATGCAGGAG  ACTGTGCGCC  ATGCTTTCGG  CGTCCGCTGC
301 GGTCTGGATT  CGATGGTGTT  GGGCGAGCCG  CAGATTTTAG  GACAGATTAA
351 GGATGCGGTC  AGGGTTGCTC  AAGAGACGGA  AAGTATGGGT  AAGAAACTCA
401 ATGCCCTGTT  CCAAAAAACC  TTTTCTGTTG  CTAAAGAGGT  CCGTACCGAT
451 ACTGCCGTCG  GCGAAAAACT  GGTPTCCATG  GCTTCCGCTT  CCGTCAAGTT
501 GGCAGAGCAG  ATTTTCCCCG  ACATCGGCGA  TTTGAATGTC  TGTGTTATCG
551 GTGCGGGTGA  GATGATTGAG  CTGGTTGCCA  CTTATTTTGC  GCGTAAAGAT
601 CCCCGGCTGA  TGACGGTTGC  CAACCGGACG  CTGGCGCGTG  CACAGGAGTT
651 GTGCGACAAG  CTCGGTGTC  ACGCGGAACC  GTGCCTGCTG  TCCGATCTGC
701 CTGCCATTTT  GCATGAGTAC  GACGTGGTGG  TTTCTTCAAC  GGCAAGCCAG
751 TTGCCCATTG  TCGGCAAAGG  TATGGTGGAG  CGCGCATTTG  AACAAAGGCA
801 GAGTATGCCG  TTGTTTATGC  TTGACTTGGC  CGTGCCGCGA  GACATTGAGG
851 CGGAAGTCGG  AGATTTGAAC  GATGCCTATC  TTTATACGGT  GGACGATATG
901 GTCAATATCG  TCCAAAGCGG  CAAGGAGGCA  AGGCAGAAGG  CCGCCGCCGC
951 CGCGGAAACG  CTGGTGTCCG  AGAAGTTTGC  CGAATTTGTC  AGGCAGCAGC
1001 AGGGCAGGCA  GAGTGTCCCG  TTAATCAGGG  CATTGAGGGA  TTGAGGAGAG
1051 AAAGCGCGCA  AACAGGTCTT  GGAATGCG  ATGAAACAGC  TTGCCAAAGG
1101 CGCAACGGCA  GAAGAGGTTT  TGGAAAGGCT  GTCGATCCAA  CTGACCAACA
1151 AGCTGCTGCA  TTCGCCGACC  CAAACCTTGA  ATAAGGCGGG  GGAAGAAGAT
1201 AAAGATTTGG  TTCACGCCGT  CGGCAGATT  TATCATTTGG  ACAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```

a622.pep
  1  MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SLDPAIHLEV DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGDLN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAEET LVSEKVAEFV RQQQGRQSVP LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLRLLSIQ LTNKKLLHSPT QTLNKAGEED
401 KDLVHAVAQOI YHLDK*

```

m622/a622 98.1% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLRASNAATEAVILSTCNRTELYCVGD					
a622	MQLTAVGLNHQTAPLSIREKLAFAAAALPEAVRNLRASNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
a622	SEEIIRWLADYHSLPIEEISPYLYTLMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m622.pep	RVAQEQUESMGKKLNALFQKTFSSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
a622	RVAQEQUESMGKKLNALFQKTFSSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
	250	260	270	280	290	300
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

```

g624.seq
1  ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
51  GATAATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTAC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATccc cgcgcTTTCa ccgCTGGCTG
151 CACcgGCacc gCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AGATTTCGCG CATCAGCATG AtaaccgcAt
251 cctgcctcat gatctTTtgg CattTTCccc aacnctggtg ggtcGGGGCG
301 GTTTCATCGG TTTTGTGTTC CCTTGTcAcC ATacggatgt gGcacAGacC
351 cgaatCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

```

g624.pep
1  MIRYLLIACG GISLLLGIIG IFPLPLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIEW HFPQXWWVGA
101 VSSVFCSLVT IRMWRPES*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

```

m624.seq
1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTCTCC TACTGTTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
151 CACCGGCACC GCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTGGG CAGTTTCCCC AACGCTGGTG GGTGCGGGCG
301 GTTTCATCGG TTTTGTGTTC CCTTGTGCGC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

```

m624.pep
1  MIRYLLIACG CISLLLGIIG IFPLPLPTTP FVLLSAACWA KASPRFYRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLMIEW QFPQRWWVGA
101 VSSVFCSLVA IWMWRPES*

```

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACG CISLLLGIIG IFPLPLPTTP FVLLSAACWAKASPRFYRWLHRHRYFGPMV					
g624	MIRYLLIACG GISLLLGIIG IFPLPLPTTP FVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60

	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
g624	HNWEQNGAVPRKAKIFAISMITASCLIMFWHFPQXWWVGAVSSVFCSLVTIRMWHRPESX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```
a624.seq
1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCT TGCTGTTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCGG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTGG CAGTTTCCCC AACGCTGGTG GGTCCGGGCG
301 GTTTCATCGG TTTTGTGTT CCTTGTGCC ATATGGATGT GCGCAGGCGC
351 CGAATCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```
a624.pep
1  MIRYLLIACG CISLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRRHYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*
```

m624/a624 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRRHYFGPMV					
a624	MIRYLLIACGCISLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRRHYFGPMV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
a624	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```
a625.seq
1  ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGTCCTTG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGCGCG TAATTTTGCC
351 GTAA
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```
g625.seq
1  atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGTCCTTG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtcgTtcc CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGCGCG TGATTTTGCC
351 gTAA
```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```
g625.pep
1  MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPME ASAVPTASRA
```

1000

51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT  
101 KLNGMRKSNV QKAVILP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq  
1 ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT  
51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC  
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG  
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC  
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGG ATGTATTCTT  
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC  
301 AACTGAACG GGATGAGGAA GAGCAATGTC CAAAAGCGCG TAATTTTGCC  
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep  
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPmie ASAVPTASRA  
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT  
101 KLNGMRKSNV QKAVILP\*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
g625	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep  
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPmie ASAVPTASRA  
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT  
101 KLNGMRKSNV QKAVILP\*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
a625	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq  
1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG  
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTATCCTG ATTACATTGA  
101 CCGCCGTATC TATGGCAATC ACGCCCAAC AAGTCCGCGC AGGCAACGAA  
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTTCC TCGGCATCTT  
201 CATCACCATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG  
251 CGCTGGGCGG GGTGTATCG CTGTTTCAG ATACGGCAGG TCATCCGATT  
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA  
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GCGGGGCGGC GATGCCCAAG  
401 CCTTAATGAC GGGTCCCCTG TTTCATTcgc TGCTGGCGGT TTCTAtgggT  
451 tCGGTATTCA TGGGCGCACT GaccTACATc gCAACgcac cgaactTCAT